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New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 56; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0023975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bjorck LH, Rasmussen M;
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                                                                                                                                                                                AAY71038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyog
H. pylori secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/Aa1980.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/Aa1981.DAT:*
| SIDSI/gcgdata/hold-geneseqy-emb1/Aa1981.DAT:*
| SIDSI/gcgdata/hold-geneseqy-geneseqp-emb1/Aa1982.DAT:*
| SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1983.DAT:*
| SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1985.DAT:*
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| SIDSI/gcgdata/hold-geneseqy/geneseqp-emb1/Aa1989.DAT:*
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Streptococcus pyog
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
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/SIDSI/gcgdata/hold-geneseqy-embl/AA1997.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
                                                                                                        (without alignments)
273.300 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                      October 13, 2002, 03:04:37; Search time 11.3797 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                               28
                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
                                                                                                                                                             129
1 SDALEALADQTDALQSEEAAVVKADNAA
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Maximum Match 100%
Listing first 45 summaries
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AAY71045
AAW20445
AAW20638
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AAY71046
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AAY71042
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AAY71044

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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H. pylori ORF 09ce
Novel human diagno
E.coli alkaline ph
Chlamydia trachoma
C glutamicum prote
                                                                                                                        Drosophila melanog
Native RSP3 protei
Chlamydomonas prot
Tagged Chlamydomon
Tandem tagged RSP3
                                                        Peptide #11249 enc
Arabidopsis thalia
Arabidopsis thalia
                                                                                                   A rat calcium/calm
Murine p/CIP prote
Murine pCIP protei
                                                                                                                                                                                          Arabidopsis thalia
Arabidopsis thalia
Streptococcus pneu
                                                                                                                                                                     Arabidopsis thalia
Arabidopsis thalia
                             C glutamicum prote
Peptide #10862 enc
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Arabidopsis thalia
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Drosophila melanog
                                           Human brain expres
                                                                                Staphylococcus aur
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Pseudomonas aerugi
                                                                                                                                                                                    Human protein SEQ
pylori ORF
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                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes strain SF370 GRAB protein fragment #3.
                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                         AAM37212
AAG31518
AAG31517
                                                                               AAU34319
AAU37320
AAU36317
                                                                                                   AAY54580
AAW99481
AAW81029
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AAG61028
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AAY81672
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ABB65976
              AAW11567
AAY36771
AAG90301
ABB43356
AAM64267
                                           AAM77089
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AAW61234
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                                                                                                   502
1362
1447
1637
515
516
527
527
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572
2076
2186
476
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296
296
344
358
358
371
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Gaps

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Length 141; Indels

Score 129; DB 21; Pred. No. 7.6e-11; Mismatches 0;

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100.0%; 100.0%;

Query Match 100. Best Local Similarity 100. Matches 28; Conservative

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           The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus. Antibodies against GRAB are useful for purifying alpha2M from a sample. The present sequence is one of the repeat regions of GRAB protein from S. pyogenes strain S7370 corresponding to residues 92-119. This fragment is useful in vaccine composition.
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                                                                                                                                                                                                                                                                                Length 28;
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100.0%; Pred. No. 1.2e-11;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                Local Similarity
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141 AA

Sequence

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The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
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                                                                                                                                                                                                                        GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
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100.0%; Pred. No. 8.4e-11;
tive 0; Mismatches 0;
1 SDALEALADQTDALQSEEAAVVKADNAA 28
              1 SDALEALADQTDALQSEEAAVVKADNAA 28
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                                                                                                      AAY71044 standard; Protein; 155 AA.
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Best Local Similarity
Matches 28; Conserv
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Streptococcus pyogenes.
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                                                            02-NOV-1999;
                                                                                02-NOV-1998;
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                                        11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                            Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                           New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
                                                                                                              GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
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                                                                                         Streptococcus pyogenes strain SF370 GRAB protein fragment #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71041 standard; peptide; 159 AA.
                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 57-58; 67pp; English.
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                                                                      (first entry)
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                                                                                                                                                       Streptococcus pyogenes.
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nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 AA;
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                                                                    29-AUG-2000
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                                                AAY71041;
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immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain KTL3.

The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                       The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective
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/label= alpha2-macroglobulin_binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes strain SF370 mature GRAB protein.
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150..155
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/note= "repeat region"
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115..159
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 62-63; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71039 standard; Protein; 184 AA.
99WO-GB03631
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                                                                                                                                                                                      Bjorck LH, Rasmussen M;
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99WO-GB03631,
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                                 Region
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                                                                                                                                                                                              New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Length 184;
/note= "consensus sequence for gram-positive
surface cell wall anchored proteins"
160..184
/label= Membrane_spanning_region
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100.0%; Pred. No. 1e-10;
.ve 0; Mismatches 0;
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/label- alpha2M_binding_site
34..68
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/label- Mature_GRAB_protein
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'label= Signal_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71042 standard; Protein; 217 AA.
                                                                                                                                                                                                                                                                                                                                                    and useful in vaccine composition
                                                                                                                                                                                                                            Claim 5; Page 56; 67pp; English
                                                                                            99WO-GB03631
                                                                                                                98GB-0023975
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nes 28; Conservative
                                                                                                                                                        Rasmussen M;
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                                                                                                                                    (ACTI-) ACTINOVA LTD.
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                                                                                                                                                                                                                                                                                                                                                                         184 AA;
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                                                                                                               02-NOV-1998;
                                                                                            02-NOV-1999;
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus, Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a full-length GRAB protein from S. pyogenes strain SF370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,\cdot\,
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                                                                                                                                                                                                   for gram-positive
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                                                                                                                                                                                               /note= "consensus sequence for gram-
surface cell wall anchored proteins"
193..217
/label= Membrane_spanning_region
                                                                                                                                 /label - Cell_wall_spanning_region
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'label - Repeat_region_1
                                                                     /label- Repeat_region_2
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                                                                                                     .192
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                                  120..147
                                                                                                                                                                    183,.188
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nes 28; Conserv
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Gaps

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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain AP49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                              Length 271;
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                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded by GYG"
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Misc-difference 187
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95US-0487032.
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Matches 28; Conservative
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                                                                                                                                                                                 271 AA;
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                                                                                                                                                       composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis.
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                                                                                                                                         a protective immune response binding protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                     New alpha2M binding protein for generating to group A streptococcus and purifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                              Claim 5; Page 59-60; 67pp; English
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             98GB-0023975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                    Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bjorck LH, Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
                                        (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ACTI-) ACTINOVA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365572/31.
                                                                                              WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD00563
                                                                                                             N-PSDB; AAD00561
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           02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                       composition
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                                                                    Bjorck LH,

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acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coll hosts.

222 AA;

Sequence

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This sequence represents a H. pylori secreted or periplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as petential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (AFCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a H. pylori secreted or periplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORR of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 18; Length 192; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori secreted or periplasmic protein, 02ce10216orfl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 72; Page 1062; 1481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW20638 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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52.28;
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95US-0487032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASTR ) ASTRA AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORPs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least for treating or proteins are claimed, as are probes containing at least for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of the licobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acids and proteins - used to develop products for the detection, prevention and treatment of H. pylori
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Score 57; DB 18; Length 222;
Pred. No. 2.2;
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                                 Indels
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                                                                                                                                                                                                                                                                H. pylori ORF 09ce10413_35336707_f2_9 secreted protein.
                                                                                                                                                                                                                                                                                              Vaccine; probe; diagnostic; ORF; cell envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 19;
Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claims 27, 31; Page 201-202; 279pp; English.
Ouery Match

44.2%; Score 57; DB
Best Local Similarity 52.2%; Pred. No. 2.2;
Matches 12; Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                              secreted protein; cellular protein.
                                                                                                                                                                        AAY10994 standard; Protein; 412 AA.
                                                                               4 LEALADQTDALQSEEAAVVKADN 26
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52.2%;
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96US-0739150.
96US-0759739.
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                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 52.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-271811/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASTR ) ASTRA AB.
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                                                                                                                                                                                                                                                                                                                                                                         WO9818323-A1.
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06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections
                                                                                                                                                                                                     AAY10994;
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                                                                                                                                        RESULT 1
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alkaline phosphatase (BAP) that has higher activity and similar thermal stability compared with the corresponding wild-type E.coli BAP. In this mutein, one wild-type amino acid residue has been substituted (see features table). Optionally, at least one amino acid is inserted between residues 6 (Pro) and 7 (Val) of the wild-type enzyme. The modified enzyme is useful as an immunoassay label. Note: This sequence does not appear in the specification but has been derived by modifying an E.coli BAP sequence according to the numbering given in the sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a specifically claimed modified bacterial
                                                                                                                                                                                                                                                                                             Bacterial alkaline phosphatase; BAP; mutein; variant; inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Gln329 is replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified bacterial alkaline phosphatase enzymes · useful as immunoassay labels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boulain J, Cattolico L, Ducancel F, Menez A;
                                                                                                                                                                                                                                                E.coli alkaline phosphatase mutant Q329A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BOUL/) BOULAIN J.
(COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers Misc-difference 330
                                                                                                               AAW11567 standard; Protein; 450 AA.
581 AVIQLTPQTEAVRSEDAPVAPRDN 604
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                                                                                                                                                                                                    (first entry)
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Best Local Similarity 34.1
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-1997.
                                                                                                                                                                                                    20-OCT-1997
                                                                                                                                                                                                                                                                                                                      immunoassay.
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                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a dood supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating and disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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45.8%; Pred. No. 1.5e+02;
tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laim 20; SEQ ID No 60627; 103pp; English
                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #30259
                                                                                                                                                      ABG30268 standard; Protein; 1164 AA
                         ::|| :| || || || || || 49 IQALQEQIDALDSQEKVVSKWDN 71
  4 LEALADQTDALQSEEAAVVKADN 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-2001; 2001WO-US08631
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23-AUG-2000; 2000US-0649167
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Best Local Similarity
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N-PSDB; AAS94455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              40200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                              18-FEB-2002
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ä
                                     Gaps
                                   Indels 13;
   DB 18; Length 450;
                                                                                         :|:: || || || 294 NDSVPTLAOMTDKAIELLSKNEKGFFLOVEGASIDKADHAA 334
                                                                    1 SDALEALADQTDA------LQSEEAAVVKADNAA 28
                                  .;
8
Score 48.5; DB Pred. No. 80; 6; Mismatches
                                                                                                                                                                                            Š.
                                                                                                                                                                                            AAY36771 standard; Protein; 258
                                                                                                                                                                                                                                                             07-OCT-1999 (first entry)
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3 ALEALADQTDALQSEEAAVVKADN 26

Matches

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ABB43356 standard; Peptide; 73 AA.
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Ikeda M,
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                                                         (KYOW ) KYOWA HAKKO KOGYO KK.
                2000JP-0159162.
2000JP-0280988.
  99JP-0377484
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2000US-0608408
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                                                                                      Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Patent Office.
                                                                                                                              WPI; 2001-376931/40.
N-PSDB; AAH65520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 AA;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                             03-AUG-2000;
  16-DEC-1999;
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                 -APR-2000;
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                                                                                      Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                Claim 17;
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ABB43356
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                                                                                                                                                                                                                                                                                                                                                                                                             AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, and venerallymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                             Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 20; Length 258; Pred. No. 69;
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Chlamydia trachomatis cellular envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C glutamicum protein fragment SEQ ID NO: 4055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 668-669; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia trachomatis
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97FR-0016034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic acid synthesis.
                                                                                                   Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                             WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AA;
                                                                                                                                                                                                                                                                        (GEST ) GENSET
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                                                                                                                               W09928475-A2
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17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG90301;
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Query Match Matches

RESULT 16 AAG90303

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The present invention provides a number of nucleotide and protein arequences from the Coryneform bacterium Corynebacterium glutualcum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, tramins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe.
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Ochial K, Yokol H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 4055; 246pp + Sequence Listing;
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S, Hayashi M,
Ozaki A;
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Gaps

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Indels

7; 22;

Length 73;

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                       Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed probe encoded protein SEQ ID NO: 37395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                     DB
                                                                                                                                             2; Mismatches
                                                                                                                     Score 45.5;
Pred. No. 26;
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                                                                                                                                                                                      2 DALEALADQTDALQS----EEAAVVK 23
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2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                     35.3%;
48.1%;
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2000GB-0024263.
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                                                                                                                                                                                                                                                                 AAM77089 standard; Protein;
                                                                    the probes of the invention
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                             Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53
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Best Local Similarity
Matches 13; Conserv
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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04-OCT-2000;
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                                                                                              Sequence
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    8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain expressed single exon probe encoded protein SEQ ID NO: 36372.
                                                                                                                                           measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human: brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                      Claim 27; SEQ ID NO 35991; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                          Length 73;
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                                                                                                                                The invention relates to a single exon nucleic acid
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              DR;
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              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
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2000US-0608408.
2000US-0632366.
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              Hanzel DK,
                                       WPI; 2001-483447/52
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                                                                                                                                                                                                                                                                73 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157275-A2
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27-SEP-2000;
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              Penn SG,
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                                                                                   probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                       The present invention provides a number of single exon nucleic acid
Example 4; SEQ ID NO: 37395; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                             Length 73;
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990S-0139454
990S-0139455.
990S-0139456.
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99US-0134218.
99US-0134219.
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99US-0136392.
99US-0136782.
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99US-0138847.
99US-0139119.
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99US-0132484
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99US-0135124
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  termination sequence.
                          Arabidopsis thaliana.
                                                    EP1033405-A2
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10-JUN-1999;
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19-APR-1999;
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23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                          Peptide #11249 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta .
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                                                                                                                                                                  Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
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48.1%; Pred. No. 26;
iive 2; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
47 DILEQTAAQVDALQGHLQQMEQEALVK 73
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                                                             AAM37212 standard; Protein; 73
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2000US-0234687.
2000US-0234687.
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2000US-0207456.
2000US-0608408.
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                                                                                                                (first entry)
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 2.5e+02;
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990S-0154018.
990S-0154039.
990S-0155139.
990S-0155486.
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990S-0156596,
990S-0157117,
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990S-0158029,
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Best Local Similarity 61.9%;
Matches 13; Conservative
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26 - CCT - 1999;
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25-FEB	25-FEB-19 05-MAR-19	09-MAR	23-MAR 25-MAR	29-MAR	01-APR	OB-APR	16-APR	19-APR	21-APR	23-APR	23-APK	30-APR	30-APR	04 - MAY	-MAY	-MAY	06-MAY	07 - MAY	II-MAY	14 - MAY	14 - MAY	14-94	14 - MAY	IB-MAY	19-MAY	20-MAY	21-MAY	24 - MAY	25-MAY	27-MAY	28-MAY	NOC-TO	NOD-50	00 - 70	08-JUN	10-JUN	10-JUN	14-JUN	16-JUN	16-JUN	17-JUN	18-JUN	18-JUN	18-JUN	NOC-81	19-11V	18-JUN	18-JUN	18-JUN	18-JUN	18-JUN	18-JUN	21-JUN	22-JUN	NUD-67	24 - TIN	28 - TUN	29-JUN	30-JUN	01-JUL	01-JUL	02-JUL-19)
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990S - 014 9 08 5.
990S - 015 08 6.

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Bseudomonas aeruginosa and Enterococcus facefalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                      Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
Xu HH;
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                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5; DB 22;
Pred. No. 1.3e+03;
3; Mismatches 9;
                                                                                                                                                                                                            Example 3; Seq ID No 5815; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU37320 standard; Protein; 2186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 DALNQLATDETDAIDNVTNATTNAD 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DALEALA-DQTDALQSEEAAVVKAD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%;
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2000US-207727P.
2000US-242578P.
2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conservat
                                                                                                                   WPI; 2001-611495/70.
N-PSDB; AAS52178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2076 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200170955-A2.
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                          Haselbeck R,
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                                                                                        Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5; DB 21
Pred. No. 2.8e+02;
}; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU34319 standard; Protein; 2076 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
          990S - 0156458
990S - 0156458
990S - 0157753
990S - 0157753
990S - 0157822
990S - 0158222
990S - 0158232
990S - 0159293
990S - 0159293
990S - 0159330
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990S - 0159638
990S - 0159638
990S - 0159638
990S - 0160761
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990S-0161920.
990S-0161992.
990S-0161993.
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61.9%;
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99US-0161360
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Best Local Similarity
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                      05-0CT-1999;
06-0CT-1999;
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2-OCT-1999;
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5-OCT-1999;
                                                                                     07-0CT-1999;
08-0CT-1999;
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14-0CT-1999
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26-0CT-1999
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21-OCT-19
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AAU34319
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Carr GJ;

genes essential to

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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential case themselves and the encoded proteins. The prokaryotes used are been contained as a sequence in the identification of potential new targets of invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen to a wide variety of organisms. The present sequence is also useful to screen a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium/calmodulin dependent protein kinase; CaMK-VI; CaMK-IV; CaMK VI related peptide; CARR; neuronal plastitity; eplicpsy; kainate-induced seizure; selzure; central nervous system; hippocampus; acute brain insult; stroke; trauma; hypoxia; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A rat calcium/calmodulin dependent protein kinase designated CaMK-IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "residue thought to be crucial for activation of the kinase by phosphorylation"
                                                                                                                                                                                                                                                           New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                    Ohlsen KL, Zyskind JW, Wall D, Trawick JD,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "residue involved in ATP binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "putative catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 22;
Pred. No. 2.7e+02;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute brain insult; stroke; trauma; hypoxia; is
neurodegenerative disease; Alzheimer's disease
                                                                                                                                                                                                                                                                                                                             Example 3; Seq ID No 11910; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
52..324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY54580 standard; Protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.98;
    22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000 (first entry)
                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.9
Best Local Similarity 43.3
Matches 13; Conservative
                                                                                                                                                                                      WPI; 2001-611495/70.
N-PSDB; AASS4176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                    Haselbeck R,
                                                                                                                                           Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
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AAY54580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are convention is also useful for the identification of potential mew targets for antibiotic development. The antisense nucleic acids can also be used invention is also useful for the identification of potential mew targets for antibiotic development. The antisense nucleic acids can also be used to indentify proteins used in proliferation, to expresse proteins.

The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms this wipe.int/pub/published_pct_sequences.
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                                                                                                                    Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2186;
                                                                                                                                                                                                                                                    New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                               Zyskind JW, Wall D, Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa cellular proliferation protein #307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation protein; design,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45.5; DB 22;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                      Example 3; Seq ID No 12913; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.3%;
48.0%;
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2000US-207727P.
2000US-242578P.
2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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                                                                                                               Ohlsen KL,
                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 48.0 es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                                                                                                                                         Xu HH;
                                                                                                                                                                                 WPI; 2001-611495/70.
N-PSDB; AAS55179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200170955-A2.
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                               Haselbeck R,
Yamamoto RT,
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RESULT 25 AAU36317

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This sequence represents the amino acid sequence of the mouse p/CIP (p300/CBP/co-integrator-associated protein) polypeptide. The protein can regulate gene expression so are potentially useful therapeutically, e.g. aqainst (breast) cancer, Inflammatory disease (e.g. atherosclerosis)
                                                                    "there appears to be 20 amino acids missing
between these positions in the sequence given
in the specification"
                               between these positions in the sequence given
                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding p/\text{CIP} and NcoA-2 polypeptides - are used to identify agents that regulate gene expression, e.g. for treatment of cancer, inflammatory disease and osteoporosis
               /note= "there appears to be 20 amino acids missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIB1; amplified in breast cancer; cancer; steroid; receptor; coactivator; SCR; estrogen; ER; estrogen dependent transcription; breast cancer; lung cancer; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1402
/label- Potential_C_terminus
/note- "This position encoded by stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine pCIP protein (ortholog of human AIB1 protein).
                                                                                                                                                                                                                                                                                    Torchia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
                                             in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                    Glass CK, Rose DW, Rosenfield MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW81029 standard; Protein; 1447 AA.
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1053 QALESKQDVFQGQEAAVMMDQKAA 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Fig 1; 100pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.98;
                                                                                                                                                                                              98WO-US12263
                                                                                                                                                                                                                          97US-0049452
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                                                           Misc-difference 1044..1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA .:
                                                                           /note-
 Misc-difference 44..45
                                                                                                                                                                                                                                                                                                                  WPI; 1999-080883/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX26000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or osteoporosis.
                                                                                                                                    W09856806-A1
                                                                                                                                                                                              12-JUN-1998;
                                                                                                                                                                                                                          12-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9857982-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999
                                                                                                                                                                 17-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW81029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; p/CIP; p300/CBP/co-integrator-associated protein; gene expression;
breast cancer; inflammatory disease; atherosclerosis; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a calcium/calmodulin dependent protein kinase (CaMK-IV). The specification also describes another CaMK designated CaMK-IV). The specification also describes another CaMK campared CaMF or campared peptide, designated CAMF. The CAMF peptide is produced by alternative splicing of the CaMF-VI gene, and plays a role in kinase-mediated neuronal plasticity which is associated with epilepsy. A large part of CAMF (48 out of 55 amino acids) is highly homologous with the carboxy-terminus of human doublecortin. It is possible the calcium overload in a cell, triggered by kainate-induced seizures, leads to activation of CaMK-VI. This acts as a modulator of the kinase, e.g. by acting as a substrate or by irreversible binding to the activated kinase. The mammalian CAMF protein may be used for the treatment and/or prevention of seizures
                                                                                                                                                                                                                                                     Mammalian calcium/calmodulin dependent protein kinase related protein useful as a modulator of calcium/calmodulin dependent protein kinase activity, useful for treating seizures and damage to the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     portion may no again and or damage to the central nervous system, particularly the hippocampus. CARP peptides may also be used to treat acute brain insults (e.g. resulting from stroke, trauma, hypoxia, and ischemia), and neurodegenerative diseases (e.g. Alzheimer's disease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 2.9e+02;
3; Mismatches 4; Indels
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                                                                                                                                                                                              (MEDI-) DIV MEDICAL PHARMACOLOGY LEIDEN AMSTERDA
227..234
/note= "Ser/Thr kinase motif"
346..364
                                           /note= "regulatory domain"
                                                                                                                                                                                                                                                                                                                                Disclosure; Page 34-36; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW99481 standard; Protein; 1362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.9%;
                                                                                                                                   98EP-0202654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAAKAAADETMKLQSEE 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine p/CIP protein.
                                                                                                                                                                                                                          WPI; 2000-138770/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                    nervous system
                                                                                                                                   06-AUG-1998;
                                                                                                                                                                 06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-1999
                                                                         EP978562-A1
                                                                                                     09-FEB-2000
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   Domain
Domain
                               Domain
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Gaps

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Length 1362; 10; Indels

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N-PSDB; ABL04445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9820031-A1.
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                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW61907;
                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                     (SCR-I) family of nuclear receptor co-activators that interact with cestrogen receptors (ER) to enhance ER-dependent transcription.

The AIBI gene is amplified and over-expressed in certain cancers in particular breast cancer and steroid hormone responsive cancers.

The AIBI polypeptide can be used to identify compounds which inhibit ER-dependent transcription. Increased expression of the AIBI gene indicates aberrantly proliferating cells, thus detection of increased expression of the AIBI gene or an increase in the number of copies of the AIBI gene can be used to disgnose cancer or a predisposition towards developing cancer. Compounds which inhibit expression of AIBI or compounds which inhibit interaction of AIBI with steroid receptors or nuclear co-factors can be used for reducing the proliferation of cancer cells. This sequence is of the murline pcIP protein, mouse ortholog of AIBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                             New isolated steroid receptor co-activator, AIB1 - used to develop products for the diagnosis and treatment of steroid-responsive tumours, e.g. breast, lung, prostate or colon cancers or melanomas
                                                                                                                                                                                                                       The AIB1 protein is a member of the steroid receptor coactivator-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 34.9%; Score 45; DB 20; Length 1447; Local Similarity 41.7%; Pred. No. 9.8e+02; les 10; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 7818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                Disclosure; Page 39-42; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB60342 standard; Protein; 1637 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 EALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L1 PWD,
 98WO-US12689
                          97US-0049728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                    (USGO ) US GOVERNMENT
                                                                              Weltzer P, Trent JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                     WPI; 1999-080946/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEKE ) PE CORP NY.
                                                                                                                      N-PSDB; AAV99919
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 17-JUN-1998;
                          17-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB60342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the native RSP3 protein, a Chlamydomonas pf14 gene product. The gene can be tagged by using the method of invention of tagging genes, transcripts and proteins in cells in a single recombinational event. The method comprises producing a tagged gene by inserting a DNA sequence into an intron of a gene by selecting a DNA sequence having a 5, portion free of any nucleotide sequence selected from AAV43548 to AAV43551, a
                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tagged gene; tagged transcript; hybrid intron; protein tag; protein isolation; recombination; subcellular structure analysis; transcriptional regulation; viral infection; Chlamydomonas; pf14 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tagging genes, transcripts and proteins - using tag-creating DNA inserted into intron of gene to create 2 hybrid introns separated by new exon encoding protein tag
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                                                                                      Disclosure; SEQ ID NO 7818; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1637;
                                                                                                                                                                                                                                                                                                                                                                                                                    34.9%; Score 45; DB 22; Length 16
47.8%; Pred. No. 1.1e+03;
...mafrches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Native RSP3 protein (pf14 gene product).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 22; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LEALADQTDALQSEEAAVVKADN 26
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                                                                                                                                                                                                                                                                                                                                                                                                    1637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JARV/) JARVIK J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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runction of proteins. The products, methods and uses are particularly used for proteins that are unstable, are difficult to purify, or share epitopes with a number of other proteins. The methods overcome the inefficiency of epitope tagging caused by reading frame obstacles and orientation obstacles.

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Gaps

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Indels

Score 44.5; DB 19; Pred. No. 3.5e+02; 4; Mismatches 7;

Query Match 34.5%; Best Local Similarity 51.7%; Matches 15; Conservative

516 AA;

Sequence

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AAW70357 standard; Protein; 527 AA.

RESULT 32 AAW70357 (first entry)

14-DEC-1998

AAW70357;

Length 516;

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                                                     splice acceptor site in a known gene, sequence identical to a known splice donor site in a known gene, an open reading frame (ORF) 3N-1 nucleotides in length, the ORF encoding a known peptide tag recognisable by a known reaction characteristic of the known peptide tag and sequences selected form CAGG and TAGG. The DNA sequence is inserted into the intro within the gene to create a tagged gene, and the tagged gene is incubated within a cell so as to maintain intact or to introduce the tagged gene within the genome of the cell. The method is used for isolating proteins, RNA and genes, for analysis of subcellular structures, cellular responses and transcriptional regulation, for the study of viral infection and for
nucleotide sequence selected from AAV43552 to AAV43560 and nucleotide sequences identical to a known spilce branch site in a known gene, sequences identical in length to a known spacer region between splice branch and acceptor sites in a known gene, sequences identical to a known
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                  DB 19; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Target nucleotide; epitope; gene tagging; epitope tagging.
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                34.5%; Score 44.5; DB 19;
51.7%; Pred. No. 3.5e+02;
iive 4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                           368 ADAVEAAAAELTA-QAEEAANAKWEADKA 395
                                                                                                                                                                                                                                                                                                                          1 SDALEALADQTDALQSEEAAVVK--ADNA 27
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW70356 standard; Protein; 516 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0762106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydomonas protein RSP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-1998 (first entry)
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.7
Matches 15; Conservative
                                                                                                                                                                                                        diagnosis of disease
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                                                                                                                                                                                                                                     515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9826094-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW70356;
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The tagged chlamydomonas protein RSP3 is an example of a target nuclectide with an oligonucleotide encoding an epitope inserted. The epitope is encoded by the oligonucleotides nucleotide sequence independently of the reading frame. The epitope and methods disclosed can be used for the tagging of genes, transcripts and polypeptides. They can be used for e.g. discovering new genes, determining the size and abundance of proteins produced by newly discovered genes, tracking the movement of proteins within cell membranes, monitoring receptor binding and internalisation of exogenous proteins, identifying the components of function of proteins complexes, purifying proteins, discovering the function of proteins. The products, methods and uses are particularly used for proteins that are unstable, are difficult to purify, or share epitopes with a number of other proteins. The methods overcome the inefficiency of epitope tagging caused by reading frame obstacles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epitope tagging of genes, transcripts and polypeptides - using oligonuclectide comprising a nucleotide sequence encoding the epitope independently of the reading frame of the nucleotide
                                                 Target nucleotide; epitope; gene tagging; epitope tagging.
                                                                                                                       Location/Qualifiers
                Tagged Chlamydomonas protein RSP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2B; 46pp; English.
                                                                                                                                       147..157
/note= "Taq""
                                                                                                                                                                                                                                                                 97WO-US22472.
                                                                                                                                                                                                                                                                                                  96US-0762106.
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                                                                                                                                                                                                                                                                                                                                     JARV/) JARVIK J W.
                                                                                    Chlamydomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV33278.
                                                                                                                                                                                           WO9826094-A1.
                                                                                                                                                                                                                                                                 09-DEC-1997;
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                                                                                                                                                                                                                              18-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                       Jarvik JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                         Region
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The Chlamydomonas protein RSP3 is an example of a target nucleotide sequence into which is inserted an oligonucleotide encoding an epitope. The epitope is encoded by the oligonucleotides nucleotide sequence independently of the reading frame. The epitope and methods disclosed can be used for the tagging of genes, transcripts and polypeptides. They can be used for e.g. discovering new genes, determining the size and abundance of proteins produced by newly discovered genes, tracking the movement of proteins within cell membranes, monitoring receptor binding and internalisation of exogenus proteins, identifying the components of functional protein complexes, purifying proteins, discovering the

- using an

Epitope tagging of genes, transcripts and polypeptides · using oligonucleotide comprising a nucleotide sequence encoding the epitope independently of the reading frame of the nucleotide

WPI; 1998-348546/30.

N-PSDB; AAV33277

Disclosure; Fig 2A; 46pp; English.

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RESULT 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide tag recognisable by a known reaction characteristic of the known peptide tag and sequences selected form CAGG and TAGG. The DNA sequence is inserted into the intron within the gene to create a tagged gene, and the tagged gene is incubated within a cell so as to maintain intact or to introduce the tagged gene within the genome of the cell. The method is used for isolating proteins, RNA and genes, for analysis of subcellular structures, cellular responses and transcriptional regulation, for the study of viral infection and for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                   Tagged gene; tagged transcript; hybrid intron; protein tag; protein isolation; recombination; subcellular structure analysis; transcriptional regulation; viral infection; Chlamydomonas; pf14 gene.
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tagging genes, transcripts and proteins – using tag-creating DNA inserted into intron of gene to create 2 hybrid introns separated by new exon encoding protein tag
                                                                               3,
                                   Length 527;
                                                                               Indels
                                       DB 19;
                                       Score 44.5; DB 19;
Pred. No. 3.6e+02;
; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                 Tandem tagged RSP3 pf14 gene product) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 22-23; 66pp; English.
                                                                                                                                          :||:|| | : | |:||| | | | | | 380 ADAVEAAAAELTA-QAEEAANAKWEADKA 407
                                                                                                                     1 SDALEALADQTDALQSEEAAVVK--ADNA 27
                                                                                                                                                                                                                                                              AAW61908 standard; Protein; 552 AA
                                       34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US20150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       960S-0705404
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JARV/) JARVIK J W.
                                                        Local Similarity
nes 15; Conserv
527 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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  Seguence
                                     Query Match
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                                                            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                               3;
   Length 552;
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                                                               Indels
Score 44.5; DB 19;
Pred. No. 3.8e+02;
4; Mismatches 7;
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Pred. No.
                                                                                                                                                                    1 SDALEALADQTDALQSEEAAVVK--ADNA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #1068.
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2000US-0649167.
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Ouery Match 34.5
Best Local Similarity 51.7
Matches 15; Conservative
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N-PSDB; AAS65264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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23-AUG-2000;
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990S-0145087.
990S-0145089.
990S-0145192.
990S-0145145.
990S-014518.
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990S-0145276.
990S-0145913.
990S-0145918.
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99US-0147935.
99US-0148171.
99US-0148319.
          990S-0139492.
990S-0139454.
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990S-0139458.
990S-0139461.
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990S-0139763.
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99US-0142154.
99US-0142055.
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990S-0146386.
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99US-0147302
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99US-0144884
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05-AUG-1999
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                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
  Gaps
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 7; Indels
                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 75231.
Mismatches
                                                                                    AAG58293 standard; Protein; 274 AA.
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                   DALEALADOTDALQSEEAAVVK 23
                              8 DSLQLLQDEEDSAANEEGLVLR 29
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99US-0123180.
99US-0123548.
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990S-0128714.
990S-0129845.
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9905-0132485
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99US-0134941.
99US-0135124.
99US-0135353.
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99US-0136021.
99US-0136392.
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99US-0137502
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99US-0132407
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99US-0138847
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                                                                                                                           18-OCT-2000 (first entry)
 8; Conservative
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                                                                                                                                                                                                                                                                                                              23 - MAR - 1999;
25 - MAR - 1999;
25 - MAR - 1999;
01 - APR - 1999;
06 - APR - 1999;
16 - APR - 1999;
13 - APR - 1999;
23 - APR - 1999;
30 - APR - 1999;
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19 - MAY - 1999;
10 - JUN - 1999;
27 - MAY - 1999;
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06 - JUN - 1999;
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10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
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 Matches
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                                                                              AAG58293
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 79109.
                            AAG61028 standard; Protein; 274 AA
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990S-0125248.
990S-0126264.
990S-0126785.
990S-01207462.
990S-0120744.
990S-0130749.
990S-013049.
990S-013049.
990S-0130489.
990S-0131449.
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990S-0132486.
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990S - 0135722

990S - 0137222

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990S - 013724

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                                                                            (first entry)
                                                                                                                                                                            Arabidopsis thaliana
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05 - MAR - 1999

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01-JUN-1999;
03-JUN-1999;
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07-JUN-1999;
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14-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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   RESULT 36
                AAG61028
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            9905-0148684
9905-0149178
9905-0149175
9905-0149725
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9905-0149929
9905-0149902
9905-0149902
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990S-0151303.
990S-0151438.
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990S-0154039
990S-0154779
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990S-0156458
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99US-0151065.
99US-0151066.
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990S-0160981.
990S-0161404.
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99US-0160770.
99US-0160814.
99US-0160815.
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13-AUG-1999
113-AUG-1999
113-AUG-1999
117-AUG-1999
120-AUG-1999
121-AUG-1999
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124-AUG-1999
125-AUG-1999
126-AUG-1999
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127-AUG-1999
128-SEP-1999
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RR 22-70N-1999 9918-0134650
RR 22-70N-1999 9918-0134690
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20-AUG-1999;
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25-AUG-1999;
26-AUG-1999;
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29 - SEP - 19
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Arabidopsis thaliana protein fragment SEQ ID NO: 75230.
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21-JUN-1999;
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                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; cancer; neukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy .
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llarity 47.6%; Pred. No. 2e+02;
Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 3417-3418; 6221pp; English.
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                                                                                                                                                                        03-FEB-2000; 2000US-0560875.
20-JUN-2000; 2000US-0560875.
20-JUN-2000; 2000US-0590075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
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          Human protein SEQ ID NO 1174.
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es 10; Conserv
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                                                                                      Homo sapiens.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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990S-0128234.
990S-0128714.
990S-0129845.
99US-0130077.
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990S-0132048
990S-0132484
990S-0132485
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99US-0123548.
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                          termination sequence
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09-MAR-1999)
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99US-0151065.
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 22 - JUN - 1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 2.2e+02;
Mismatches 9; Indels
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39.1%;
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99US-0161992.
99US-0161993.
99US-0162142.
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Best Local Similarity 39.1
Matches 9; Conservative
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Arabidopsis thaliana

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99US-0123788.
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13-SEP-1999; 15-SEP-1999;

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WPI; 1998-272224/24
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Matches 11; Conserv
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                                           N-PSDB; AAV27419
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Pred. No. 2.2e+02;
5; Mismatches 9; Indels
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The present sequence represents a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein

can be useful in vaccines for inducing protective antibodies against

Streptococcus pneumoniae, for treatment or prevention of infection e.g.

pneumonia, otitis media or meningitis. Probes based on the nucleic acid

are used to detect Streptococcus infection (by usual hybridisation or

amplification methods), also for isolating Streptococcus genes or their

allelic variants. The protein can be used similarly to detect specific

antibodies in standard immunoasasys, especially for diagnosing or

monitoring infections. Antibodies which bind the protein are used to

detect corresponding antigans, to purify the protein and for passive

immunisation (optionally coupled to a toxin). Vaccines are administered,

e.g. by injection, orally or through the skin, typically at 0.01-1000
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                                                                                                                                                                                                                                                                            Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
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                                                                            Kunsch CA;
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                                                                            Hromockyj A, Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 87; 118pp; English.
(HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 ADQTDALQSEEAAVVKADNA 27
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Title: Perfect score:

Sequence:

protein

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Scoring table:

Minimum DB s Maximum DB s

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AL427196 CLONE BAO
AU180004 AU180004
BMC29212 IpSkn0005
AU17958 AU17963
AU1657981 SWOVL3CAN
AU17973 AU180137
BMS55271 AU180137
AU179259 AU179732
AU179269 AU179269
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BU144391 GOGGOB.Y
BU114733 BU114733
AU44840 T3 end of
BU101775 BU1011893
BU114733 BU114733
AU439757 T7 end of
BU101283 BU101893
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AG676392 ENTHHYTR
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BH161951 ENTRB12TR
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AU180092 AU180092
AL439268 T7 end of
AL439268 T7 end of
BJ139410 BJ119410
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
Bolotin-Tukuhara,M., Bon,E., Durnen,P., Casaregola,S.,
Malpertuy,A., Dujon,B., Durnen,P., Lepingle,A., Llorente,B.,
Baurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wincker, P., Artiguenave, F.
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Blandin, G., Ozier-Kalogeropoulos, O.,
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FEBS Lett. 487 (1), 91-94 (2000)
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BG44681
AL959039
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CNS0794Y
BJ001775
BJ0001775
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CNS07270
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COMMENDAL LIUE PALALMINELES.

COMMENDEL Frame+ p2n. model - DEV-xlh

CD=/cgn2_1/USPTQ_Spool/US09847539/runat_10102002_093106_5005/app_query.fasta_1.526

DB=SST -QFWT=fasted SUFFIN=xed.fr.st - MINMATCH=0.1 - LOOPEXT=0.

UNITS=bits -START=1 - END=-1 - MARRIX=blosum62 - TRANS=human40.cd1 - LIST-45

- DCCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=40 - MODE=LOCAL

- USTFMT=pct - NORM=xct - HERPSIZE=S00 - MINLEN - MAXELN=200000000

- USER-01509847539_eCGN 1_1_763_erunat_10102002_093106_5005 - NCPU-6 - ICPU-3

- NO_XLPXY - NO_MMAP - LARGEQUERY - NEC_SCORES=0 - WAIT - LONGLOG - DEV_TIMEOUT=120

- WARN_TIMEOUT=30 - THREADS=1 - XGAPDF=10 - XGAPDRT=0.5 - FGAPDP=6 - FGAPEXT=7
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1143.085 Million cell updates/sec
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                      GenCore version '5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                            nucleic search, using frame_plus_p2n model
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Lough the Gaston Cremicus, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: 2 rue Gaston Cremicus, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: 2 rue Gaston Cremicus, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - %06: 1 random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exvazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces hauverii, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxiatuus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Genomic exploration of the hemiascomycetous yeasts: 1. A set yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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/db_xref="taxon:5482"
/clone="BD0AA002F07"
/clone_lib="BD0AA"
/note="end : T7"
a 246 c 196 g 3
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689 bp mRNA linear EST 20-FEB-2001 L0-5660T3 Ice plant Lambda Uni-Zap XR expression library, 0 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L0-2660 5', BF480699.
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/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/db_xref="taxon:3544"
/clone_lib="loe plant Lambda Uni-Zap XR expression library
/ 0 hours NaCl treatment"
/ 1 hours NaCl treatment"
/dev_stage="Six week old"
/dev_stage="Six week old"
/note="Yeator: Lambda Uni-Zap XR, Bluescript SK-; Site_l:
ECORI: Site_2: Xho!"
110 +
                                                                                                                                                                                                                                        Gommon ice plant.
Mosembryanthemum crystallinum
Mosembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Caryophyllidae; Caryophyllidae; Caryophyllidae; Caryophyllidae; Mascaceae; Mesembryanthemum.
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
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Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, US
Tel: 775-784-1918
Fax: 775-784-1650
TCAGAAGCAGATGAAACACCAGAAGTG 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: Seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces ruxii, saccharomyces huyveringes bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces Riuyveriomyces thermoclolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSO738M 1061 bp DNA linear GSS 07-JUL-2001 clone BA0AB017F12 of library BA0AB from strain CLIB 210 of Kluyveromyces lactis, genomic survey sequence.
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                                                                                                                                418 -------CCAACCGAGGAGAAGGCTGCAGAGCCAGCCAAGGAAGCCGCAAAG 462
                                                                                                                                                                                                                                                                                                                                                      143 GluargGlnasnValasnThrLeuProThrThrGly-------GluGluSer 157
                                                                                                                                                                            116 AspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThrLysAsp--- 134
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76 GluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAsp 95
                                                                                                                                                                                                                                                                                                                                                                                    96 GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSer
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Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
                                           382 GAAGAAAGAAGCCCGAAGCTGAGGGAGCCGCAAAG-----
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FEBS Lett. 487 (1), 66-70 (2000)
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AUR80004 Medaka liver cDNA library (OLe) from HNI Oryzias latipes AUR80004 Medaka liver cDNA library (OLe) from HNI Oryzias latipes for choriogenin Hminor, complete cds, mRNA sequence.
AUI80004
AUI80004.1 GI:13428841
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 GAAGAAGCGGCAGAAGAGGCA-----GCAGCGGCAGAAGAAACCGATGCCACAGAAGCA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 AlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGlu
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Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
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Graduate School of Science, University of Tokyo
Hongo 7-31, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
                                                                                                                                                                                                                                                    1061
46
20
50
14
/organism="Kluyveromyces lactis"
/strain="CLIB 210"
/variety="lactis"
/db_xref="taxon:28985"
/clone="BAOAB017F12"
                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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126 GACTCGGAGGAAATTGAAGACAATTCCT 99
                                                                                                                            /clone_lib="BA0AB"
282 c 190 g
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Best Local Similarity:
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BM029212 475 bp mRNA linear EST 05-NOV-2001 IpSkn00051 Skin cDNA library Ictalurus punctatus cDNA 5', mRNA
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Ostariophysi; Siluriformes;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 475)
Marsil,A., Cao,D., Li,P., Ju,Z., Kocabas,A., Feng,J., Patterson,A.,
Mickett,K.D. and Liu,Z.
Transcriptome analysis of channel catfish (Ictalurus punctatus):
Initial analysis of gene expression and microsatellite-containing unpublished (2001)
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/dstref='taxon:8090"
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/clone_lib="Medaka liver cDNA library (OLe) from HNI"
/tisxue_type="adult"
/ 169 c 52 g 94 t
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This clone was isolated from Medaka liver cDNA library (OLe). Location/Qualifiers
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The Fish Molecular Genetics and Biotechnology Laboratory,
                                                                                                                                                                                                                                442
39
119
114
4
                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                   Gaps:
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112.00
45.67%
30.71%
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Best Local Similarity:
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Cell
                                                                                                                                    /organism="Ictalurus punctatus"
/db_xref="taxon:7998"
/clone_lib="Skin cDNA library"
/note="Organ: Skin; Vector: pSport1; Site_1: Not1; Site_2: Sal1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU179963 Medaka liver cDNA library (OLe) from HNI Oryzias latipes cDNA clone OLe17.07a similar to gb(AB025967† Oryzias latipes mRNA for choriogenin Hminor, complete cds, mRNA sequence.

AU179963.1 GI:13428800
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostel;
Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygil; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.

1 (bases 1 to 570)
Naruse, K., Mitani, H. and Tanaka, M.
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                                            AL 36849,
 Department of Fisheries and Allied Aguacultures
                                                                                                                                                                                                                                                                                           475
37
28
45
11
                            Auburn University
203 Swingle Hall, Auburn University, Auburn,
Tel: 334 844 4054
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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               and Molecular Blosciences
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Best Local Similarity:
Query Match:
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               AUTHORS
TITLE
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Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThrLysAspThrLys 136
                                                                                                                                                                                                                                 /clone_lib="Medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGAGGATTCTGAGGTTTTGAAGGGTACTGAGGCTGCTGAGGATTCTGAGGATGTTGAG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 GAGGATACTGAGGCTGATGAGGCTGCTGAGGTTTTGAAGGATACTGAGGCTGCTGAGGAT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TCTGAGGTTTTGAAGGATACTGAGGCTGCTGAGGATGCTGAG 156
                         Contact: Kiyoshi Naruse
Contact: Kiyoshi Naruse
Carduate School of Science, University of Tokyo
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4410
Fax: 81-3-5841-4410
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAla---SerSerAspAlaLeu
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 EST Project in University of Tokyo (2001)
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Indels:
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/organism="Oryzias latipes"
/strain="HNI"
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                                                                                                                                                                                                      /db_xref="taxon:8090"
                                                                                                                                                                                                                                                                              84 9
                                                                                                                                                                                                                   /clone="OLe17.07a"
                                                                                                                                                                                                                                                               /dev_stage="adult"
203 c 84 c
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A1057981
A1057981.1 GI:3331847
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112.00
45.678
30.718
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/note="Vector: lambda Unizap XR; Site_1: EcoR I; Site_2: Xho I; Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptease and oligo(dr) followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Br. S. Williams, email genome@smith.edu."
                                                                                    volvulus
Unpublished (1995)
Unpublished (1995)
Contact: Steven A. Williams
Molecular Parasitology
Smith Coilege Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 GCGGCGAAAACGTCAGAAACGAATGCTGCAGCGTCACAACAATCAGCCGCCACGTCTGCN 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCACCGCGCCACAAAGCGTCAGAGGCCGCCACTTCAGCACGAGATGCGGTGGCCTCA 313
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1 (bases 1 to 615)
Williams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J.
Genes expressed in infective third stage larvae of Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="SMOvL3CAN21G06"
/clone_lib="Onchocerca volvulus infective larva cDNA
(SAW94WL-OvL3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --------AATGCCAGGTCATCTGAAACAGCAGGGAACGGAGC 166
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38
18
48
35
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Matches:
Conservative:
Mismatches:

    615
/organism="Onchocerca volvulus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sierra Leone"
/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: pBluescript SK.
Location/Qualifiers
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AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
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Best Local Similarity:
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                                           DEFINITION
                                                                                                                                      ORGANISM
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                                                                          ACCESSION
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Medaka liver cDNA library (OLe) from HNI Oryzlas latipes cDNA clone OLe19.11e similar to gb|AB025967| Oryzlas latipes mRNA for choriogenin Hminor, complete cds, mRNA sequence.
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil; Neopterygil; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygil; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzinae; 1 to 344)
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                                                                                                                                                                                                                                                                                                                                                                        Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLE).
Location/Qualifiers
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                                                                                                                                                                                                                                   Naruse, K., Mitani, H. and Tanaka, M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
Contact: Klyoshi Naruse
Department of Blological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
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Matches:
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/dov_stage="adult"
a 132 c 41 g 74 t
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Globodera rostochiensis.

Globodera rostochiensis

Bukaryota; Metazoa Nematoda; Chromadorea; Tylenchida; Tylenchidae; Heteroderinae; Globodera.

Tylenchoidea: Heteroderidae; Heteroderinae; Globodera.

MCGATTER, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hiller, L., Kucabo, T., Theising, B., Bowers, Y., Globons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Site_2: EcoRI; The library was donated for sequencing Geert Smant from Wageningen University, Laboratory of Nematology, The Netherlands."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1810
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The Washington Univ. Nematode EST Project, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
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BM355271.1 GI:18089902
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AU180091 610 bp mRNA linear EST 21-MAR-2001 AU180091 Medaka liver cDNA library (OLe) from HNI Oryzias latipes CDNA clone OLe19.04e similar to pir|A48048| egg envelope protein wf winter flounder, mRNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
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/dev stage="adult"
185 c 106 g 141 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
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                                                             AspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer
                                                                                               GATACTGAGGCTGATGAGGCTGCTGAGGTTTTTGAAGGAT---ACTGAGGCT----GCT
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Naruse, K., Mitani, H. and Tanaka, M. Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
Contact: Kiyoshi Naruse
Contact: Kiyoshi Naruse
Coppartment of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Klyoshi Naruse
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4410
Email: naruse@blol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
                                                         SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla
                                                                                             442 ACTGAAGAGCCC-----TCAACAGACGAAGCATCTTACGGGTACTGAAGAGTCT
                                                                                                                                 122 AlaThrProIleAlaLeuAspValLysLysThrLysAspThrLysProValValLysLys
                                                                                                                                                                         493 TCAACA------GACAAAGCATCATCTACGGATACTGAAGAGTCTTCAACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 AlaileGluAspLysGluAlaThrThrAlaileGluAlaAla---SerSerAspAlaLeu
                                                                                                                                                                                                           142 GluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGluSerAsnPro 159
                                                                                                                                                                                                                                   /clone="OLE13.10d"
/clone_lib="Medaka liver cDNA library (OLE):
/tissue_type="liver"
/dev_stage="adult" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 517)
Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="HNI"
/db_xref="taxon:8090"
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34.82%
14.16%
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Best Local Similarity;
Query Match;
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JOURNAL
COMMENT
                   388
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AUTHORS
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EST 21-MAR-2001
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Oyozias latipes

Euvaryota: Hatipes

Euvaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Addianlchthyidae; Oryzlinae; Oryzlas.

1 (bases 1 to 453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU179269 Medaka liver CDNA library (OLe) from HNI Oryalas latipes CDNA clone OLe06.03e similar to gb|AB025967| Oryalas latipes for choriogenin Hminor, complete cds, mRNA sequence.
   198 GAGGCTGTTTAGGATTCTGAGGTTACTGAGGCTGATGAGGCTGCTTAGGATTCTGAGGAT 139
                                                                                               378 AATACTCATCTACTTCACAAGAGTGAAATGTTGATGGTGGAGTCTGAGGATTTTGAGATT 319
                                                                                                                                                                                                                                                                                                                                                               99 AlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrp 118
                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GluLysAlaAlaThrProIleAlaLeuAspValLysLysThrLysAspThrLysProVal 138
                                                                                                                                                                                                                                              258 GCTGCTTAGGATTCTGAGGATACTGAGGCTGCTGATCATTCTGATGTTTTGAAGGGTACT 199
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                                                                                                                                  63
                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biological Sciences Graduate School of Science, University of Tokyo Graduate School of Science, University of Tokyo Hongo 7-1, Bunkyo-ku, Tokyo 113-0033, Japan Tel: 81-3-5841-4410
Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
                                                                                                                                                                                                                                                                                                                                                                                  138 ACTGAGGCGCTGAGGATTCTGAGGTTTTGAAGGGTACTGAGGCTGCTGAGGATTCTGAG
                                                                                                                                  45 IleGluAspLysGluAlaThrThrAlaIleGluAlaAla---SerSerAspAlaLeuGlu
                                                                                                                                                                                                                                                                                     83 ------AspasnalaalaSeraspalaLeuGlualaLeualaaspGlnThrasp
                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GATGTTGAGGCT------GCTGAGGATTCTGAGGATTTTGAAGGATACTGAGGCTGCT
                                                          64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Naruse, K., Mitani, H. and Tanaka, M.
Medaka EST Project in University of Tokyo (2001)
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/organism="Oryzias latipes"
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/db_xref="taxon:8090"
/clone="OLe60.03e"
/clone="Ilb="Medaka liver cE
/tissue_type="liver"
/dev_stage="adult"
a 159 c 59 g 88 t
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Matches:
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Contact: Kiyoshi Naruse
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EST.
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109.50
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E 1 (bases 1 to 610)

S Narues, K., Mitani, H. and Tanaka, M. Medaka EST Project in University of Tokyo (2001)

L Onpublished (2001)

L Onpublished (2001)

Contact: Kiyoshi Naruse

Department of Biological Sciences

Graduate School of Science, University of Tokyo
Hongo 77-31, Bunkyo ku, Tokyo 113-0033, Japan

Tel: 81-3-5841-4443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU180168 Medaka liver cDNA library (OLe) from HNI Oryzias latipes cDNA clone OLe20.04g similar to pir|A48048| egg envelope protein wf
                                                                                                                                                   99 AlaLeuGinSerGiuGiuAlaGiuValValGinSerAspAsnAlaAlaSerAspAlaTrp 118
                                                                                                                                                                                                                             186 ACTGAGGCGGCTGAGGATTCTGAGGTTTTGAAGGGTACTGAGGCTGCTGAGGATTCTGAG 127
                                                                                                                                                                                                                                                                               119 GluLysAlaAlaThrProlleAlaLeuAspValLysLysThrLysAspThrLysProVal 138
366 TTGAAGGATACTGAGGCTGCTGAGGCTGCTGAGGCTTCTGAGGCTGCTGAGG 307
                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="HNI"
/db_xref="taxon:8090"
/clone="0.0420.04g"
/clone=lib="Medaka liver cDNA library (OLe) from HNI"
                                                        82
                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: naruse@blol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualiflers
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                                                      64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla---
                                                                                           306 GCTGCTTAGGATTCTGAGGATACTGAGGCTGCTGATCTTTTGATGTTTTGAAGGGTACT
                                                                                                                                83 ------AspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAsp
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/organism="Oryzias latipes"
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189 c 104 q
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Best Local Similarity:
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Query Match:
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AU177381
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1 (bases 1 to 715)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                       290 TCTGATGTTTTGAAGGGTACTGAGGCTGTTTAGGATTCTGAGGATACTGAGGCTGATGAG 231
                                                                                                                                                                                                                                                                                                                                                                                                 112 AsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLys 131
                                                                                                                                                                            389 ------TTGAAGGATACTGAGGCTGCTGAGGCTGCTGAGGCTGCTGTGT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
                                                                                                                                                         38 AspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAla
                                                                                                                                                                                                                                                                             77 AlaAlaValValLysAla------AspAsnAlaAlaSerAspAlaLeuGlu
                                                                                                                                                                                                                                                                                                                                                                   230 GCTGCTTAGGATTCTGAGGATACTGAGGCGGCTGAGGATTCTGAGGTTTTGAAGGGTACT
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@enes.nig.ac.jp.
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    Conservative:
               Mismatches:
Indels:
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/dev_stage="stage 25"
154 c 232 g 59 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Xenopus laevis"
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BJ064193.1 GI:17425031
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50.00%
31.06%
14.09%
 Percent Similarity:
Best Local Similarity:
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                      Query Match:
DB:
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Japanese medaka.

Japanese medaka.

Japanese medaka.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostei;
Actinopterygii; Percomorpha; Aberinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1 (bases 1 to 548)

Naruse, K., Mitani, H. and Tanaka, M.
Medaka EST Project in University of Tokyo (2001)

N. Unpublished (2001)

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Tel: 81-3-5841-4443
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/db_xref="taxon:8090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU177381 519 MRNA linear EST 21-MAR-20
AU177381 Sugano-Kawakami 5' end enriched cDNA library (OLA) from
HNI Oryzias latipes CDNA clone OLA30.05b similar to 9b|AB025967|
Oryzias latipes mRNA for choriogenin Hminor, complete cds, mRNA
                                                                                                                                                                                                                                                                                                                   331 CAGAAAAAGCCGAGGCAGCCGCTGCGGCACTGAAGAAGAAAGCGGAAGCGGCAGAAGCA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThr 132
                                                                                                                                                                                                                                                                    109 GAGCGGTTAGCGGCTCAGGAGCAGAAAAAGCAGGCTGAAGAAGCCGCAAAAACAGGCCGAG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AlaAlaSerAspAla-----LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
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                                                                                                                                                                                                                                                                                                                                                                                                                     65 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn
                                                                                                                                                                                                                   26 GluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAla---
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715
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43
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This clone was isolated from Sugano-Kawakami
library (OLa).
Location/Qualifiers
                                           Conservative:
Mismatches:
Indels:
  Length:
Matches:
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0.137
108.50
51.948
32.568
13.968
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GA_Ea0022N09f Gossyptum arboreum 7-10 dpa fiber library Gossyptum arboreum cDNA clone GA_Ea0022N09f, mRNA sequence.
/organism="Oryzias latipes"
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                                                                                                                                                                                                                                                                                                                                                                                               103 GluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
                                                                                                                                                                                                                                                                        24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln
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330 GCTGAGGATTCTGAGGTTTTGAAGGGTACTGAGGCTGCTGAGGATTCTGAGGATGTTGAG
                                                                                                                                                                                                                                                                                                                                                       270 GCTGCTGAGGATTCTGAGGTTTTGAAGGATACTGAGGCTGCTGAGGATTCTGAGGATGTT
                                                                                                                                                                                                                                                                                                                             44 AlaileGluAspLysGluAlaThrThrAlaileGluAlaAla---SerSerAspAlaLeu
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Indels:
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Matches:
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Seq primer: TAATACGACTACACTATAGGG
High quality sequence stop: 631.
Location/Qualifiers
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Gossypium arboreum
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107.00
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32.748
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Best Local Similarity:
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BG443972
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AUTHORS
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AU179899.1 GI:13428736
EST.
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                                                                                                                                                                                                                                                                                                 404
                                                                                                                                                                                                                 24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln 43
                                                                                                                                                                                                                                                                                                                             82
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Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
Fax: 81-3-5841-4443
Email: naruse@blol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
                                                                                                                                                                                                                                                                                       44 AlaileGluAspLysGluAlaThrThrAlaIleGluAlaAla---SerSerAspAlaLeu
                                                                                                                                                                                                                                                                                                                            GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla
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                                           others
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139
14
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Mismatches:
Indels:
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Matches:
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(OLa) from HNI"
/tissue_type="whole b
/dev_stage="adult"
a 189 c 81 g
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AU179899/c
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TITLE
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BG445649 881 bp mRNA linear EST 15-MAR-2001 GA_Ea0029A12f Gossypium arboreum 7-10 dpa fiber library Gossypium
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/db.tref="txxon:29729"
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/clone="GA_Ea0034C23r"
/clone="Ib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 GAGGITGCATCAAACTGCACTTCATGAGGAGAAACTGAAGAATCAGTGAAGGAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 -----GTTGAAGTTGAAACCAAGGAGGTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 CAAGAAGCTACAACAGATGAAGTAGTTGCCGAAGCTCCTGCAGCGGAAGCAGCTGCCGAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (93 GAGCCAAAG-----GAAGCGGAGCCTGCGGCGGTGGCAGTCGAGGAACCTGAAGCCTCG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 ValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeu 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AspValLysLysThrLysAspThrLysProVal-----ValLysLysGluGluArg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 AlaLeuArgAsnGluGluArgAlaIleAspGluLeuLys---LysGlnAlaIleGluAsp 47
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI" 150 c 230 g 206 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ArgilelleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         857
28
28
58
58
58
                             Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fmail: rwingClemson.edu
Total High Quality bases = 618
Seq primer: TAATACGACTACTATAGG
High quality sequence stop: 846.
1. .857
Corganism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-847-539A-6 (1-159) x BM360707 (1-857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 CAAACCGTTGAAACCAAAGAAACTACA 399
                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. coli"
of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.243
107.00
44.97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.17%
13.77%
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                 JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG445649
                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
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               /organsa...
/strain="AkA"
/cultiva="8400"
/db_xref="taxon:29729"
/clone="16—Ea0022N09f"
/clone=lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. col1"
/lab_host="E. col1"
/lab_host="E. col1"
/lab_tost="E. col1"
/lab_tost="E. col1"
/lab_tost="E. col1"
/lab_tost="E. col1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gossyptum arboreum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossyptum.
1 (bases II to 857)
Wing R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oo, DP mRNA linear EST 09-JAN-2002
arboreum cDNA clone GA_Ea0034C23r, mRNA sequence.
BM360707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 GAGGTTGCATCAGTTCAAACTGCACTTCATGAGGAGAAAACTGAAGAATCAGTGAAGGAT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 GAGACTCCTAAGGAAACAGTGCCAGAACCAGTTGCCGAGGAGATCAAGGAAACCACTGAA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 ValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeu 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AspValLysLysThrLysAspThrLysProVal------ValLysLysGluGluArg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 LysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAsp 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 GlnThrAspAlaLeuGlnSerGluGluAlaAlaValLySAlaAspAsnAlaAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 ------GTTGAAGTTGAAACCAAGGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ArgilelleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeu
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239
288
248
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Matches:
Conservative:
Mismatches:
Indels:
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107.00
44.978
26.178
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Best Local Similarity:
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Source
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KEYWORDS
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128 AspValLysLysThrLysAspThrLysProVal----
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                                                                                                                                                                                                                                                                                        Gossypium arboreum.
Gossypium arboreum
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107.00
44.978
26.178
13.778
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Best Local Similarity:
Query Match:
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                                                                                                                                     RESULT 20
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                                                                            SM Gossyplum arboreum.
SM Gossyplum arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

I (bases I to 881)
S Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
L Unpublished (2000)
Contact: Wing RA
Clemson University
I00 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:29729"
/clone="GA_Ea0029A12f"
/clone_11b="Gossypium arboreum 7-10 dpa fiber library"
/tlssue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GAGGTTGCATCAGTTCAAACTGCACTTCATGAGGAGAAAACTGAAGAATCAGTGAAGGAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GAGCCAAAG-----GAAGCGGAGCCTGCGGGGGGGGGCCAGCCTCGAAGCCTCG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGAAGTTGAAACCAAGGAGGTG 287
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237 g 205 t ' 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 AlaLeuArgAsnGluGluArgAlalleAspGluLeuLys---LysGlnAlalleGluAsp 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 LysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAsp 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ArgilelleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 GlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSer
arboreum cDNA clone GA_Ea0029A12f, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            881
28
28
28
58
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                             1. .81.
/organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence start: 10
High quality sequence stop: 715.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-847-539A-6 (1-159) x BG445649 (1-881)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host-"E. coll"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="8400"
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162 c 23
                                 BG445649.1 GI:13355301
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107.00
44.978
26.178
13.778
                                                                    Gossyplum arboreum,
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Best Local Similarity:
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DB:
                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
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                                                                                                                                                    REFERENCE
AUTHORS
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                                 VERSION
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossyplum.

I (bases 1 to 887)

Ning, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, J., Wood, T.C., Lealie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

IL Upublished (2000)

Contact: Wing RA

Clemson University

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Tel: 864 656 7288

Fax: 864 656 7288
                                                                                                                                                                                                                                                             BG444821 887 bp mRNA linear EST 15-MAR-2001 GA_Ea0025L07f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0025L07f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="8400"
/db_xref="taxon:29729"
/db_xref="dA_Ea0025L07f"
/clone_ilb="GA_Ea0025L07f"
/clone_ilb="GGSSSppium arboreum 7-10 dpa fiber library"
/close_type="Fibers isolated from bolls harvested 7-10
                                 82 GAGGTTGCATCATCAAACTGCACTTCATGAGGAAAACTGAAGAATCAGTGAAGGAT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ValLysLysGluGluArg 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI" 161 c 241 g 213 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 ArgilelleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysteu
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Matches:
Conservative:
Mismatches:
Indels:

    .887
    /organism="Gossypium arboreum"

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Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 664.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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                                                                                                       145 GlnAsnValAsnThrLeuProThrThr 153
                                                                                                                                           390 CAAACCGTTGAACCAAAGAAACTACA 416
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double-stranded cDNA.was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonuclectide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster.
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                                                                                                                                                                                                                                                                                            sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1: Rhabditidae; Peloderinae; Caenorhabditis.
1: (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ACACCTGCAGTTATTGAAGCCGAAGCTGCAGCCGAAGCTGAAAACACTGCTACAGATGCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 GCCGAAGCTGAAAACACTGCTACAGATGCA-----TTAGCTACACCTGCAGTTATT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 GAAGCCGAAGCTGTAGCCGAAGCTGAAACCATTGCTGCAGATGCATTATCTACACCTGCA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GGGGGTACTGATGCTGAACTTGCGGCTGAAGCTGAAACACTGCTACAGATGCATTAGCT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 ValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeu 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 TTAGCTACACCTGCAGTTATTGAAGCCGAAGCTGTAGCCGAAGCTGAAACCATTGCTGCA
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 07-JUN-2001
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Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabame
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A1959039 546 bp mRNA linear EST 07-JUN-2001
fd06g08.yl Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3730142 5' similar to contains element L1 repetitive element
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                                                           202 GAGCCAAAG-----GAAGCGGAGCCTGCGGCGGTGGCAGTCGAAGCTGGAAGCTCG 255
                                                                                                                                                                                                                                   108 ValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeu 127
                                                                                                                                   88 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluVal 107
                                                                                                                                                                                      ------GTTGAAGTTGAACCAAGGAGGTG 279
                                                                                                                                                                                                                                                                                                                                                                                            322 GAGACTCCTAAGGAAACAGTGCCAGAACCAGTTGCCGAGGAGATCAAGGAAACCACTGAA 381
                                                                                                                                                                                                                                                                                         280 GTAGAAGAACCAAAGGCTGTTACTGAG-------GAGCCAGTAGTAGAG
                                                                                                                                                                                                                                                                                                                                            128 AspValLysLysThrLysAspThrLysProVal-----ValLysLysGluGluArg
                                  GlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSer
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Zebrafish Washu MPIMG EST"
/sex="mixed"
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/db_xref="taxon:7955"
/clone="IMAGE:3730142"
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WashU Zebrafish EST Project 1998
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Location/Qualifiers
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Query Match:
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Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
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                                                                                                                                                            1. .620
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/clone="ykil83bil"
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elegans L1 stage"
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                                                                 Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                            A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i
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Matches:
Conservative:
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/dev_stage="Li"
150 c 141 g 129 t
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                                                                                                                                                                                                                                                      /sex="hermaphrodite"
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    AUTHORS
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Direct Submission

La Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
3 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces Kluyveromyces thermotolerans, Kluyveromyces lactis var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Varromya lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                       Pichla angusta.
Pichla angusta.
Pichla angusta
Eukaryota; Pascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichla.

1 (bases 1 to 947)
Blandin, G, Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, B.
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Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
Meloritugny, J., Dulon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potler, S.,
Saurin, W., Tekala, F., Toffano-Nloche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Wincker, J.
Win
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AL434840.1 GI:12218253
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BJ000182 BF01SSA CDNA Oryzias latipes CDNA clone MF01SSA012D06 5',
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Contact: Takeda Shin i Centact: Takeda Shin i Centact: Takeda Shin i Centact: To Genetic Resource Information National Institute of Genetics 1111 Yata. Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856

Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actihopterygii; Neopterygii; Teleostei; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                       ------AspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                             SerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProlleAlaLeuAspVal 129
                                                                                                                                                                                                                              192 TTGGAT---TCAGCAGATGACAGCCAAGACTCTACAGATGAGCCA---AGTCAAGAAACA 545
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/db_xref="taxon:8090"
/clone="MF01SSA012D06"
/clone_lib="MF01SSA cDNA"
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/tissue_type="whole embryo"
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Location/Qualifiers
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
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Modaka EST Project in Takeda's lab
Modaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
Ill Yatas Mishina, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                  AGCAGCAGAGAGAGAGAGAGCTG---GAAGAGAGACTCACTGGCA-----ACTGA 720
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/tissue_type="whole embryo"
/dox stage="segmentation stage 20
/dox 5193 g 118 t
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Mismatches:
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/strain="Hd-rR"
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/clone-"MF01SSA027A11"
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Modaka EST project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
National Institute of Genetics
Tel: 81-55-81-6856
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzilnae; Oryzias.
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160 GATGCTGGGACAAAAGAGCCAGCTGTTACAGAAGCAGGTGGAACAGCTGAACCTTCAGCT 219
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                                                220 GATTCTCACCTCAAATGTCTATGACGACAACTCT------GGGGACAACACC
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/tissue_type="whole embryo"
/dv_stage="segmentation stage 20
143 c 180 g 131 t
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/organism="Oryzias latipes"
/strain="Hd-rR"
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BJ011593.1 GI:17357315
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Alignment Scores:

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Granton Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Peteostei; Euteleostei; Meoteleostei; Actinopterygii; Peteostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianchthydae; Oryzlinae; Oryzlas.

RS Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H., Medaka EST Project in Takeda's lab Contact: Tadasus Shin-i Center For Genetic Resource Information

AL Unpublished (2001)

Contact: Tadasus Shin-i
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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T7 end of clone BD0AA007F08 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
AL439757
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Candida tropicalis
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycetlas;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 968)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
                                                                                                                                                                                                                                                                                                                                                                   260 GATTCATCTGACAGTGAAATGTCTATGATGACAACTCT------GAGGACAACAGC 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 TCTGACGATGAGTCCAAAGAAACATCTAAAGCTGCTGCAGAGGTCAAGACCACTGAGAAA 490
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                                                                                                                                                                                                                                                                                                                                                                                                        42 LysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  551 TTGGAT----TCAGCAGATGACAGCCAAGACTCTACAGATGAGCCA----AGTCAAGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnValAsnThr
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                                                                                                                                                                                                                                                                                                                                              22 GlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLys
                                                                                     0 - 25"
1 others
                                                                                                                                                          710
34
42
74
19
5
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                                                                                     /dev_stage="segmentation stage 20
149 c 186 g 137 t 1
                                                                                                                                                                         Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAla-
                                                                                                                                                          Length:
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                                                                                                                                                        0.277
105.50
44.978
20.128
13.588
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Best Local Similarity:
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                                                                                                    237
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KEYWORDS
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Direct Submission

L Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 seqref@genoscope.cns.fr - Web:

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
by contact of the sequence of this sequence and for the sequence of
                                                                                     Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Dulon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAsp 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 ThralalleGlualaalaSerSerAspalaLeuGlualaLeuAlaAspGlnThrAspAla 71
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Mismatches:
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Location/Qualifiers
1. .968
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FEBS Lett. 487 (1), 91-94 (2000)
20584726
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/clone_lib="BDGAA"
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46.75%
26.62%
13.58%
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LysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGlu 46
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Pred. No.:
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ORIGIN
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                                                                                                               62
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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/dec_stage="Five day old etiolated seedling"
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/lab_host="E. coli SoLR"
/lab_host="E. coli SoLR"
/site_l: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Roots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
                                                                                                                                                                                                                                                                                                            Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
i (bases 1 to 473)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                    BE405838 473 bp mRNA linear EST 21-JUL-2000 WHE0437_A10_A19ZS Wheat etiolated seedling root cDNA library Triticum aestivum cDNA clone WHE0437_A10_A19, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Andérson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 51055955773
Fax: 5105595818
Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 Asn ----- Alaala SerAspAla TrpGluLysAlaAla Thr Prolle Ala LeuAsp 128
                         149 CCAGATTTGTTGTCAGATTTCGGATGCATTCAGAAGCACTGGCATTAGAGTTAGAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Strategene SK primer. 
Location/Qualifiers
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24
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                                                                         129 ValLysLysThrLysAspThrLysProValValLysLysGlu 142
                                                                                                89 TCGGAACCAGAAAAGAATCGGCACCAGAAGTAGAAGCAGAA 48
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Mismatches:
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Best Local Similarity:
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No.:
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                                                                                                                                                RESULT 29
BE405838
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AJ395963 AKÉZ426 Gallus gallus cDNA clone 24ml7rl, mRNA sequence.
AJ395963
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.

1 (bases 1 to 755)
Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
Contact: Buerstedde JM
                                                                                                                                                                                                                                                                      242 GAGAAGAAAGAGGCTGACACTGTTGCTCAGGAAGAAGAAA-----GAGGCTGACACT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 LysAspThrLysProValValLysLysGluGluArgGlnAsnValAsnThrLGuProThr 152
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                                                                                                                                                                                              122 ACTGAAGTGGAGATGAAAGATGCTGAAGAAGCCAAAGTCACTGACCTGGACCTGGAGATG 181
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61
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Martinistr. 52, 2025! Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Quallflers
2 AAACCTGCCAAAGGGGGAAGGCCCTCAAGCTCTAAGAAAGGCAAAAAGGGGAAACAGGAG
                                                  47 AspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAla
                                                                                                                                                                                                                                                                                                                                          -----AspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsn
                                                                                                                                                                                                                                             81 ---LysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAla-------
                                                                                                                                              67 AspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal····
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="dkfz426"
/tissue_type="Bursa of
124 c 185 g 1
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/db_xref="taxon:9031"
/clone="24m17r1"
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48.15%
25.19%
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Best Local Similarity:
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Query Match:
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BJ006142
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/db_xref="taxon:3544"
/db_xref="taxon:3540"
/clone="ib="ib="fee plant Lambda Uni-Zap XR expression library
/ 0 hours NaCl treatment prescreened for removal of highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 22-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesembryanthemum crystallinum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 530)
Cushman, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM300555 530 bp mRNA linear EST 22-JAN-200 GAG053902_21480 Ice plant Lambda Unit-2ap XR expression library, 0 hours NaCl treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCA053H02 5,
                                                                                                                                                                                                                                                 196 ---AAAGAAAAGCAGCAAGAAGTTGAAGCATTAGTTCTGGAACTGAACAGCTGAAACAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 GAACAAGCCTCATATAAGCAACAGAGTGAGGCAGCACCAACAAGCAATCGCATCCTTAAAG 312
                                                                                                                                                                                                                                                                                                                                                                   95 AspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla 114
                                                                                                                                                                                                                                                                                                                                                                                                     313 GAGCAAGTCAGTGCTTTG-----GAAGCTGAGGCAGTGAAGACAAGGGAATCTCTA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                          115 SerAspAlaTrpGluLysAlaAlaThrProlleAlaLeuAspValLySLysThrLysAsp 134
                                                                                                                                                                                                                                                                                                  46
                                                                                       17 LeuThrAsnLeuLeuGlyAsnAlaProGluLysLeuAla-----LeuArgAsnGluGlu 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An expressed sequence tag database for the common ice plant,
                                                                                                                                                           35 ArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIle
                                                                                                                                                                                                                           55 GluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer
                                                                                                                                                                                                                                                                                                75 GluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAla
                                                                                                                                                                                          145 CAGAAACTAAATAGCGCCAAGAAGAAAGCAGACGATTCAAGCAGAAAAATG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 ThrLys ----- ProvalvalLysLysGluGluArgClnAsn 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesembryanthemum crystallinum Unpublished (1997)
Contact: Cushman JC
Coppartment of Blochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 530.
Location/Qualifiers
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                                                      US-09-847-539A-6 (1-159) x AJ395963
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Seg primer: T3 20mer
13.51%
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BM300555
   Query Match:
DB:
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AUTHORS
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BM300555
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BJ006142 MF01SSA CDNA Oryzias latipes CDNA clone MF01SSA089B12 5', BJ006142 MF01SSA089B12 5', BJ006142 MF015SA089B12 5', BJ006142
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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                                                                                                                                          SK-; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 LysProValVal------LysLysGluGluArgGlnAsnValAsnThrLeuProThr 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 ACCAAAGAAGCTGAGACCAAGAAAGAAGAAGTCCCAAAAGCAGCTGAAGCTGAACCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 GCAAAG------CCAACGAGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TTGACGAACGAGGGGGCG-------GCGCCGGCGCCGGGGAGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
abundant transcripts"
/tissue_type="leaf"
/dev_stage="six-week-old"
/note="Vector: Lambda Uni-Zap XR, Bluescript Scorif Site_2: XhoI" 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                530
117
44
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42
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 GCCGCTGCAGAAGAAGGTTGAGAGGACCAAACCC 404
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                         186
                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                   /sex="mixture of female and male"
/tissue_type="whole embryo"
dev_stage="segmentation stage 20
139 c 176 g 125 t
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
                                                                                                                                                                        /organism="Oryzias latipes"
 Medaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                      /clone_lib="MF01SSA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                     /db_xref="taxon:8090"
/clone="MF01SSA094C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-847-539A-6 (1-159) x BJ006464 (1-666)
                                                                                                                         Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                  176 g
                                                                                                                                                                                        /strain="Hd-rR"
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AZ676392
AZ676392.1 GI:11813538
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103.50
45.22%
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Best Local Similarity:
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Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
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                                                                          /gtrain="Hd-rR"
/db_xref="taxon:8090"
/clone="MF01SSA089B12"
/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage=""segmentation tage 20 -
a 125 c 162 g 110 t
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    /organism="Oryzias latipes"

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                Email: tshini@genes.nig.ac.jp.
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AZ676392 938 bp DNA linear GSS 14-DEC-2000
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390 TCTGACGATGAGTCCAAAGAAACATCTAAAGCTGCTGCAGGGGTCAAGACCACTGAGAAA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: klwan@pkrisc.cc.ukm.my
PCR PRimers
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/db.xref="taxon:5759"
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/note="Vector: PHOSI; Site_i: Bst i; Constructed at The
/note="Vector: PHOSI; Site_i: Bst i; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77.450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
712 Medical Center Dr., Rockville, MD 20850, USA
713 Medical Center Dr., Rockville, MD 20850, USA
719: 301 838 934 834
724: 301 938 9354
725: 301 938 9354
737 Medical Center Dr., Rockville, MD 20850, USA
726: 301 938 9354
737 Medical Center 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 GlualaalaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAla---
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Conservative:
Mismatches:
Indels:
                     Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 938)

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from HM:: IMSS sheared DNA library
Unpublished (2000)

Contact: Brendan J Loftus
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Class: shotgun
   Entamoeba histolytica
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103.00
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30.088
13.268
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Best Local Similarity:
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                                                                                  AUTHORS
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BG930118 537 bp mRNA linear EST 31-DEC-2001 etsHEST0539 EtH11 Eimeria tenella cDNA clone etsHk077 5', mRNA sequence.
                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="vector: Lambda ZaPII; Site_1: EcoRI; Site_2: XhoI; Sporozoites were excysted in vitro from E. tenella H ocoysts, purified by column chromatography and mRNA extracted using a FASTTRACK kit (Invitrogen). cDNA was synthesised and a Uni-ZAP XR library was constructed using cDNA synthesis kit. ZAP-cDNA synthesis kit. ZAP-cDNA synthesis kit. TaP-cDNA synthesis kit and labrary was amplified once through E. coli XLI-Blue
                                                                                                                                                                                                                                                                                                                      Ng.S.T., Jangi, M.S., Shirley, M.W., Tomley, F.M. and Wan, K.L. Comparative EST analyses provide insights into gene expression in two asexual developmental stages of Eimeria tenella Unpublished (2001)
Contact: Wan KL
Centre for Gene Analysis and Technology
Universiti Kebangsaan Malaysia
4360 UMB Bangi, Selangor DE, Malaysia
Tel: 6 03 8292997
Fax: 6 03 8293249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GAAGCAGCAGCAGAATCTGAGGAAGCAGCAGCAGCAGAAGACAGCGAGAGACTTGGC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GCAGCAGACGACGAGGAAGCNGCAGCAGACGACGAGGAAGCAGCAGCAGCAGCAGCAG
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42
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. 537
/ Organism="Eimeria tenella"
/ Strain="Houghton"
/ db_xref="taxon:5802"
/ clone="etsHk077"
/ clone="etsHk077"
/ da_ste="sporozoite"
/ lab_host="XL1-Blue MRF"
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Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                            0.488
102.50
44.44%
26.11%
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Best Local Similarity:
Query Match:
                                                                                               218
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9
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KEYWORDS
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S E1-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
Library for gene discovery and sequence-ready map construction unpublished (1999)

Other GSSs: RPCI93-EcoRI-6D15.TJ
Contact: Najib M. E1-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ648620 628 22-JUN-1999 RPCI93-ECORI -6D15.TV RPCI93-ECORI -6D15.TV RPCI93-ECORI -6D15, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: T?
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPC193-EcoRI"
/note="Vector: pBACe3.6; Site_l: Eco RI; Site_2: Eco RI;
Constructed for The Institute for Genomic Research by
Bohul Zhao in Pieter de Jong's Laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucel TREU927/4 GUTat 10.1 agarose embedded DNA was
                                                                                                                                                                                                            135
                                                                                                                                                                                                                                                                                      427
                                                                                                                                                                                                                                                                                                                  135 rLysProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThrThrGlyGl 155
                                                                                                                                                                                                                                                                                                                                      128 CGCTCACGGTCTCGGCGTGAAGACGAAGCTGAAGAAGAAAGCGGCAGCAGCAGCAGCTCT 187
                                                                                                                           85 AlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln------ThrAspAlaLeu 100
                                                                84
 ---AlaLeuAlaAspGln 68
                                                                                                                                                                                      GlnSerGluGluAlaGluValValGlnSerAspAsn-----------AlaAlaSer
                                                                                                                                                                                                                                                                      69 ThrAsp-----AlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn
                                                                                            CGCGACGAGGATGTTTCGGAAGCAGCAGCAGAGAGTCCAGGGGCCGCGCGAGCAGCAGCAAGA
                                                                                                                                                                                                                                                     116 AspalaTrpGluLysAlaAlaThrProIle-AlaLeuAspValLysLysThrLysAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927/4 GUTat 10.1"
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Trypanosoma bruce1
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AQ648620
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DEFINITION
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partially digested with a combination of Eco RI and Eco RI methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII segment). High molecular weight fragments were ligated in pBACe3.6 vector digested with Eco RI or Bam Hi. respectively. The average insert size is 141 Kb. Total coverage (both segments): > 90 X the haploid non-minichromosomal genome." I others
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201 GACGCAGCCCGTACAAAAGAGACGTTGCTCAGAAGGAGGTGGATCGTTTGAAATCCGGG 260
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Eukaryota: Fungl: Ascomycota; Saccharomycotina; Saccharomyceto
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

J. (bases 1 to 790)
Bolotin-Fukuhara,M. Toffano-Nloche,C., Artiguenave,F.,
Duchateau-Nguyen,G., Lemaire,M., Marmeisse,M., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ValAspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 CATCAGCAGAATCTCAATGAAGCGCGAGAACAGTAGAAAAACTTCAGAAAGAGTATGAC
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Integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
               GA_Ba0009A22f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ba0009A22f, mRNA sequence.
                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="8400"
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/clone_idA_Ea0009A22f"
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/clone_lib-"Fibers isolated from bolls harvested 7-10
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153 t 2 others
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Conservative:
Mismatches:
Indels:
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/strain="AKA"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
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201 g 15
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Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 504.
Location/Qualifiers
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BG440614.1 GI:13350265
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                                                                                                                                                                                                                                                                                                                         Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : Sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces ervazzii, Zygosaccharomyces rouxii, saiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenil var. hansenii, Pichia sonbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                         Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lephingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Hucker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
press. 11, 3-12 (2000)
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/strain="CLIB 210"
/variety="lactis"
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/clone="BA0AB008E01"
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                                                                                                                                                                                                                                                                                                                               CNSO6MOG 107-2001 1076 bp DNA linear GSS 17-JUN-2001 T3 end of clone AUOAA006A09 of library AUOAA from strain CBS 3082 of Saccharomyces kluyveri, genomic survey sequence.
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Souclet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souclet,J.L., Aigle,M., Artiguenave,F., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvegilse,C., Ozler Ralogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces kluyveri.
Saccharomyces kluyveri
Saccharomycetels; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 1076)
Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,
Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
                                                                                                                                                 281 GTAGAAGAACCAAAGGCTGTTACTGAGGAGCCAGTAGTAGAGGAGGACTCCTAAGGAAACA 340
                                                                               341 GTGCCAGAACCAGTTGCCGAGGAGTCAAGGAAACCACTGAACANACCGTTGAAACCAAA 400
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                                        121 AlaAlaThrProIleAlaLeuAspValLys------LysThrLys
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FEBS Lett. 487 (1), 56-60 (2000)
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/db_xref="taxon:4934"
/clone="AU0AA006A09"
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/note="end : T3"
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Pred. No.:
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CNS06MOG/c
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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REFERENCE
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TITLE
JOURNAL
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AUTHORS
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AUTHORS
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Entamoeba histolytica.

Entamoeba histolytica.

Entamoeba histolytica.

Entamoeba histolytica

Entamoeba histolytica

Entamoebidae; Entamoeba.

Entamoebidae; Entamoeba.

Entamoebidae; Entamoeba.

Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1: IMSS sheared DNA library (2001)

Contact: Brendan J Loftus

Department of Entaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica HM1: IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH161951 868 bp DNA linear GSS 24-SEP-2001
ENTRB12TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_llb="Entamoeba histolytica Sheared DNA"
/note="Vector: pH0S1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
                                                                                                                                                                                                                                           :::||| ||| |||
832 GATGCTGAAGAAACCGAAAGAAGAAGAAGAAGAAGATTCAAGG 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                772 GAAGCACTAGCGGAAGAAGCAGAAAGAGCTGAGGCTACCGAAGCGGCACTGGAAAGAGT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 AspGlnThrAspAlaLeuGlnSerGluGluAla-------GluValValGlnSer 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLys
                                                                                                                                                                                                                                                                                                                 43 Ginalaile---GluaspLysGlualaThrThralaileGlualaala----Ser
                                                                                                                                                                                                                                                                                                                                                                                                                    SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla
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     232
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                          Conservative:
Mismatches:
                                                                             Indels
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High quality sequence start: 13
High quality sequence stop: 861.
                                                                                                           Gaps:
                                                                                                                                                        US-09-847-539A-6 (1-159) x CNS06MOG (1-1076)
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1. .868
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BH161951.1 GI:15735389
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102.00
50.81%
28.23%
13.13%
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                                                  Similarity:
                             Percent Similarity:
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Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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97 BASE COUNT ORIGIN

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 0.907 101.50 50.82% 31.15% 13.06% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: Score:

US-09-847-539A-6 (1-159) x BH161951 (1-868)

610 GAAGCAAAAGCCAAAGAAGAAGCTGAAGCAAAAGCTAAAGAAGAAGAGCTGAAGCAAAAGCT 551 ò ద ò

53 AlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAla-----AspGlnThr

g

ò qq

70 AspAlaLeuGlnSerGluGluAla-----AlaValValLysAlaAspAsnAlaAla 86

87 SerAspAlaLeuGluAlaLeuAla---AspGlnThrAspAlaLeuGlnSerGluGluAla 105

δ

106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125 a ð q

146 AsnVal 147

ò q 256 GAAGTT 251

Search completed: October 13, 2002, 06:10:13 Job time : 1886.39 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 13, 2002, 03:46:02; Search time 68.8717 Seconds (without alignments) 399.383 Million cell updates/sec Run on:

Title: Perfect score:

US-09-847-539A-6 777 1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database

sp_invertebrate:*
sp_mammal:*
sp_mhtc:*
sp_organelle:*
sp_phage:* sp_unclassified:* sp_virus:*
sp_vertebrate:* sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:* sp_rodent:* sp_plant:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp_rvirus:*

sp_archeap:*

		Description	Q9x5c4 streptococc	Q9s6q4 streptococc	09s6g3 streptococc	Q9x5c6 streptococc	Q9x5c5 streptococc	Q55105 streptococc	Q54180 streptococc	Q53900 streptococc	Q91255 petromyzon	O9n4m4 caenorhabdi	Q9sck5 arabidopsis	Q53974 streptococc	Q935bl salmonella	Q54744 streptococc	Q9amm4 streptococc	Q54859 streptococc
SUMMARIES		ID	Q9X5C4	095664	095663	09x5c6	Q9X5C5	055105	054180	023300	091255	Q9N4M4	Q9SCK5	053974	Q935B1	054744	Q9AMM4	054859
		BB :	16	7	7	~	7	~	7	~	13	Ŋ	10	7	7	7	~	7
		Match Length DB	217	156	156	268	239	439	103	323	1110	7659	166	413	820	425	388	415
	% Query	Match	100.0	97.8	97.0	89.3	89.1	19.5	18.3	17.8	15.8	15.1	14.9	14.7	14.7	14.5	14.3	14.3
		Score	777	160	754	694	692	151.5	142	138.5	122.5	117	116	114.5	114.5	112.5	111	111
	Result	2	7	7	e	4	S	ø	7	8	6	10	11	12	13	14	15	16

Complete proteome; Signal; Transmembrane.

POTENTIAL.

Q95s18 drosophila Q85472 abiotrophia Q01891 enterococcu Q91853 arabidopsis Q54860 streptococc		09f1f5 enterococcu 09z4h8 enterococcu 024478 drosophila 09yfal drosophila bof810 etrochocca		Q9Ka19 streptococc Q9Ka19 enterococcu Q53975 streptococc Q47802 enterococcu Q9bhc4 leishmania	007290 streptococc 09413 enterococcu 004111 enterococcu 091cj9 staphylococ 09r169 staphylococ 099qr6 staphylococ
Q95518 O85472 Q01891 O Q9LK53 Q54860	-	Q9F1F5 Q9Z4H8 Q24478 Q9VFA1			Q07290 Q9KJJ3 Q04111 Q9LCJ9 Q9RL69 6 Q99QR6
619 5 2055 2 890 2 316 1 425 2	159 10 405 2 415 2 425 2	679 2 679 2 1096 5 1096 5	388 2 388 2 437 2 314 2 389 2		1822 2 576 2 891 2 1795 2 2478 2 2481 1
14.3 14.2 14.0 14.0	13.9 13.9 13.9	22.25.25.25.25.25.25.25.25.25.25.25.25.2	13.8 13.7 13.6 13.6	13.5 13.5 13.4 4.4	133.4 4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4
111 111 110 109 109	108 108 108 108	108 108 108	107 107 106.5 105.5 105.5	105 105 105 104.5	104.5 104 104 104 104 104
17 18 19 20 21	22 23 24 25	226 228 238 246	33 3 3 1 0 0 3 4 9 3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	33 33 39 39	4 4 4 4 4 4 4 4 5 4 5 4 5 4 8 8 8 8 8 8

ALIGNMENTS

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RX MEDILEFROM N.A.

RX MEDILEFLORD STORTON OF A TCC 700294 / SEROTYPE MI;

RX MEDILEFLORD STORTON OF A TCC 700294 / SEROTYPE MI;

RX MEDILEFLORD STORTON OF A TCC 700294 / SEROTYPE MI;

RA PRIME STATE OF A TCC 700294 / SEROTYPE MI;

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RA PRIME STATE OF A TCC 700294 / SEROTYPE MI;

RA PRIME STATE OF A TCC 700294 / SEROTYPE MI;

REMBL; AROUGST3; ARX34185.1;

REMBL; AROUGST3; ARX34185.1;

REMBL; AROUGST3; ARX34185.1;

REMBL; AROUGST3; GRAM POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC700294;
Rasmussen M., Muller H.P., Bjorck L.;
Rasmussen M., Muller H.P., Bjorck L.;
"Protein GRAB of Streptococcus pyogenes regulates proteolysis at the bacterial Surface by binding alpha2-macroglobulin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                            09X5C4;
09X5C4;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GRAB PRECURSOR (PROTEIN GRAB) (PROTEIN G-RELATED ALPHA 2M-BINDING
                                                                                      217 AA.
                                                                                               PRT;
                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                              GRAB OR SPY1357.
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                                                                                           99X5C4
RESULT 1
                                                         09X5C
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61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                  "Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin.";
J. Biol. Chem. 274:15336-15344(1999).
EMBL; AF124400; ASD26339-1; InterPro; IPR001899; Gram.Dos.anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDSPIEQPRIIPNGGTLINLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteolysis at the
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
  Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAAS--
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58.2%; Pred. No. 7.1e+38;
ive 0; Mismatches 0; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                    156 156
156 AA; 16587 MW; 19FAA98D0599D866 CRC64;
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0.1NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen M., Muller H.P., Bjorck L.;
"Protein GRAB of streptococcus pyogenes regulates bacterial surface by binding alpha2-macroglobulin. J. Blol. Chem. 274:15336-15344(1999).
EMBL. AF124403; AAD26342.1;
InterPro; IPR001899; Gram_pos_anchor.
PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.0%; Score 754; DB 2;
99.4%; Pred. No. 5e-42;
iive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AA
                                                                                                                                        STRAIN=AP1;
MEDLINE-99269061; PubMed=10336419;
Rasmussen M., Muller H.P., Bjorck L.;
"Protein GRAB of streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local Similarity 58.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=1314;
                                                      NCBI_TaxID-1314;
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NON_TER
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09X5C6
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                                                                                                                                                                                                                                                                                                        61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                                                                                                                                    94 ALEALADQTDALQSERAAVVKADNAASDALEALADQTDALQSERAEVVQSDNAASDAWEK 153
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                                                                                                                                                                                           1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                        34 VDSPIEQPRIIPHGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.
Bacterla; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                     Length
                                                                                                                                        Indels
34 217 GRAB.
217 Aa; 22836 MW; 79AA8C4FF5F3FA06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA; 16575 MW; 0C20967E2FB0D866 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                            Score 777; DB 16;
Pred. No. 2.3e-43;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 AATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 192
                                                                                                                                                                                                                                                                                                                                                                                                                    AATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
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                                                                            100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 156; Conservative
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Best Local Similarity
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NCBI_TaxID=1314;
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                                                                                                                                     datches 159;
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SEQUENCE
                            SEQUENCE
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Q9S6G3;
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Q9S6G4
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Streptococcus.
NCBI_TaxID=1306;
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                                                         121 LADQTDALQSEEAAVVKADNAASDTLEALADQTDALQSEEAAVVKADNAASDTLEALADQ 180
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                           121 LADQTDALQSEEASVVKADNAASDALEALADQTDALQSEEASVVKADNAASDALEALADQ 180
                                               TDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALD 128
                                                                                                                                                                                                                                                                                                    Rasmussen M., Muller H.P., Bjorck L.;
"Profedin GRAB of Streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin.";
J. Biol. Chem. 274:15336-15344(1999).
BMBL. AFI24402, AAD50341.1.;
InterPro: IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 TDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGE 155
         --SDALEALADO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                      Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                 89.1%; Score 692; DB 2; Length 239
64.0%; Pred. No. 8.4e-38;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                    239 239
239 AA; 24846 MW; 61AC4F6F863AF0F5 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MULTIPLE LIGAND-BINDING PROTEIN 1 PRECURSOR.
                                                                                                                                                                                         (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                           239 AA.
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STRAIN-KTL9;
MEDLINE-99269061; PubMed-10336419;
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Best Local Similarity 64.09
Matches 153; Conservative
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01-DEC-2001
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SEQUENCE
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        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                 Talay S.R., Grammel M.P., Chhatwal G.S.;
"Structure of a group C streptococcal protein that binds to fibrinogen, albumin and immunoglobulin G via overlapping modules.";
Bulchem J. 315.577-582(1996).
EMBL: X84989; CAA59349.1;
InterPro: IPR001399; Gram_pos_anchor.
InterPro: IPR001399; Gram_pos_anchor.
InterPro: IPR001399; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; I.
Pfam; PF00746; Gram_pos_anchor; I.
Pfam; PF00715; M; 6.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_I.
Signal; Transmembrane.
SIGNAL.

1 36 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 NELGNA-----PEKLALRNEERAIDELKK-------QAIEDKEATTAIEAA 57
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 SSDA------IEALADQT-----DALQSEEAAVVKAD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 --NAASDALEA-----LADQTDALQSEEAEVVQSDNAASDAWEKA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 DLEAARDAKKAVDAELAKLKAEAEALKEQLAKQAQEIEKLKESKEKAPEATQTPEKPEVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%; Score 151.5; DB 2; Length 439; 27.2%; Pred. No. 0.018; Live 25; Mismatches 46; Indels 103.
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BIOChem. J. 267:171-177(1990).
BHOChem. J. 267:171-177(1990).
EMBL; X53324; CAA37409.1; -.
STOTIENCE 103 AA; 10828 MW; E7AEE8DIC073423C CRC64;
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SEQUENCE 439 AA; 46527 MW; DOAEGC2A85D46B89 CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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MEDLINE-90226312; PubMed-2183792;
                                                   MEDLINE-96202013; PubMed-8615832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65; Conservative
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Matches 33; Conserv
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Matches 65; Conserv
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SEQUENCE FROM N.A. STRAIN=SEROTYPE C;
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DB 13; Length 1110;

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15.8%; Score 122.5;
29.4%; Pred. No. 3.8;
tive 28; Mismatches
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gattung S., Goela D., Broy M.;
"The sequence of C. elegans cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 EERQNVNTLPTTGEESN 158
                   Best Local Similarity 29.4%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 24.9%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                154 GEESNP 159
                                                                                                                                                                                                                                                                      818 EPEDEP 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
   Query Match
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09N4M4;
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                                                                                                                                                                                                                                                                                                                       Sjobring U.; "Isolation and molecular characterization of a novel albumin-binding problem from group G streptococci."; Infect. Immun. 60:3601-3608(1992). EMBL: M95520; AAA26847.1; -. HSSP; Q51911; IGAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQAIEDKEATTAIE---AASSD-----ALEALADQTDALQSEEAAVVKADNAASDALEAL 93
                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 ADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-95287814; Pubbad-7770000;
A Jacobs A.J., Kamholz J., Selzer M.E.;
Jacobs A.J., Kamholz J., Selzer M.E.;
The single lamprey neurofilament subunit (NF-180) lacks
The self lample lacks and is expressed selectively in
The self lacks man lacks and is expressed selectively in
The self lample lacks and is expressed selectively in
The self lacks lacks and is expressed selectively in
The self lacks and is expressed selectively in
The selective in the selective in the selective in the selective in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%; Score 138.5; DB 2; Length 323; 33.9%; Pred. No. 0.088; Live 25; Mismatches 36; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6903CFDCD5D373E CRC64;
                                                                                           Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF01468; GA; 2.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                       323 AA.
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                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sec 01-DEC-2001 (TrEMBLrel. 19, Last and ALBUMIN-BINDING PROTEIN (FRAGMENT)
                                                       PRT:
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34990 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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nes 39; Conservative
                                                       PRELIMINARY:
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323 AA;
                                                                                                                                                                      Streptococcus canis
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                                                                                                                                                                                                        Streptococcus.
NCBI_TaxID=1329;
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SEQUENCE
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Q53900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 DQTDALQSE-EAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTT 153
                                                                                                                                                                                                                                                    86 AS----DALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKK 141
                                                                                                                               Gaps
                                  Gaps
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                                                                                        38 DELKKQAIEDKEATTAIEAASSDALEALAD-QTDALQSEEAAVVKADNAA--SDALEALA 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6872 NAVKNVEDVVSKYQNQPQPLDVAKDDANKLKATVEQLTKLAESSDKIDPQVAKDIKDSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C. elegans cosmid ZK973.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; ARC06834; ARF40010.2; -.
Hypothetical protein.
SEQUENCE 7659 AA: 854006 WW; BBA95564D79B4FFI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 854.0 KDA PROTEIN.
8
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Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF01378; IgG_binding_B: 1.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Signal; Transmenbrane.
                                                                                                                                                                                                                  Local Similarity
hes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=90370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGEGSNP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 TGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pHCM2
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Q935B1;
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                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EAAVV---KADNAASDALEALADQTDALQSEEAEVVQS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ETTPAVQPEVAAVEESSSADAGEAAVVAPEKVENAATENAEAKVEAVAVAAPEKVEV--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 PNGGTLTNLLGNAP-----EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus dysgalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                Rigger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.9%; Score 116; DB 10; Length 166; 26.3%; Pred. No. 1.2; Live 25; Mismatches 62; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94259307; PubMed-7515368;
Jonsson H., Frykberg L., Rantamaeki L., Guss B.;
*MAG, a novel plasma protein receptor from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132964; CAB62458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3C612A36544F57FE CRC64;
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Last annotation update)
                                                                                                                                                                                (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 AA
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EMBL, 127798; AAA26921.1; -.
HSSP; P06654; 1PGX.
InterPro; IPR002989; GA.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF01468; GA; 1.
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                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 166 AA; 17373 MW;
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HYPOTHETICAL 17.4 KDA PROTEIN.
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      6985 QLAANTNTLKTATDSNN 7001
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                                                                                                                PRELIMINARY;
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01-DEC-2001
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Matches 4
                                                                                                             Q9SCK5
Q9SCK5;
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146 VDTIESESSKALAAAAARSEAAAABALNSKQAAAGSEANAKASENAAAASQQAAATSESNA 205
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                                                                                                                                                                                                                                                                          264 -- NGKTLKGETTTKAVDAETAEKAFKQYANENGVDGVWTYDDATKTFTVTEMVTEVPGDA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KAATPIALDVKKTKDT-----KPVVKKEERQNVNTLPT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 PTEPKKPEASIPLVPLTPATPIAKDDAKKDDTKKDDTKKEDAKKPEAKKEEAKKAATLPT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Bakers S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N, Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Gaps
                                                                                                                                                                                                                                    36 AIDELKKQAIED------KEATTAIE---AASSDALEALADQTDALQSEEAAVVK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 IDELKKQAIEDKEATTAIEAASSDAL-----EALADQTDALQSEEAAVVKADNA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
SMALVE 413:848-652(2001).
EMBL; AL513384; CAD09918.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.7%; Score 114.5; DB 2; Length 850; 31.0%; Pred. No. 9.4; ive 20; Mismatches 44; Indels 25
                                                                                                Length 413;
                                                                                                                                                                  Indels
CHAIN 35 413 POTENTIAL.
SEQUENCE 413 AA; 44004 MW; F04DC71044F9E50F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       850 AA; 90917 MW; 21271493A07A6563 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE PHAGE TAIL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enterica subsp. enterica serovar Typhi.
                                                                                                DB 2;
                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                        82 ADNAASDALEALADQTDALQSEEA-EVVQSDNAASDAWE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    850 AA.
                                                                                                14.7%; Score 114.5; [ 26.2%; Pred. No. 4.2;
                                                                                                                                                                  15; Mismatches
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Matches 40; Conservative
                                                                                                                                                                  Conservative
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Gaps

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93 LADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVN···· 148
                                                                                                                                                                                                                                                                                                      61 A---LEALADQTDALQSEEAAVVK-----ADNAASDALE----ALADQTDALQSE 103
                                                                                                                                                                                                                         54 IEAASSDALEALADQTDALQSEEAAVVK-------ADNAASDALE----A 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pedersen K., Hallbeck L., Arlinger J., Jahromi N., Erlandsson A.C.;
Protestigation of the potential for microbial contamination of deep
grantic aquifers during drilling using 16S rRNA gene sequencing and
culturing methods.";
FEMS Microbiol. Meth. 0:0-0(0).
EMBL: 869324; CAA49165.1; -.
InterPro; IPR001899; Gram_pos_anchor.
Printy: PR00746; Gram_pos_anchor.
PRINTS; PR00018; GPOSANCHOR.
Signal; Transmembrane.
                                                                                                                                                               6 EQPRIIPNGGTLTNLLGNAPE-----KLALRNEERAIDELKKQAIED-----KEATTA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TLTNLLGNA-------PEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                     56;
                                                                                                     14.3%; Score 111; DB 2; Length 388; larity 27.9%; Pred. No. 6.5; Conservative 24; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

14.3%; Score 111; DB 2; Length 415;
Best Local Similarity 29.0%; Pred. No. 7.1;
Matches 54; Conservative 18; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Podbielski A.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                        388 AA; 42177 MW; 189EBAB2A5F9AAAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
2696EB2457B76E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
               Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSNUCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Receptor; Transmembrane.
SEQUENCE 388 AA; 42177 MW; 189EBAB2A5F9AAAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 AA.
 InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                            149 ----TLPTTGEE-SNP 159
                                                                                                                                                                                                                                                                                                                                                          | | : | | | : | | 348 AQTKRQLPSTGEETINP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                     Ouery Match
Best Local Similarity
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Q54859;
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EMBL; AF324061; AAK11611.1;
206 RASKEAAAASQTAALQSEQVAAAHADSAKSEA-EKA------KKFADLLDVNNVLHKD 256
                                                                                                                                                                                                                                                                                                                                                     rung D.L., Hollingshead S.K.; "DNA sequencing and gene expression of the emm gene cluster in an M50 ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 TLTNLLGNAPE-----KLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQ 68
                                                                                                                                                                                                                                     Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Indels
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                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                 group A streptococcus strain virulent for mice."
Infect. Immun. 64:2193-2200(1996).
EMBL; US2008; AAB06612.1;
InterPro; IPR001189; Gram_pos_anchor.
Pfan; PR00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.5%; Score 112.5; I 30.4%; Pred, No. 5.8; ive 19; Mismatches
                                                                                                                                                               Created)
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                                                                                                                                  PRT;
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01,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 30.49 tes 49; Conservative
                                                                                                                               PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SEQUENCE FROM N.A.
                             143 ERQNVNTLP 151
                                                        257 --QNLADLP 263
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1314;
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                                                                                                                            054744
054744;
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MRP50.
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                                                                                                  RESULT 14
054744
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                                                                                                                                                                                                                                                                                RESULT 19
Q01891
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                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                        SSDALEALADQTDAL--QSEEAAVVKADNAASDALEALADQ----TDALQSEEAEVVQSDN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : || :: | | :| :| :| 343 RREE-RALKEERDRLTAEAEKQAAAEEAKIAAEEAKIAAEEALLAEAAAQKAAEEAKALK 401
275 ANAEKEKLQSQAAALEKQLEATKKELADLQAKLAATNQEKEKLEAEAKALKEQL-AKQVE 333
                          --TLPTTG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PIEOPRIIPNGGTLTNLLGNAPEKLALRNE-----ERAIDELKKQAIEDKEATTAIEAA 57
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP.
STRAIN-Y, CN BW SP.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AY060997; AAL28645...
SEQUENCE 619 AA, 68641 MW; 7DDCB26ADIAB9CEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Abiotrophia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 31.5%; Score 111; DB 5; Length 61 Similarity 31.5%; Pred. No. 11; Conservative 20; Mismatches 43; Indels
                       104 EAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXTRACELLULAR MATRIX BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                              Last sequence update)
Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                   Created)
                                                                                                                                                         PRT;
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MEDLINE-99081722; Pubmed-9864195;
                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, HL01392P.
                                                                                                                                                           PRELIMINARY;
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                                                                       EE-SNP 159
                                                                                              EETTNP 391
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Q95S18;
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Q95518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weidlich G., Wirth R., Galli D.;
"Sex pheromone plasmid pAD1-encoded surface exclusion protein Enterococcus faecalis.";
Mol. Gen. Genet. 233:161-168(1992).
EMBL: X62658; CAA44526.1;
PIR; S22452; S22452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 POTENTIAL.
390 SURFACE EXCLUSION PROTEIN SEA1.
98227 MW; DCEDC2F131F634FB CRC64;
                                                                                                                                       DB 2; Length 2055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 110; DB 2; Length 890; 29.1%; Pred. No. 19; tive 24; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         108 VQSDNAASDAWEKAATPI--ALDVKKTKDTKPVVKKEERQNVNTLPTT 153
                                                                                                                                                                                  Indels
                                                                                          215642 MW; 9699C11DDE93E2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SURFACE EXCLUSION PROTEIN SEA1 PRECURSOR.
                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001699; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Plasmid; Signal; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                            ; Pred. No. 43; 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : | : || : || ATDTQAVDDQQKVV-DQAQTDVNQQQAVVEE 171
                                                                                                                                       Score 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALDVKKTKDTKPVVKKEERQNVNTLPTTGEE 156
                                                                                                                                                                                                                               18 TNLLGNAPEKLALRNEERAIDE----LKKQAIED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92293110; PubMed-1603060;
Streptococcus defectivus.";
Infect. Immun. 67:50-56(1999).
EMBL, FAC67776; AAD03320.1; -.
NON TER 2055 2055
SEQUENCE 2055 AA; 215642 MW;
                                                                                                                                     14.3%;
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Best Local Similarity 29.1%
Matches 44; Conservative
                                                                                                                                                            Best Local Similarity 25.6%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus.
NCBI_TaxID=1351;
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46194 MW; CBE382280190D0CD CRC64;

425 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl, TAC and BAC clones.";
DNA Res. 7.217-221(2000).
EMBL; AP000375; BAB01411.1; -. SEQUENCE 316 AA; 35639 MW; 743F0166E7E93230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podbleiski A., Weber-Heynemann J., Cleary P.P.;
Immunoglobulin-binding FerA, Enn proteins and M proteins of group A Streptococct, evilved independently from a common ancestral protein.";
Med. Microbiol. Immunol. 183:33-42(1994).
EMBL: X73159; CAA51682.1;
InterPro: IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor: 1.
PRINTS; PR00015; GPOSANCHOR: 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                            -----AAVVKADNA----ASDALEALADQT-DALQSEEAEVVQSD 111
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            27 KLALRNEERAIDELKK-----QAIED-----KEATTAIEAASSDALEALADQTDALQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 AEEHARERLNVAVLESDFRSLAVVKESAAEELTETEALRACRDETLKTLEMSEREIEDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 NAASDAWEKA----ATPIALDVKK-------TKDTKPVVKKEERQN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                             Length 316;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, P1 CLONE:MJG19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                             DB 10;
            316 AA
                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 7;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                 14.0%; Score 109; D
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MEDLINE-20363099; Pubmed-10907853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-M2;
MEDLINE-94261050; PubMed-8202029;
                                                                                                                                                                                                                                                                                                                                                                                    48; Conservative
           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                        STRAIN-COLUMBIA;
                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                            Nakamura Y
                                                                                                                                                                                                                                                                                                                                                             Query Match
          Q9LK53
Q9LK53;
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Q54860;
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                                                                                                                                                                                                                                                                                                                                                           97 TDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKK-----EERQNVN-- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 LOSEEAAVVKADNAASDALEALADQTDALOSEEAEVVQSDNAASDAWEKAATPIALDVKK 131
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                      -----PEKLALRNEERAIDEL---KKOAIED 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 PNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADGTDA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN'1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DECLINED PROTEIN UDRING SEED DEVELOPMENT.
Fagopyrum esculentum (Common buckwheat).
Fagopyrum, viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Polygonaceae; Fagopyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN—CV. KITAYUKI; TISSUE—IMMATURE SEED;
FUJINO K., FURATSUKI; TISSUE—IMMATURE SEED;
FUJINO K., FURATSUKI H., Inada M., Shimono Y., Kikuta Y.;
FUJINO K., FURATSUKI H., Inada M., Shimono Y., Kikuta Y.;
"Expression and sequence analysis of cDRAs corresponding to genes differentially expressed during seed development of buckwheat (Fegopyrum esolentum Moench).";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, D87983; BAA21761.1; *.
SEOUENCE 159 AA; 16696 MW; 56862A34D99E607E CRC64;
                                                                                                                                                                                                                                             48 KEATTAIEAASSDALE----ALADQTDALQSEEA----AVVKADNAASDALE----ALADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 PN---TTTLQENEKSEVAQVEEVAAVEQVETPAVE--EAPAAVEEAPAAVEEAPA
                                                               903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
      Length 425;
                                                               Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FC-RECEPTOR PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                            59;
14.0%; Score 109; DB 2; 26.6%; Pred. No. 9.8; iive 27; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.9%; Score 108; DB Best Local Similarity 30.1%; Pred. No. 3.8; Matches 41; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                         EQPRIIPNGGTLTNLLGNA------
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111 VEEV----EEEKQQV 121
      Query Match
Best Local Similarity 26.6
Matches 53; Conservative
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DB 2; Length 415;
                                        25; Mismatches
                    11;
Score 108;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE-96396849; PubMed-8803952;
  13.9%;
27.5%;
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Query Match 13.9°
Best Local Similarity 27.5°
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Matches 53; Conserv
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                                                                                                                       STRAIN-M TYPE 76;
MEDLINE-89282846; PubMed-2660147;
Heath D.G., Cleary P.P.;
"Fc-receptor and M-protein genes of group A Streptococci are products of gene duplication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 IDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVN----- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 L-AKQAEELAKLKADKASG-----AQKP---DTKPGNKEVPTRPSQTRTNTNKAPMAQTK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 KEATTAIEAASSDALE----ALADQTDALQSEEA---AVVKADNAASDALE----ALADQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 EQPRIIPNGGTLTNLLGNA-------PEKLALRNEERAIDEL---KKQAIED 47
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
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"Different alleles of the fcrA/mrp gene of Streptococcus pyogenes encode M-related proteins exhibiting an identical immunoglobulin-binding pattern.";
Med. Microbiol. Immunol. 185:39-47(1996).
BEMBL: X78482: CAA55229.1;
InterPro: IPROU1899: Gram_pos_anchor.
Pfam: PF00746; Gram_pos_anchor.
PRINTS; PRO0015; GPOSANCHOR.
PRINTS; PRO0015; GROS_ANCHORING; UNKNOWN_1.
Receptor: Signal: Tansmembranchor.
SIGNAL.
1 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.9%; Score 108; DB 2; Length 405; 27.5%; Pred. No. 11; tive 25; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 41 POTENTIAL.
415 AA; 45256 MW; B4C67D8E230EE6DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            405 AA; 44299 MW; 9B73D62D515B41F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 86:4741-4745(1989).
EMBL; M22532; AAB95296.1; -.
InterPro; IPR001899; Gram_pos_anchor.
PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                  FC-RECEPTOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 AA.
                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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MEDLINE-96396849; PubMed-8803952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, 01-DEC-2001 (TrEMBLrel. 19, FC-GAMMA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             411
>405
405
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                                                                                                                                                                                                                                                                                                                       Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-1314;
                                                            NCBI_TaxID=1314;
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01-DEC-2001
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SEQUENCE
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P95813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 L-AKQAEELAKLKADKASG----AQKP---DTKPGNKEVPTRPSQTRTNTNKAPMAQTK 378
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       Gaps
                                                                                                                              6 EQPRIIPNGGTLTNLLGNA-----KKQAIED 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krebs B., Kaufhold A., Boyle M.D.P., Podbielski A.;

"Different alleles of the fcrA/mrp gene of Streptococcus pyogenes encode M-related proteins exhibiting an identical immunoglobulin-binding pattern.";

Med. Microbiol. Immunol. 185:39-47(1996).

EMBL: X78483, CASA55232.1;

InterPro: IPROUB899; Gram_pos_anchor.

Pfam: PF00746; Gram_pos_anchor.

PRINTS; RROUGLS; GPOSANCHOR.

PROSTITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                  48 KEATTAIEAASSDALE----ALADQTDALQSEEA---AVVKADNAASDALE----ALADQ
48;
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67; Indels
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425 AA; 46558 MW; 1DD73FB2CF76DAD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 03, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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Gaps

16;

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RC STRAIN-OREGON R;

MEDLINE-96154790; PubMed-8586650;

RA Whitfield W G.F., Chaplin M.A., Osgema K., Parry H., Glover D.M.;

RA Whitfield W G.F., Chaplin M.A., Osgema K., Parry H., Glover D.M.;

RA Whitfield W G.F., Chaplin M.A., Osgema K., Parry H., Glover D.M.;

RA The 190 kba centrosome-associated protein of Drosophila melanogaster contains four zinc finger motifs and binds to specific sites on projytene cromosomes.";

L. Call Sci. 108.3377-3387(1995).

R PyBase; Fagno000283; Can190.

R InterPro; IPR000288; ER, target.

BR InterPro; IPR000886; ER, target.

InterPro; IPR000865; ER, target.

BR Ffam; PF00651; BTB; 1.

BR Ffam; PF00651; BTB; 1.

BR RART; SM00225; BTB; 1.

BR ROSITE; PS00014; ER_TARGET; UNKNOWN_1.

BR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.

BR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.

BR PROSITE; PS000157; ZINC_FINGER_C2H2_2; 2.

KW DNA-binding; Metal-binding; Zinc_finger.

SEQUENCE 1096 AA; 121736 MW; 5CD5C54BD6B5D39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                           83 DNAASDALE----ALADQTDALQSEEAEVVQSDNAASDAWEKAATFIALDVKKTK---DTK 136
                                                                                                                                                                                 282 --TVKDAMEKAKQLVDSIQAVDSENAEIKKRNADALAKYQKAKA--ELDAKNAKIKAENE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQS-DNAASDAWE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVAELREAVTASEGEDDVHLEADNIRKELLDELIARAEK-POQEKDIVQSEENATTEALD 985
                                                                                                               26 EKLALRNEERAIDELKKQAIEDKEATTAIEAAS---SDALEALADQTDALQSEEAAVVKA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 IPNGGTLTNLLGNAPEKLALRNE-----ERAIDELKKQAIEDKEATTAIEAAS----SD 60
                Length 679;
                Query Match 13.9%; Score 108; DB 2; Length 67; Best Local Similarity 27.3%; Pred. No. 19; Matches 36; Conservative 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UJUN-2001 (TrEMBLrel. 17, Last annotation update)
CENTROSOME-ASSOCIATED ZINC FINGER PROTEIN.
CEN190 OR CP190 OR CG6384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                          PRT; 1096 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.9%; Score 108; DB 21.8%; Pred. No. 33; ive 42; Mismatches
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Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                               137 PVVKK-EERONV 147
                                                                                                                                                                                                                                                                  338 AIAKRNKERODL 349
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Q24478;
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                                                                                                                                                                                                                                                                             MEDLINE-20553452; PubMed-10998166;
De Boever B.H., Clewell D.B., Fraser C.M.;
De Boever Recalls conjugative plasmid pAM373: complete nucleotide sequence and genetic analyses of sex pheromone response.";
Mol. Microbiol. 37:1327-1341(2000).
EMBL; ARG002565; ARG40452.1;
EMBL; PR002565; ARG40452.1;
Pfam; PF00746; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor.
PROSTIE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 DNAASDALE---ALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTK---DTK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 EKLALRNEERAIDELKKQAIEDKEATTAIEAAS---SDALEALADQTDALQSEEAAVVKA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muscholl-Silberhorn A.B.;
"Cloning and expression of Asa373, a novel adhesin unrelated to the other sex pheromone plasmid-encoded aggregation substances of Enterococcus faecalis.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132039; CAB38226.1; ...
                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 108; DB 2; Length 655; 27.3%; Pred. No. 18; tive 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             655 AA; 72823 MW; 6A1E75FAF89C1893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 37 POTENTIAL.
679 AA; 75614 MW; 5E50706E9D92553A CRC64;
                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AGGRECATION SUBSTANCE PROTEIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AGGREGATION SUBSTANCE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1
Signal; Plasmid.
                                                                                                                                                         Enterococcus faecalis (Streptococcus faecalis).
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                                    655 AA
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                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 27.3% les 36; Conservative
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 PVVKK-EERQNV 147
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                             NCBI_TaxID-1351;
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                                                                                                                                                                          Plasmid pAM373
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                                                                                                                                                                                                             Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                         EP0041.
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0924HB;
                                  09F1F5
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Matches
RESULT 26
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Query Match
Best Local 3
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P95810
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                                                                                                                                                                                                                                                                    RX STAIN-BERKELEY;
RA Admanstdes F.E. Holt R.A., Evans C.A., Gocayne J.D.,
RA Admanstdes F.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admanstdes F.E., Scherer S.E., 11 P.M., Hoskins R.A., Galle R.E.,
RA Admanstdes S.E., Richards S.E., Ashburner M., Henderson S.N.,
Sutton G.G., Wortnan J.R., Yandlell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Andrews-Fenninchof C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Andrews-Fenninchof C., Baldwin D.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Burtis K.C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Burtis N.L., Harvy D., Heiman T.J., Herrandez J.R., Houck J.,
RA Hartis N.L., Harvy D., Heiman T.J., Herrandez J.R., Houck J.,
RA Hull M. Kalush F., Karpen G.H., Ke.Z., Kennigon J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke.Z., Kennigon J.A., Ketchum K.A.,
Alulu X., Mattei B., McIntosh T.C., Morison D.L.,
Merkulov G., Milshian N.V., Mobarry C., Morris D., Wolknefi A.,
Reinert K., Remington K.A., Holly W., Nelson D.L.,
Ra Balazdolo M., Pittann G.S., Pan S., Pollard J., Wolk R., Shie B.C., Siden-Klamos I., Simpson M., Strong K., Snell H.,
Rabardon M., Pittann G.S., Pan S., Pollard J., Wang X.,
Wallam S.H., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,
Wallam S.H., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
Rabence S. Bence Sequence of Drogophila melanogaster.",
R. Schence S. Shien S. 19512000.
                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Trācheata; Hexapoda; Insecta;
Pteryyota; Neoptera: Endopteryyota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS5007; BTB; 1.
PROSITE; PS5007; ETB; 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 1096 AA; 121678 MW; 5CD5C5492B948D39 CRC64;
                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                               Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000210; BTB_POZ.
InterPro; IPR000886; ER.target.
InterPro; IPR00082; Znf-C2H2.
Pfam; PF000961; BTB; 1.
SMART; SM00225; BTB; 1.
SMART; SM00255; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0000283; Cen190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2185-2195(2000).
EMBL; AE003708; AAF55159.1;
                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                PRELIMINARY;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                CEN190 PROTEIN.
CEN190 OR CG6384.
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                                Q9VFA1
RESULT 29
               09VFA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSDALE----ALADQTDALQSEEA---AVVKADNAASDALE----ALADQTDALQSEEAE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |: || :| || :| || :| 305
247 EKEKLQSQAAALEKQLEATKKELADLQAKLAATNQEKEKLEAEARALKEQL-AKQAEELA 305
                                                                                                                             61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQS-DNAASDAWE 119
                                                                                                                                                                                                                         107 VVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVN------TLPTTGEE- 156
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            11 IPNGGTLTNLLGNAPEKLALRNE-----ERAIDELKKQAIEDKEATTAIEAAS----SD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 KLKADKASG----AOKP---DTKPGNKEVPTRPSQTRTNTNKAPMAOTKROLPSTGEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 TLTNLLGNA------PEKLALRNEERAIDEL---KKQAIEDKEATTAIEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96396849; pubMed=8803952;

Krebs B., Kaufhold A., Boyle M.D.P., Podbielski A.;

"Different alleles of the fcrA/mrp gene of Streptococcus pyogenes

encode M-related proteins exhibiting an identical immunoglobulin-

binding pattern.";

binding pattern.";

EMBL; X78848; CAA552351; --

InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                  26;
  DB 5; Length 1096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; Score 107; DB 2; Length 384; 28.4%; Pred. No. 12; ive 23; Mismatches 60; Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                     986 RSVIDEDDLVPPTQVSTEQMEIDEPAAEKAAENNEDIRTADEKEA 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
8DF120B6AA30BAD5 CRC64;
                                                                                                                                                                                                                                                                                        120 KAAT-----PIALDVKKTKDTKPVVKKEERQNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Signal; Transmembrane.
SIGNAL
SIGNAL
SEQUENCE 384 Aa; 41708 MW; BDF120B6AA30BAD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 AA.
                                                    Mismatches
                           33,
  13.9%; Score 108;
                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSANCHOR.
                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TremBirel, 03, 01-DEC-2001 (TremBirel, 19, FCRAB PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03,
                           21,88;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
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053474;
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Best Local Similarity 28.5% Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                         Katerov V., Schalen C., Totolian A.A.; "Sequencing of genes within the vir regulon of Streptococcus pyogenes type MI5-en opacity factor-positive serotype with low opacity factor expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete incleotide sequence of the defective Sakai-VTI prophage carrying the shiga toxin 1 genes of the enterchemorrhagic Escherichia coli 0157:H7 defived from the Sakai outbreak."; Gene 258:127-139(2000).

EMBL; AP000400; BAB19560.1; -.

Interpreto; IPR000087; Collagen.

SEQUENCE 437 AA; 44183 MW; 408C870ACD31E14D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 LADLQAKLAATNQEKEKLEAEAKALKEQL-AKQAEELAKLKADKASG-----AQKP---D 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TLTNLLGNAPE-----KLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQ 68
                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%; Score 107; DB 2; Length 388; 30.4%; Pred. No. 12; Live 18; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 AA; 41957 MW; 2C7320D575A5C899 CRC64;
                              Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 VKKTKDTKPVVKKEERQNVN------TLPTTGEE-SNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 TKPGNKEVPTRPSQTRTNTNKAPMAQTKRQLPSTGEETTNP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Gen. Genet. 245:78-85(1994).

EMBL; S75411; AAB3326.1.1;

InterPro; PPROUS99; Gram_pos_anchor.

Pfam; PF00746; Gram_pos_anchor; 1.

PRINTS; PROU015; GPOSANCHOR.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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   Created)
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MEDLINE-20564182; PubMed-11111050;
                                                                                                                                                                                                                                                                                                                          MEDLINE-95147851; PubMed-7845360;
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01,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 30.49
Matches 49; Conservative
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                        01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
   (TrEMBLrel.
                                                                                                                                              Streptococcus pyogenes.
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NCBI_TaxID-83334;
                                                                                                                                                                                                                                  NCBI_TaxID=1314;
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                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                               FCRA15
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Q9EYE8
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Length 437;

DB 2;

Score 106.5;

13.78;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ebel F., Delbel C., Kresse A.U., Guzman C.A., Chakraborty T.; 
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Infect. Immun. 64:4472-4479(1996).
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"Characterization of two virulence proteins secreted by rabbit enteropathogenic Escherichia coll, EspA and EspB, whose maximal expression is sensitive to host body temperature.";
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MEDLINE-99141579; PubMed-9987106;
Nougayrede J.P., Marches O., Boury M., Mainil J., Charlier G., Pohl P., De Rycke J., Milon A., Oswald E.;
"The long-term cytoskeletal rearrangement induced by rabbit enteropathogenic Escherichia coli is Esp dependent but intimin "Aanendent.";
                                    67; Indels
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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MEDLINE-97427930; PubMed-9284118;
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300 L-AKQAEELAKLKADKASG-----AQKP---DTKPGNKEVPTRPSQTRTNTNKASMAQTK 350
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Analysis of genes encoding two unique type IIa immunoglobulin G-
binding proteins expressed by a single group A streptococcal
isolate.";
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5989493B3D4AD5EA CRC64;
        389 AA; 42424 MW; 68F2EC0FCF15C5EC CRC64;
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                                                                                    13.6%; Score 105.5; DB 2; ilarity 27.4%; Pred. No. 15; Conservative 26; Mismatches 68;
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EMBL; X72932; CAA51436.1; -.
InterPro: IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSANCHOR:
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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FCRA64/14 PROTEIN PRECURSOR.
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Best Local Similarity 27.5%
Matches 53; Conservative
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Best Local Similarity
Matches 54; Conserv
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"Complete Nucleotide Sequence and Analysis of the Locus of Enterocyte
Effacement from Rabbit Diarrheagenic Escherichia coli RDEC-1.";
Effacement from Rabbit Diarrheagenic Escherichia coli RDEC-1.";
EMEL: X99670; CAA67984.1;
EMBL: X99670; CAA67984.1;
EMBL: APO59113; AAC64708.1;
EMBL: AFO54121; AAC6280.1;
EMBL: AFO4421: AAC6280.1;
EMBL: AF144009; AAD34584.1;
EMBL: AF144009; AAD34583.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21153569; PubMed=11254564;
Zhu C., Agin T.S., Elliott S.J., Johnson L.A., Thate T.E., Kaper J.B.,
Boedeker E.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 GGAISSVLG-----ILGSFAAINSATKGASDIAQKTASTSSKAIDAASDTATKTLTKA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 TESVADAVEDASSVMQQAMTTATRAASRTSDVADDIADSAQRASQLAENAADAAQKASRA 212
                                                                                                                                                                                                                                                                                                                        MEDLINE-98254123; PubMed-9593291; Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K., Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.; The complete sequence of the locus of enterocyte effacement (LEE) from enteropathogent Escherichia coli E2348/69."; Mol. Microbiol. 28:1-4(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF007557; AAD01409.1; -
InterPro: IPR01999; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor.
PRINTS; PR00015; GPOSANCHOR.
PRINTS; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                          Krejany E.O.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.6%; Score 105.5; 28.7%; Pred. No. 12; ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                STRAIN-E65/56, 84/110-1, AND 83/39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 28.79 nes 45; Conservative
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[7]
SEQUENCE FROM N.A.
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Q47802
ID Q4780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus dysgalactiae.
Bacterla; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                 Enterococcus faecium (Streptococcus faecium).
Bacteria: Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jonsson H. Mueller H.-P.:
The type-III FC receptor from Streptococcus dysgalactiae is also
alpha 2-macroglobulin receptor ";
Eur. J. Blochem. 220:819-826(1994).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBIN G BINDING PROTEIN MIG PRECURSOR (IGG BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 105; DB 2; Length 524;
; Pred. No. 22;
31; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Teng F., Murray B.E., Weinstock G.M.;

"Characterization of an enterococcal secreted antigen.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL: AF167575; AAF87092.1;

EMBL: AF212196; AAF86217.1;
                                                                                                                                                                                                                                                                                                                                                                                                                an enterococcal secreted antigen."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C40.UPW; -. InterPro; IPR000064; NLPC_P60. InterPro; IPR000064; NLPC_P60. Ffam; PF00877; NLPC_P60; 1. SEQUENCE 524 AA; 55494 MW; E7BEIA611FAD9569 CRC64;
                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                      524 AA
                                                                                                                                                                                                                                                                                                                                                                                          Teng F., Murray B.E., Weinstock G.M.; "Characterization of an enterococcal s
Submitted (JUL-1999) to the EMBL/GenBa
                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%;
23.6%;
                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
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Matches 33; Conservative
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                                                                                                    PRELIMINARY;
                                                                                                                                                                                                         SECRETED ANTIGEN SAGA.
351 RELPSTGEETTNP 363
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1352;
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Q53975
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SUMILARITY).

SIMILARITY:

SIMILARITY:

THE RECION OF THE MEMBRANE PROTEIN. CELL WALL (BY SIMILARITY).

THE RECION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER STREPTOCOCCAL TYPE-III FOR RECEPTORS.

THE RECION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER STREPTOCOCCAL TYPE-III FOR RECEPTORS.

REMBL: 229666, CAR82764.1; -.

REMBL: 22966, CAR82764.1; -.

REMBL: 229666, CAR82764.1; -.

REMBL: 22966, CAR82764.1; -.

REMBL: 22966, CAR82764.1; -.

REMBL: 229666, CAR82764.1; -.

REMBL: 229674, CAR82764, CAR82764, CAR82764, CAR82764, CAR82764, CAR82764, CAR
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2-5.
6 x 3 AA REPEATS OF (DEVP]-(DE)-(AT)-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 IDAPELTPALTTYKLIVKGNTFS---GETTTKAV--DAETAEKAFKQYANENGVYGEWSY 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 OYANENGVDGVWTYDDATKTFTVTEMVTEVPGDAPTEPEKPEASIPLVPLTPATPIAKDD 593
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                                  Vasi J., Svensson J., Frick I.M., Mueller H.-P.,
"Five homologous repeats of the protein G-related protein MIG
cooperate in binding to goat immunoglobulin G.",
Infect. Immun. 67:413-416(1999).
-1- FUNCTION: BINDS TO THE CONSTANT FC RECION OF IGG WITH HIGH
AFFINITY. N-TERMINUS MEDIATES BINDING TO PLASMA PROTEINASE
INHIBITOR ALPHA 2-MACROGLOBULIN AFTER COMPLEX FORMATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNOGLOBIN G BINDING PROTEIN MIG.
ALPHA 2-MACROGLOBULIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (BY SIMILARITY).
MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
Z X 24 AA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-2.
5 X 70 AA TANDEM REPEATS
(IGG CONSTANT REGION-BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%; Score 105; DB 2; Length 66.
23.9%; Pred. No. 29;
:ive 21; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 KKTKDTKPV------VKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4A41CEEF7977862A CRC64;
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2-2.
2-3.
MEDLINE=99081771; Pubmed=9864244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 VVQSDNAASDAW------
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STRAIN-FRIEDLIN;
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SEQUENCE
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MEDLINE-96032304; PubMed-7559345;
PHJimoto S., Tomita H., Wakamatsu E., Tanimoto K., Ike Y.;
*Physical mapping of the conjugative bacteriocin plasmid pPD1 of
Enterococcus faecalis and identification of the determinant related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of a region of Enterococcus faecalis plasmid pPD1 encoding pheromone inhibitor (ipd), pheromone sensitivity (trac), and pheromone shutdown (traB) genes.";
J. Bacteriol. 177:5567-5573(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQTD-ALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPI 125
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-97074879; PubMed-8917306;
Hirt H., Wirth R., Muscholl A.;
"Comparative analysis of 18 sex pheromone plasmids from Enterococcus
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NCBI_TaxID=5664;
                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 OPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALA
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MEDLINE-96032393; PubMed-7559344;
Nakayama J., Yoshida K., Kobayashi H., Isogai A., Clewell D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       faccalis: detection of a new insertion element on pPD1 and implications for the evolution of this plasmid family."; Mol. Gen. Genet. 252:640-647(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632C8BDC8E79EB2C CRC64;
047802; 052199;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-12000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                 Enterococcus faecalis (Streptococcus faecalis).
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                                                                                                                                 SURFACE EXCLUSION PROTEIN PRECURSOR (SEA1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the pheromone response.";
J. Bacteriol. 177:5574-5581(1995).
BMBL; x96976; CAA65662.1;
EMBL; D78016; BAA11202.1; -.
Signal; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSSIBLE R27-2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 843 AA; 93049 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leishmania major.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 SSEA-----QKEAAALAEAEAAADEPAEATKMVSLVQGEIDNLADSIADEFLKQ 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith H.E., Reek F.H., Vecht U., Gielkens A.L.J., Smits M.A.; "Repeats in an extracellular protein of weakly pathogenic strains of Streptococcus suis type 2 are absent in pathogenic strains."; Infect. Immun. 61:318-3326(1993).

EMBL: X71880; CAA50714.1; ...
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                                                                                                                                                                                                                                                                                                                                                         Length 924;
                                                                                                                    STRAIN-FRIEDLIN:
MEDLINE-98146435; PubMed-9477341;
MEDLINES A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.
Smith D.F.;
                                                                                                                                                                                                               "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
EMBL; ALS90734; CAG73243.1; -.
NON TER 924 924
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Saunders D., Murphy L., Silva W., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                          99390 MW; 28F42FB20499E85A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                        45;
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EDKQAEIKKLTDAVAKTLATIRDNADK-RTQEAEKAQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches
                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 104.5; ilarity 25.9%; Pred. No. 46; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 104.5; 24.5%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSDALEALADQTDALQSEEAAVVKADNAASDALEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93328288; PubMed=8335363;
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Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                               924 AA;
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ses 37; Conserv
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                                                                                                SECUENCE FROM N.A.
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01-NOV-1996 (
01-OCT-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-1890;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 13, 2002, 03:33:22; Search time 22.9572 Seconds (without alignments) 268.169 Million cell updates/sec Run on:

US-09-847-539A-6 777 1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		Description	4 str	P19909 streptococc		P03764 bacteriopha	Q47500 escherichia	Q47125 escherichia	P19934 escherichia		P76072 escherichia		Q90988 gallus gall		P39922 hydra atten	P17953 enterococcu	gallus	-		P39653 streptococc		Q9zf28 klebsiella	Q01042 herpesvirus	_	P50532 xenopus lae	Q98987 serinus can	P28668 drosophila		P77611 escherichia	Q11142 mycobacteri	P44678 haemophilus	P08089 streptococc		20	P27379 bacterlopha
SUMMARIES		ΙĐ	SPG1_STRSP	SPG2_STRSP	SANT_PLAFN	STF_LAMBD	CE05_ECOLI	CE10_ECOLI	TOLA_ECOLI	YIO9_YEAST	STFR_ECOLI	MRP4_STRPY	SCII_CHICK	E4L3_MOUSE	MYS3_HYDAT	ASA1_ENTFA	CALD_CHICK	NFM_CHICK	MRSP_STAAU	DEXT_STRDO	AK15_RAT	IF2_KLEOX	IE68_HSVSA	IF2_ENTCL	XCPC_XENLA	NEUM_SERCA	SYEP_DROME	ICAL_HUMAN	RNFC_ECOL1	HBHA_MYCTU	TOLA_HAEIN	M6_STRPY	M12_STRPY	HLES_DROME	VP06_BPPRD
		DB	-	-	7	П	-	П	-	-	-	П	-	Н	-	-	П	, 1	, ,	~	7	-	-	-	7	7	-	7	-	-	-	٦	-	-	-
		Match Length	448	593	309	774	490	490	421	1679	1120	388	1189	929	539	1296	771	857	1637	1337	464	896	407	897	1290	241	1714	708	740	198	372	483	264	1077	166
ď	Query	Match	24.2	24.1	16.9		14.2	•		13.8	13.6	13.5	13.3	13.1	13.1	13.1	13.0	12.9	12.9	12.8	12.7	12.7	12.7	12.7	12.7	12.6	12.4	12.3	12.3	12.2	12.2	12.2	12.2	12.2	12.0
		Score	188	an a	131.5	110.5	110	110	108.5	107	105.5	105	103	102	101.5	101.5	101	100	100	99.5	<u>ნ</u>	66	98.5	98.5	98.5	86	96	95.5	95.5	92	95	95	95	94.5	93.5
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P13692 enterococcu	P26041 mus musculu O74191 schizosacch	Q14203 homo sapien O9hp81 halobacteri			
P54_ENTFC ABPX_YEAST	MOES_MOUSE FKB4 SCHPO	DYNA_HUMAN HTR2_HALN1	HTR2_HALSA MAPB_RAT	MYH8_HUMAN RSP3_CHLRE	G19P_HUMAN HTR6_HALN1
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516	576 361	1278	764	1937	527 778
12.0	12.0	11.9	11.8	11.7	11.6 11.6
93.5	93	92.5	91.5	91	90.5
34	36	80 G 60 E	40	42	44 45

ALIGNMENTS

SPG1_STRSP STO1_STRSP STANDARD; PRT; 448 AA. AC POR654:			<pre>RN {1,000</pre>				
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Immunoglobulin G binding protein G precursor (IGG binding protein G)
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 X 5 AA REPEATS OF [DE]-D-A-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 AWEAAA-AADALAKAKADALKEFINYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ALEALADQTDALQSEEAAVVKADN -- AASDALEAL -- ADQTDALQSEEAEVVQSDNAA - 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VDSPIEDTPIIRNGGELTVLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA 93
SUBCELLULAR LOCATION: Type I membrane protein. Cell wall. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                     IMMUNOGLOBULIN G BINDING PROTEIN G.
                                                                                                                                                                                                                                                                                            PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.28; Score 188; DB 1; Length 448; 38.98; Pred. No. 9.4e-06; Live 20; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A0759060C8F9E6CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                            ALA-RICH.
2 X 37 AA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                  2 X 55 AA REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 ISEATDGLSDFLKSOTPAEDTVKSIELAEAKVLANRE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 AA
                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
                                                                                                                                                                                                                    InterPro; IPR002988; GA.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR0010724; IgG_bind_B.
Pfam; PF01468; GA; 2.
Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEINS
                                                                                                                                                                                                                                                                        Pfam; PF01378; IgG_binding_B; 2. PRINTS; PR00015; GPOSANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 AA; 47567 MW;
                                                                                                                     EMBL; M13825; AAA03664.1; -. PIR; A24496; A24496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                       PDB; 1PGA; 30-APR-94.
PDB; 1PGB; 30-APR-94.
PDB; 1PGX; 15-UUL-92.
PDB; 1IGC; 03-UUN-95.
PDB; 2IGD; 01-NOV-94.
PDB; 2IGD; 20-UUL-98.
PDB; 1FCC; 20-UUL-95.
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01-FEB-1991 (
15-JUL-1999 (
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P19909;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Filpula D., Alexander P., Fahnestock S.R.;
"Nucleotide sequence of the protein G gene from Streptococcus GX7805,
and comparison to previously reported sequences.";
Nucleic Acids Res. 15:7210-7210(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guss B., Eliasson M., Olsson A., Uhlen M., Frej A.-K., Joernvall H., Flock J.-I., Lindberg M.; "Structure of the IgG-binding regions of streptococcal protein G."; EMBO J. 5:1567-1575(1986).
Streptococcus sp. (strain G148).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Struct. Biol. 5:470-475(1998).
-!- SUBGELUIAR LOCATION: Type I membrane protein. Cell wall.
-!- SIMILARIFY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R EMBL; X06173; CAA29540.1; -.
R EMBL; X00428; CAA68489.1; -.
R EMBL; X004128; CAA27638.1; -.
R PTR; S00128; S00128.
R PTR; A26314; A26314.
R PDB; 1G84; 22-41L-98.
R InterPro: IPR001899; Gram_pos_anchor.
R InterPro: IPR001899; Gram_pos_anchor.
R InterPro: IPR001899; Gram_pos_anchor.
R InterPro: IPR00746; Gram_pos_anchor.
R Pfam; PF01746; Gram_pos_anchor.
R Pfam; PF01778; IgG_binding_B; 3.
R Pfam; PR00313; GPOSANCHOR.
R PRINTS; PR000134; GPOSANCHOR.
R PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
R PGOSTTE; PS00343; GRAM_POS_ANCHORING; 1.
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MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malakauskas S.M., Mayo S.L.;
"Design, structure and stability of a hyperthermophilic protein
variant.";
                                                                                                                                                                                                                                                                                                                          Structure and evolution of the repetitive gene encoding
                                                                                                                                                                                                                                                         Olsson A., Eliasson M., Guss B., Nilsson B., Hellman
Lindberg M., Uhlen M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                               streptococcal protein G.";
Eur. J. Biochem. 168:319-324(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=GX7805;
MEDLINE=88015586; PubMed=3658689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86300657; PubMed-3017704;
                                                                                                                                                                                               STRAIN-G148;
MEDLINE-88029445; PubMed-3665928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98290449; PubMed-9628485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 114-593 FROM N.A. STRAIN-G148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 371-427.
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593
567
588
593
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=1306;
                                                             Streptococcus
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SIGNAL
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271 15-1. 286 15-2. 33694 MW; 63574C51D62024FC CRC64;

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SEQUENCE
            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 40:775-783(1985).
-1- FUNCTION: S ANTIGENS ARE SOLUBLE HEAT-STABLE PROTEINS PRESENT
IN THE SERA OF SOME INPECTED INDIVIDUALS.
-1- SUBCELLULAR LOCATION: PARASITOPHOROUS VACUOLE.
-1- POLYMORPHISM: DITERSITY IN S-ANTIGEN IS MAINLY DUE TO POLYMORPHISM
IN THE REPETITIVE REGIONS.
                                                                                                CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                              94 AWEAAA-AADALAKAKAADALKEFNKYGVSDYYKNLINNAKTVEGVKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ALEALADQTDALQSEEAAVVKADN--AASDALEAL---ADQTDALQSEEAEVVQSDNAA- 114
                                                                                                                                                                       60; Indels 16; Gaps
                                                                                                                                                                                              1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                           "Conserved sequences flank variable tandem repeats in two S-antigen genes of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-8176931; Pubwed-3886159;
Cowman A.F., Saint R.B., Coppel R.L., Brown G.V., Anders R.F.,
                                                                                   5 AA REPEATS OF [DE] - D-A-K-K.
                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
5-antigen protein precursor.
Plasmodium falciparum (isolate NF7 / Ghana).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                               24.1%; Score 187; DB 1; Length 593; 38.9%; Pred. No. 1.5e-05; Live 20; Mismatches 60; Indels 1
                                                                                                                      048BAA760D5B2920 CRC64;
                                    1-3.
2 x 55 AA REPEATS.
2-1.
 AA REPEATS.
                                                                                                                                                                                                                                                                                               115 -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                               |:| : : | : :|
153 ISEATDGLSDFLKSOTPAEDTVKSIELAEAKVLANRE 189
 37
                                                                      2-2.
3 x :
1-1,
1-2.
                                                                                                                         63291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M10130; AAA29758.1; -. PIR; B22011; YAZON7.
                                                                                                                                                            Local Similarity 38.9
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                        215
290
427
427
555
564
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309
56
86
256
                                                                                                                       593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5842;
SANT_PLAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria;
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kemp D.J
                                                                                                                                                Query Match
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                                              DOMAIN
REPEAT
REPEAT
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                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: The common laboratory strain of bacteriophage lambda; lambda PaPa; carries a frameshift mutation relative to Urlambda; lambda paPa; carries a frameshift mutation relative to Urlambda virions have thin, jointed tail fibers (side tail fibers) that are absent from lambda wild type. Relative to lambda PaPa, Urlambda has expanded receptor specificity and adsorbs to E.coli cells more rapidly.
-: SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
-: CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS CORRECTED IN POSITION TO 396 TO RECREATE THE ORIGINAL STF PRIOEIN.
                                                                                                                                                                                 85 A---ASDALEAL-ADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTK-DTKPVV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION AS STF.
MEDLINE-22165720; PubMed-1531648;
Haggaard-Ljungquist E., Halling C., Calendar R.;
"DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizontal transfer of tail fiber genes among unrelated
                                           Gaps
                                                                               26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEA-LADQTDALQSEEAAVVKADN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Bacteriophage lambda PaPa: not the mother of all lambda phages."; Science 258:1145-1148(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10710;
                                         6
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  Length 309;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDIINE-83189071; PubMed=6221115;
Sanger F., Coulson A.R., Hong G.F., Hill D.F., Peter
"Nucleoride sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
                                       45;
DB 1;
                                                                                                                                                                                                                                                                                                                                                                                  STF_LAMBD STANDARD; PRT; 774 AA. P03764; P03745; 21-JUL-1986 (Rel. 01, Created) CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Side tail fiber protein.
  16.9%; Score 131.5; DB 34.1%; Pred. No. 0.032;
                                         29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J02459; AAA96555.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 174:1462-1477(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93068310; PubMed-1439823;
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hendrix R.W., Duda R.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage lambda.
                      Best Local Similarity
                                                                                                                                                                                                                                          140 KKEERQ 145
                                                                                                                                                                                                                                                                               216 KSDEAE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteriophages.
                                         43;
    Query Match
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4

Indels

48;

Mismatches

20;

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Conservative
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
                                                                                                                                 142 EERQ 145
                                                                                                                                                         262 LERQ 265
      42;
                                                                                                                                                                                                                                                                                     Colicin 10.
                                                                                                                                                                                                                    CE10_ECOLI
Q47125;
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"Evidence that the immunity protein inactivates colicin 5 immediately prior to the formation of the transmembrane channel.";
J. Bacteriol. 177:6966-6972(1995).

-I- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING TO DISSIPATION OF CELLULAR ENBRGY.

-I- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.

-I- SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
                                                                                                                                                         87 SDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALD----VKKTKDTKPVVKKE 142
                                                                                                                                                                                                            Gaps
                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                     32;
                                                                                         14.2%; Score 110.5; DB 1; Length 774; 27.4%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110; DB 1; Length 490; Pred. No. 1.3;
                                                                                                                    Indels
                                                                 774 AA; 77527 MW; CDD1DF85E919123B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 POTENTIAL.
53137 MW; 187614D103B953E2 CRC64;
                                                                                                                  18; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X87835; CAA61102.1; -. InterPro; IPR000293; Channel_collcin. Pfan; PF01024; COlicin; PRINTS; PR00280; CHANLCOLICIN. PRODOM; PD00260; CHANLCOLICIN. PRODOM; PD00276; CHANNEL_COLICIN; I. PROSTTE; PS00276; CHANNEL_COLICIN; I. Antibiotic; Bacteriogin; Plasmid; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                    490 AA
EMBL; J02459; AAA9657.1; ALT_FRAME.
PIR; A04389; QXBP1L.
PIR; A04370; QXBP2L.
InterPro; IPR004089; Chemotaxis_transducer.
Fiber protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96074329; PubMed-7592492;
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15-DEC-1998 (Rel. 37, Last seq
16-CCT-2001 (Rel. 40, Last and
Collcin 5.
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                                                                                                                 37; Conservative
                                                                                                                                                                                                                                             143 ERONVNTLPTTGEES 157
                                                                                                                                                                                                                                                                    280 --- NARSSETAAERS 291
                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Best Local Similarity
                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-562;
                                                                                                                                                                                                                                                                                                                                  CE05_ECOLI
Q47500;
                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dependent uptake via the Tsx receptor and to pore formation.";
Mol. Microbiol. 16:57-67(1995).
-1- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF
TRANSMEMBRARE TOXINS DEPOLARIZE THE CYTOPLASHIC MEMBRARE, LEADING
TO DISSIPATION OF CELLULAR ENERGY.
-1- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE
AGAINST, ESCHBERCHIA COLI AND CLOSELY RELATED BACTERIA.
-1- SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
                                                                154 AAEK-ALREAERQRDEIARQ-----QAETAHLLAMAEAAEAEKNRQDSLDEEHRAVEVAE 207
                                                                                                                                               84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKT--KDTKPVVKK 141
                                                                                                                                                                                         208 KKLAEAKAELAKAESDVQSKQAIVSRVAGELENAQK-----SVDVKVIGFPGWRDVQKK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKT--KDTKPVVKK 141
24 APEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKAD 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pcoll0.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilsl H., Braun V.;
"Novel colicin 10: assignment of four domains to TonB- and TolC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 490;
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Pfam; PF01024; Colicin; 1.
PRINTS; PR00280; CHANNCOLICIN; 1.
PROSTE; PS00276; CHANNEL_COLICIN; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
Antiblocic; Bacterioch; Plasmid; Transmembrane.
ERANSMEM 497 467, 467
ERANSMEM 490 AA; S3342 MM; 700E864DA3F97F5R C
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Last annotation update)
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MEDLINE-95379494; PubMed-7651137;
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16-OCT-2001 (Rel. 40, Last anno
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FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A

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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nasamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
208 KKLAEAKAELAKAESDVQSKQAIVSRVAGELENAQK-----SVDVKVTGFPGWRDVOKK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1657.
STRAIN-KIZ. / MG1657.
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                        Levengood S.K., Webster R.E.; Nucleotide sequences of the tolA and tolB genes and localization their products, components of a multistep translocation system in Escherichia coll.; J. Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97133271; PubMed-8978668;
Derouiche R., Gaviol1 M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.; Frilamentous phage infection: crystal structure of 93p in complex with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levengood S.K., Beyer W.F. Jr., Webster R.E.; "Tolla membrane protein involved in colicin uptake contains an extended helical region.":

Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tola central domain interacts with Escherichia coli porins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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MEDLINE-99332679; Pubmed-10404600;
                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                         421 AA.
                                                                                                                                                                                                                                            Tola protein.
TOLA OR CIM OR EXCC OR LKY OR B0739.
                                                                                                                                                         PRT;
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MEDLINE-97061202; Pubmed-8905232;
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                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                              Escherichia col1
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                142 EERQ 145
                                                                   262 LERQ 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AASDA----LEALADQTDALQSEEAEVV------QSDNAASDAWEKAATPIALDVKKT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 ERLAAQEQKKQAEEAAKQAELKQKQAEEAAAKAAADA-KAKA-EADAKAAEEA----AKK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AAADAKKKAEAEAAKAAAEAQKKAEAAAALKKKAEAAEAAAEARKKAATEAAEKAKAE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKLALRNEERAIDELKKQA-IEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C / AAB72;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Walandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.;
                                                                                         SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                       EcoGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                        AND LAMB.
-1. SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA HELICAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycottna; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
             COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OF BACTERIOPHAGE DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 195.1 kDa protein in DNA43-UBI1 intergenic region.
YIL140C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 108.5; DB 1; Length 421; 32.6%; Pred. No. 1.4; ive 25; Mismatches 43; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeal; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1679 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                          EMBL, AE001177, AAC73833.1; -.
EMBL, D90713, BAA35405.1; -.
PIR, JV0057; JV0057.
PDB; 1TOL; 20-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                             EMBL; M28232; AAA24683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 KDTKPVVKK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AEKKAAAEK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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35
48
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Best Local Similary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YIO9_YEAST
P40457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIO9_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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Streptococcus
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P30141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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DD4CD
DD4CDD
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 LQS----EEAAVVKAD------NAASDALEALADQTDALQSEEAEVVQSDN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97251357; PubMed-9097039;
Alba H., Baba T., Frjita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., K., Mori H., Mori T., Moromura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 LTNLLGNAPEKL----ALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1625;
STRAIN-KIZ. / MG1625;
PUDNed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
May B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 107; DB 1; Length 1679; 26.8%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Side tail fiber protein homolog from lambdoid prophage Rac.
STFR OR B1372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 1679 AA; 195141 MW; 298950CC52202DBF CRC64;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1380 SSSDAFEK----LKVNMEKEKDRIIDERTKEFEKKLQETLNKST 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 AASDAWEKAATPIALDVKKTKD-----TKPVVKK-EERQNVNT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 3:363-377(1996).
-1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                EMBL; 238059; CAA86129.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STFR_ECOLI STANDARD P76072; P77560; 16-OCT-2001 (Rel. 40, C 16-OCT-2001 (Rel. 40, L 16-OCT-2001 (Rel. 
                                                                                                                                                                                                                                                                             PIR; S48385; S48385
SGD; S0001411; MLP2
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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STFR_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 HAADAADSARAASTSAGQAASSAQSASSSAGTASTKATEA····SKSAAAAESSKSAAAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GTLTNLLGNAPE----KLALRNEERAIDELKKQAIEDKEATTAIEAASSD----ALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AP4 / SEROTYPE M4;
MEDLINE-92269579; PubMed-1588817;
Stenberg L., O'Toole P., Lindahl G.;
Stanpy group A streptococcal strains express two different immunoglobulin-binding proteins, encoded by closely linked genes characterization of the proteins expressed by four strains of
                                                                                                                                                                                                                                                                                                            EcoGene; EG13370; stfR.
InterPro; IPR0401089; Chemotaxis_transducer.
Hypothetical protein; Fiber protein; Repeat; Complete proteome.
SEQUENCE 1120 AA; 113779 WW, 542E59D71EE795B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MRP protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Fibrinogen- and Ig-binding protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 13.6%; Score 105.5; D
1 Similarity 31.5%; Pred. No. 6.3;
41; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 AA
                                                                                                                                                                                               EMBL; AE000234; AAC74454.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 6:1185-1194(1992).
                                                                                                                                                                                                                            EMBL; D90774; BAA14966.1; -. EMBL; D90775; BAA14975.1; -. HSSP; P04002; IWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 ALDVKKTKDT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 SAGAAKTSET 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 41; Conserv
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SEQUENCE
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                                                                                                                                                  MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCII.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF
                                                                                                                                                                                                                                                                                            181 EIAKLQSEAATLENLLGSAKRELTELOAKLDTATAEKAKLESOVTTLENLLGSAKRELTD 240
                                                                                                                                                                                                                                                                                                                                 97 TDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVN------ 148
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                      6 EQPRIIPNGGTLTNLLGNA-------PEKLALRNEERAIDEL---KKQAIED 47
                                                                                                                                                                                                                                                                                                                     48 KEATTAIEAASSDALEA----LADQTDALQSEEA---AVVKADNAASDALE----ALADQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Cell Biol. 127:303-318(1994).

-:- FUNCTION: MITOSIS-SEPCIFIC CHROMOSOME SCAFFOLD PROTEIN THAT COLOCCALIZES WITH TOPOISOMERAEI II. MAY FUNCTION IN CHROMOSOME COLOCCALIZES WITH TOPOISOMEASE II. MAY FUNCTION IN CHROMOSOME CONDENSATION OR SISTERS CHROMATID DISJUNCTION.

-:- SUBCELLULAR LOCATION: NUCLEAR. LOCATED ALONG THE ENTIRE LENGTH THE CHROMATID ARM AXIS.

-:- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ದ
                                                                                                                             FIBRINGEN- AND IG-BINDING PROTEIN
                                                                                                                                                                                                                                                 48;
                                                                                                     IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal. SIGNAL 1 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fibroblast;
MEDLINE-95014725; PubMed-7929577;
Saitoh N., Goldberg I.G., Wood E.R., Earnshaw W.C.;
"ScII: an abundant chromosome scaffold protein is a member of family of putative ATPases with an unusual predicted tertiary structure.";
                                                                                                                                                                                                                      13.5%; Score 105; DB 1; Length 388; 26.9%; Pred. No. 2.2; tive 26; Mismatches 67; Indels
                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                  3AB19E8B6CEDA722 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                         EXTRACELLULAR
                                                                 Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
          or send an email to license@isb-sib.ch)
                                          PIR; A46173; A46173.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosome scaffold protein ScII.
                                                                                                                                                                                                  42244 MW;
                                EMBL; M87831; AAA26930.1; -.
                                                                                                                                                                                                                                   Similarity 26.9 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               149 -TLPTTGEE-SNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                      352 RQLPSTGEETTNP 364
                                                                                                                                                                                                388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
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Q90988;
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SCIL_CHICK
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Marra M., Hillier L., Kucaba T., Martin J., Beck C., Wylie T.,
Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person B.,
Swaller T., Gibbons M., Pape D., Harvey N., Schurk R., Ritter E.,
Kohn S., Shin T., Jackson Y., Cardenas M., McCann R., Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-20119278; PubMed-10652311;
Parra M., Gascard P., Walensky L.D., Gimm J.A., Blackshaw S., Chan N.,
Takakuwa Y., Berger T., Lee G., Chasis J.A., Snyder S.H., Mohandas N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular and functional characterization of protein 4.1B, a novel member of the protein 4.1 family with high level, focal expression in brain ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 EEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 LTNLLGNAPEKLA--LRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edia_MOUSE STANDARD, PRT; 929 AA.
09WV92. 09R102;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
8nand 4.1-11ke protein 3 (4.1B) (Differentially expressed in adenocarcinoma of the lung protein 1) (DAL-1) (DALIP) (MDAL-1).
EPB41L3 OR EPB4.1L3 OR DAL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 103; DB 1; Length 1189;
                                                                                                                                                                                                                                                                                                                                                                                                                              P-binding; Coiled coil; Nuclear protein.
32 39. ATP (POTENTIAL).
211 503 COILED COIL (POTENTIAL).
674 1030 COILED COIL (POTENTIAL).
1093 1120 ALA/ASP-RICH (DA BOX).
1189 AA; 134940 MW; 905EBC89EC45AD5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Azam M., Andrabi S., Lin L., Newsham I., Chishti A.H.; "Mouse DAL-1 (mDAL-1) cDNA Sequence."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 6-929 FROM N.A. (ISOFORM 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 275:3247-3255(2000).
                                                                                                                                                                                                                                               EMBL; X80792; CAA56767.1; -. InterPro; IPR003405; SMC_C. InterPro; IPR003495; SMC_N. Pfam; PF02483; SMC_C, 1. Pfam; PF02463; SMC_N; 1. Mitosis; ATP-binding; Colled NP_BIND 211 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%;
25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 TK---PVVKKEERQN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889 IKAKSAKIEKYREON 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conboy J.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMIG outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                        -I-SUBCELLULAR LOCATION: Membrane-associated.
-I-ALTERNATIVE PRODUCTS: 7 isoforms: 1/4.1B-brain (shown here), 2/4.1B-heart, 3/4.1B-kidney, 4/4.1B-brain, 5/4.1B-heart, 6/4.1B-kidney and 7; may be produced by alternative splicing. Isoform 7 is 1nferred from the cDNA sequence of ref.2.
-ITSSUE SPECIFICITY: Highest expression in brain, lower in testis, adrenal gland, heart and kidney. Also present in muscle and epithelial cells Isoform 1 is expressed in heart and soform 2 is expressed in heart and isoform 6 seems to be most abundant in kidney while isoforms 4 and 5 are predominantly expressed in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOPORM 2, ISOFORM 3, ISOFORM 5, ISOFORM 6 AND ISOFORM 7).

ACAGAIKERAKEOHPDMSVTKVVVHKETEITPEDGED -> E (IN ISOFORM 4, ISOFORM 5, ISOFORM 6 AND ISOFORM 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 7).
D -> NSLIKRIKGENVYVKHSNLMLED (IN ISOFORM 2 AND ISOFORM 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structural protein; Cytoskeleton; Glycoprotein; Alternative splicing; Membrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TDALQS--EEAAVVKADNAASDALEALADQTDALQSEEAEV-VQSDNAASDAWEK--AAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Isoform 2 (heart-specific) has the complete spectrin--
actin-binding (SAB) domain and fully interacts with spectrin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 GGTLTNLLGN-APEKLALRNEERAIDELKKQAIEDKEATTAIE---AASSDALEALAD-Q 68
                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: The complete SAB domain is present only in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1; Length 929;
8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSDSE -> RIRLR (IN REF. 2).
Q -> R (IN REF. 2).
A -> V (IN REF. 2).
V -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; F4975FF405DA44AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECTRIN--ACTIN-BINDING. CARBOXYL-TERMINAL (CTD).
                                                                                                                                                                                                                                                                                                                                                                                                               heart-specific isoforms (2 and 5).
SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 PIALDVKKTKDT---KPVVKKEERQNVNTLPTTGEE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.8; 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF152247; AAD38048.1; -.
EMBL; AF177146; AAD51365.1; ALT_INIT.
MGD; MG1:103008; EP84.113.
InterPro; IPR000299; Band_4.1.
Pfam; PF00373; Band_41; 1.
PRINTS; PR00935; BAND41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00660; BAND 41_1; 1.
PROSITE; PS00661; BAND_41_2; 1.
PROSITE; PS50057; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 26.9 tes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558
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288 2
306 3
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakano M.Y., Stidwill R.P.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN 6 HAS ATPASE
--- ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST,
TO OTHER NON MUSCLE MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 EQPRIIPNGGTLTNL-----LGNAPEKL------ALRNEERAIDELKKQ 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding.
                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, clone 203 (Fragment).
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metacoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
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Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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01-NOV-1990 (Rel. 16, Last sequ
01-NOV-1997 (Rel. 35, Last anno
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                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6087;
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P17953;
                                                                                  MYS3_HYDAT
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Matches
                                              MYS3_HYDAT
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                Galli D., Lottspeich F., Wirth R.;
"Sequence analysis of Enterococcus faecalis aggregation substance
encoded by the sex pheromone plasmid padl.";
Mol. Microbiol. 4:895-904(1990).
-I- FUNCTION: AGGREGATION SUBSTANCE ALLOWS DONOR AND RECIPIENT STRAINS
TO FORM TIGHT AGGREGATES WHICH ALLOW THE NON-MOTILE BACTERRA TO
MAINTAIN PHYSICAL CONTACT OVER A PERIOD OF TIME SUFFICIENT TO
PERMIT CONJUGATIVE TRANSFER OF THE SEX PHEROMONE PLASMID FROM
DONOR TO RECIPIENT STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL WALL REGION (PROBABLE).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAW 118
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                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein, Cell wall, SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
               Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALDI OR CAD.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1296 AA; 142285 MW; 52123A133AD23E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 EK------AATPI----ALDVKKTKDTKPV-VKKEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101.5;
pred. No. 13;
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid; Transmembrane; Cell wall; Signal.
                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 44-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S10223; HMSOIF.
InterPro; IPRO(1899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                  MEDLINE-91014689; PubMed-2120541;
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25.0%;
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                                                 NCBI_TaxID-1351;
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DOMAIN
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Plasmid
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CALD_CHICK
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation sites.";
J. Biol. Chem. 266:19971-19975(1991)
-1- FUNCTION: ACTION: AND MYOSIN-BINDING PROTEIN IMPLICATED IN THE REGULATION OF ACTOMYOSIN INTERACTIONS IN SMOOTH MUSCLE AND NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN AND ACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88293484; PubMed-3401222;
Mornet D., Audemard E., Derancourt J.;
"Identification of a 15 kilodalton actin binding region on gizzard caldesmon probed by chemical cross-linking.";
Biochem. Biophys. Res. Commun. 154:564-571(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92041815; Pubmed-1939059;
Mak A.S., Carpenter M., Smillie L.B., Wang J.H.;
"Phosphorylation of caldesmon by p34cdc2 kinase. Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yano H., Hayashi K., Haruna M., Sobue K.; ^{\circ} Identification of two distinct promoters in the chicken caldesmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (GIZZARD H-CAD; BRAIN L-CAD AND GIZZARD L-CAD).
                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (GIZZARD H-CAD ISOFORM).
                                                                           AND PARTIAL SEQUENCE (GIZZARD H-CAD ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-94071994; Pubmed-8250919; Haruna M., Hayashi K., Yano H., Takeuchi O., Sobue K.; Common structural and expressional properties of vertebrate
                                                                                                                                                                                                                                                                   Hayashi K., Kanda K., Kimizuka F., Kato I., Sobue K.; "Primary structure and functional expression of h-caldesmon complementary DNA.";
                                                                                                                             Bryan J., Imai M., Lee R., Moore P., Cook R.G., Lin W.-(
"Cloning and expression of a smooth muscle caldesmon.";
J. Biol. Chem. 264:13873-13879(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi K., Fujio Y., Kato I., Sobue K.; "Structural and functional relationships between h- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 451-756 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 201:618-626(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-15 FROM N.A. (BRAIN L-CAD ISOFORM).
                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 164:503-511(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of an avian non-muscle caldesmon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muscle Res. Cell Motil. 12:372-375(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (GIZZARD L-CAD ISOFORM).
                                                                                             TISSUE-Gizzard, and Oviduct;
MEDLINE-89340480; Pubmed-2760048;
                                                                                                                                                                                                                                 TISSUE=G1zzard;
MEDLINE=90026426; PubMed=2803315;
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MEDLINE=94271210; PubMed=8002994;
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MEDLINE-92042686; PubMed-1939602;
                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
MEDLINE-91093148; PubMed-1824698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 266:355-361(1991).
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                                                                         SEQUENCE FROM N.A.,
TISSUE-Gizzard, and
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                                   NCBI_TaxID*9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caldesmon genes.
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                                                                                                                                                                                                   -I- DOMAIN: THE N-TERMINAL PART SEEMS TO BE A MYOSIN/CALMODULIN-BINDING DOMAIN, AND THE C-TERMINAL A TROPOMYOSIN/ACTIN/CALMODULIN-BINDING DOMAIN, THESE TWO DOMAINS ARE SEPARATED BY A CENTRAL BLICAL RECION IN THE MUSCLE FORMS.

-I- PTM: IN NON-MUSCLE CELLS, PHOSPHORYLATION BY CDC2 DURING MITOSIS CANDESS CALDESMON TO DISSOCIATE FROM MICROFILAMENTS.

PHOSPHORYLATION REDUCES CALDESMON BINDING TO ACTIN, MYOSIN, AND CALMODULIN AS WELL AS ITS INHIBITION OF ACTOMYOSIN ATPASE ACTIVITY. PHOSPHORYLATION ALSO OCCURS IN BOTH QUIESCENT AND DIVIDING SMOOTH MUSCLE CELLS WITH STMILAR EFFECTS ON THE INTERACTION WITH ACTIN AND CALMODULIN AND ON MICROFILAMENTS REORGANIZATION (BY SIMILARITY).

-!- SIMILARITY: TO A TROPOMYOSIN BINDING SITE DOMAIN OF TROPONIN T.
FILAMENTS). STIMULATES ACTIN BINDING OF TROPOMYOSIN WHICH INCREASES THE STABILIZATION OF ACTIN FILAMENT STRUCTURE. IN MUSCLE TISSUES, INHIBITS THE ACTOMYOSIN APPASE BY BINDING TO F-ACTIN. THIS INHIBITATON IS ATTENDATED BY CALCIUM-CALMODULIN AND IS POTENTIATED BY TROPOMYOSIN. INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN. INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN AN MITH CALMODULIN. ALSO PLAY AN ESSENTIAL ROLE DURING CELLULAR MITHOSIS AND RECEPTOR CAPPING. SUBCELLULAR LOCATION: ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON STREAM PRODUCTS: 3 ISOFOMMS; GIZZARD H-CAD (SHOWN HERE), BRAIN L-CAD AND GIZZARD L-CAD; ARE PRODUCED BY ALTERNATIVE
                                                                                                                                           TISSUE SPECIFICITY: HIGH-MOLECULAR-WEIGHT CALDESMON (H-CALDESMON) IS PREDOMINANTLY EXPRESSED IN SMOOTH MUSCLES, WHEREAS LOW-MOLECULAR-WEIGHT CALDESMON (L-CALDESMON) IS WIDELY DISTRIBUTED IN NON-WUSCLE TISSUES AND CELLS. NOT EXPRESSED IN SKELETAL MUSCLE OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
                                                                                                                                                                                           Pfan; PF02029; Caldesmon; 1.
PRINTS; PR01076; CALDESMON.
Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
                                                                                                                                                                                                                                                   MYOSIN AND CALMODULIN-BINDING.
10 x 13 AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M).
                                                                                                                                                                                                                                                                                                                                                                                                                   TROPOMYOSIN-BINDING (POTENTIAL).
TROPOMYOSIN-BINDING (POTENTIAL).
STRONG ACTIN-BINDING.
CALMODULIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB 1; Length 771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDC2)
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PHOSPHORYLATION (
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:ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLU. POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY - ARG.
           BAA04540.1; JOINED.
                                                                                                                                                                                InterPro; IPR000075; Caldesmon.
                                                                                                                                                                                                                            e splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%;
                                                                                                           M59762; AAA48649.1;
D17552; BAA04490.1;
M26684; AAA48811.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 27.69 tes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 ERONVNTLPTTGEE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 EKAQANLLRKQEED 422
                                                                                                                                                      PIR; A32642; A32642.
HSSP; P05412; 1F0S.
                                                                                                                                                                                                                                      Repeat; Alternative
D17640; E
D17641; E
D17642; E
D17644; E
D17646; E
D17646; E
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NFM_CHICK
ID NFM_CHICK
AC P16053;
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449 VEEIIEETKVEDEKSEMEDALSAIAEEMAAKAQEEEQEEEKAEEEAVEEEAVSEKAAEQA 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PIM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS MOSCHONYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                ES DEV. 1:699-708(1987). FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, MAND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
                                                                                                                                                                                                                                                Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.,
*Identification of gene products expressed in the developing chick
visual system: characterization of a middle-molecular-weight
                                                                                                                               Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
*Isolation of the Chicken middle-molecular weight neurofilament
(NF-N) gene and characterization of its promoter.";
Nucleic Acids Res. 18:521-529(1990).
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O-LINKED (GLCNAC) (BY SIMILARITY).
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Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Indels
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4E2E0FC6AC64778B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL 2A.
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LINKER 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COIL 1B.
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                                                                                                                                                                                                                  SEQUENCE OF 259-857 FROM N.A. MEDLINE-88112814; Pubmed-3123320;
                                                                                                SEQUENCE FROM N.A.
MEDLINE-90174973; PubMed-2106668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95704 MW;
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23.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A27040; A27040.
PIR; S08061; S08061.
PIR; S15762; S15762.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546
857 AA;
                                                                                                                                                                                                                                                                                  visual system: char
neurofilament cDNA.
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                                                               NCBI_TaxID-9031;
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407
99
131
144
243
260
282
282
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DOMAIN
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CARBOHYD
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Pfam; PF00746; Gram_pos_anchor. 1.
PROSTTE; PS00343; GRAM_POS_anCHORING; FALSE_NEG.
Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 X 2 AA TANDEM REPEATS OF D-[SAG].
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 DDSSDASKVKGNVQTIEQSSANSNESDIPEQVDVTKDTTEQASTEEKANTTEQASTEEKA 117
                                                                                                                            -----SDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKD 134
                                                                                                                                                                                        569 KVKSPPAKSPPKSPPKSPVTEQAKAVQKAAAEVGKDQKA----EKAAEKAAKEEKAASP 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Gaps
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METHICILLIN-RESISTANT SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN—ISOLATE 1061;
Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
Sayolainen K.) Harge repeat-rich surface protein of methicillin resistant
Staphylococcus aureus."
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.; "Purification and characterisation of a plasmin-sensitive surface protein of Staphylococcus aureus."; Eur. J. Biochem. 236:904-910(1996).
                                                               AEEEEKEEEERAEEEAAKSDAAEEGGSKKEEIEEKEEGEEAEEEEAAKGKAEEAGAKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 624-628; 676-682; 938-948; 1156-1168; 1176-1185; 1199-1205 AND 1217-1224.
STRAIN-ISOLATE 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus/Staphylococcus group; Staphylococcus NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1637 AA.
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                                                                                                                                                                                                                                                                                                                        624 EKPATPKVTSPEKPATPEKPPTPEKA 649
                                                                                                                                                                                                                                                        135 TKPVVKK---EERQNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96270743; PubMed-8665912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1637 AA; 174573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRSP_STAAU STANDARD; F P80544; Q92F62; O1-FEB-1996 (Rel. 33, Created) 16-CCT-2001 (Rel. 40, Last sequ 01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF115379; AAD09131.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
1637
1582
1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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VDSPIEOPRIIPNGGTLTNLLGNAPEKLALR-----NEERAIDE-LKKQAIEDKEATTA 53

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1044 PAVAEQPQATEPNQAKPSVDKA--AAPEALSLIQLKQQTPAIQAKEADDPEVDETKSEVT 1101

EKAATPIALDVKKT-KDTKPVVKKEERQNVNTLPTTGEESN 158

119

EALADQTDALQSEEA--AVVKADNAASDALE--ALADQTDALQSEEAEVVQSDNAASDAW

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-6715 / UAB66;

MEDLINE-94292401; PubMed-8021165;

MEDLINE-94292401; PubMed-8021165;

MEDLINE-94292401; PubMed-8021165;

MEDLINE-94292401; PubMed-8021165;

MEDLINE-94292401; PubMed-8021165;

MEDLINE-94292401; PubMed-8021165;

MEDLINE-94292401; PubMed-802102;

MEDLINE-1762401; MEDLINE SCHOOL SCHOO
                          EXTRACELLULAR (BY SIMILARITY).

WHEBRANE ANCHOR (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
TTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                  Hydrolase; Glycosidase; Signal; Transmembrane; Repeat; Plasmid.
                                                                                                DNA-----ASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINS.
W; B494275A77A2E3D0 CRC64;
                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus downel (Streptococcus sobrinus).
                                                                                                                                                                                                                                                                             PRT; 1337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99.5;
Pred. No. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M96978; AAA21772.1; -. InterPro; IPR001899; Gram_pos_anchor. Pfam; PF00746; Gram_pos_anchor; I. PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%;
24.8%;
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                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1337
1313
1332
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1310
                                                                                                                                                                                                                                                                                                                         (Rel. 31,
(Rel. 31,
(Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pYA902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                            01-FEB-1995
                                                                                                                                                                                                                                                                          DEXT_STRDO
P39653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Si
Matches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                   DEXT_STRDO
                                                                                                111
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
A-kinase anchor protein 150 (AKAP 150) (CAMP-dependent protein kinase regulatory subunit II high affinity binding protein) (P150)
                                                                                                                                                                                                                                                                                                                                                                                                                 Bregman D.B., Bhattacharyya N., Rubin C.S.;
"High affinity binding protein for the regulatory subunit of cAMP-
"High affinity binding protein for the regulatory subunit of cAMP-
dependent protein kinase II-B. Cloning, characterization, and
expression of cDNAS for rat brain P150.";
J. BLOL, Chem. 264:4656(1989).
-1- FUNCTION: MAY ANCHOR THE KINASE TO CYTOSKELETAL AND/OR ORGANELLE-
ASSOCIATED PROTEINS, TARGETING THE SIGNAL CARRIED BY CAMP TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 KADNA-ASDALEALADQTDAL---QSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 VGQAEEATVGQAEEATVGQAGEATVSHIEKTTVGQA--EEAIVGQAEEATVGQAEEATVG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFIC INTRACELLULAR EFFECTORS.
--- SUBUNTT: BINDS DIMER OF THE RII-BETA REGULATORY SUBUNIT OF CAMP-DEPREDENT PROTEIN KASE.
--- SIMILARITY: PO OTHER AKAP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 QAEEATVGQAEEATVDQAEEATVGQAEEATVGQAGEAAVGQAEEAIVAQAEEATVGQAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 X 8 AA REPEATS.
; BDD21CF95CCBAC7F CRC64;
1102 PDSGTDKAPEAGQVDSDKAPTVKPSTPENNDNOPNNANDAD 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6;
                                                                                                    Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 99; DB 27.3%; Pred. No. 6.6; Live 24; Mismatches
                                                                                                    464
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89174725; PubMed=2538452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 ATVGOAEK ----ATVGOAEEP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 3
48335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J04597; AAA50420.1; -. PIR; A32461; A32461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 27,3 es 39; Conservative
                                                                                                                                                                                                                                         (Fragment).
Rattus norvegicus (Rat).
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 AA;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                  AK15_RAT
P24587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                             RESULT 19
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Gaps

11;

Indels

78;

ed. No. 19; Mismatches

32;

Conservative

40; Conserv

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3 SPIEQPRIIPNGCTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDAL 62

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114 EEQARREAEEAAKREAQLKAEREAAEQAKRELADKAKREAAEKDKVSNQQTDDMTKTAQA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X64346; CAA45696.1; -. EMBL; M86409; AAA46149.1; -. EMBL; S76368; AAB21116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; G36813; EDBEQ3.
PIR; S20244; S20244.
HSSP; P53041; 1A17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early protein.
                                                                                                                                                                                                                                                                                                                    73 OR ECLF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                           IE68_HSVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                     IE68_HSVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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è
                                                                                                                                                                                                                                                                                                                                                                                               "Sequence of the infB gene from Klebsiella oxytoca.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION OF PROTEIN SYNTHESIS IN VITRO, PROTEIS FORMYLMETHIONYL-TRNA FROM SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S RIBOSOMAL SUBUNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DQTDALQSEEA----AVVKAD-NAASDALEALAD------QTDAL-QSEEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLUIAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: USING ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME, THE GENE TRANSLATES INTO THREE ISOZYMES: ALPHA, BETA AND GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNAPEKLALRNEERA------IDELKKQAIEDKEATTAIEAASSDALEALA 66
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                ъ,
                                                                                                                                                                                                                                                                                                                                                         Steffensen S.A.D.A., Poulsen A.B., Fage-Larsen J., Korsager Mortensen K.K., Sperling-Petersen H.U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INITIATION FACTOR IF-2-ALPHA.
INITIATION FACTOR IF-2-BETA.
INITIATION FACTOR IF-2-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 99; DB 1; Length 896; Pred. No. 13; 37; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ClEB16F88FE39B6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initiation factor; Protein biosynthesis; GTP-binding; Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                     (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR IF2-BETA.
FOR IF2-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IF-2 FAMILY.
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                                                               PRT;
                                                                                                                                                                  Translation initiation factor IF-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ002735; CAA05698.1; -.
EMBL; AJ002735; CAA05699.1; -.
EMBL; AJ002735; CAA05700.1; -.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98095 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.78;
22.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD186100; IF2; 1. PROSITE; PS01176; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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896
159
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                          Klebsiella oxytoca
                                                                                                                                                                                                                                                                        NCBI_TaxID=571;
                                                                                                       30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                        Klebsiella.
                                                             IF2_KLEOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
NP_BIND
SEQUENCE
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INIT_MET
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NP_BIND
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Best Local
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                                         IF2_KLEOX
                                                                                   SOTT TITITE TO BE SEED FOR THE SECOND SECOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92230228; PubMed-1314457;
Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
*Analysis of nucleotide sequence of the rightmost 43 kbp of
herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
organization between HVS and Epstein-Barr virus.";
Virology 188:296-310(1992).
-- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 AND
HSV-2 IE-68 (US1), EHV-1 65, EHV-4 (ORF4), PRV RSP40, AND VZV 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIA--LDVKKTKDT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 APEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEA-----LADQTDALQSEEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B. Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
                                        106 EVVQSDNAASD----AWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure of the herpesvirus saimiri genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLU-RICH (ACIDIC).
FFD399CA82CE136C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 98.5; DB 1; 26.3%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Immediate-early protein.
                                                                                                                                                                                                                             407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 KPVVK-----KEERQNVNTLPTTGEESN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=92333688; PubMed=1321287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 G
46617 MW;
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us-09-847-539a-6.std.rsp

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114 EEQAQREA-EITAKREAELKAEREAAEKAKRDASDKAKRDAAEKDKVSNQQTDEMTKTAQ 172
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1196
1290
                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                       15-JUL-1998
                                                                                                                                            01-0CT-1996
                                                                                                       XCPC_XENLA
P50532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                  RESULT 23
XCPC_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                 Steffensen S.A.D.A., Poulsen A.B., Fage-Larsen J., Korsager B., Mortensen K.K., Sperling-Petersen H.U.;
"Sequence of the infe gene from Enterobacter cloacae.";
Submitted (NOV-1997) to the EMBL/Genbank/DbBJ databases.
"I- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION OF PROTEIN SYNTHEESTS IN VITRO, PROTECTS FORNYLMETHIONYL-TRNA FROM SPONTANEOUS HYDROLYSIS AND PROMOFTES ITS BINDING TO THE 30S RIBOSOMAL SUBBNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||:|| :: | |:: | 54 GSAPDKLTLQRKTRSTLANPGTGGKSKSVQIEVRKTRTFVKRDPQEAERLAAEEQAQREA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 IEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALA-----DQTDAL-QSEE 104
                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- ALTERNATIVE PRODUCTS: USING ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME, THE GENE TRANSLATES INTO THREE ISOZYMES:
ALPHA, BETA AND GAMMA.
-1- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INITIATION FACTOR IF-2-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INITIATION FACTOR IF-2-BETA. INITIATION FACTOR IF-2-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5F66372D567798BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor; Protein biosynthesis; GTP-binding;
initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR IF2-BETA.
FOR IF2-GAMMA.
G-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.7%; Score 98.5; DB 1; 21.8%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
(BY SIMILARITY)
                                                                    30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Translation initiation factor IF-2.
                                 897 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches
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InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ002736; CAA05703.1; -. EMBL; AJ002736; CAA05704.1; -.
                                                        (Rel. 39, Created)
(Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97892 MW;
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PROSITE; PS01176; IF2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
399
405
451
451
505
897 AA;
                                                                                                                   Enterobacter cloacae
                                                                  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          STRAIN-ECLAU9501;
                                                                                                                                                      NCBI_TaxID=550;
                                                     30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                          Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initiation f
Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                IF2_ENTCL
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INIT_MET
DOMAIN
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NP_BIND
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           RESULT 22
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entities requires a license agreement (See http://www.lab-sib.ch/announce/or send an email to license@lab-sib.ch).

EMBL: U13673: AAARARATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: REQUIRED FOR BOTH ASSEMBLY AND STRUCTURAL MAINTENANCE OF MITOTIC CHROMOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBGUNT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERODIMER.
-1- SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E MAS RECRUITED TO THE CHROMATIN AND
FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
-1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COLLED-COLL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-1- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 QTDALQSE----EAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAAT 1.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
105 AEVVQSDNAASD----AWEKAATPIALDVKK-TKDTKPVVKKEERQNVNTLPTTGEESN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirano T., Mitchison T.J.; "A heterodimeric colled-coil protein required for mitotic chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 NLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEA------ASSDALEALAD 67
                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 98.5; DB 1; Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coil; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALA/ASP-RICH (DA-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                              (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL)
                                                                                                                                                                                                        PRT; 1290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLY.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                   Chromosome assembly protein XCAP-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95042742; PubMed-7954811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146988 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    condensation in vitro."; Cell 79:449-458(1994).
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1027
1129
1290
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Pfam; PF02483; SMC_C;
Pfam; PF02463; SMC_N;
Mitosis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                        SYEP_DROME
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                                                                                                                                                                                                                          RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNAPTIC PLASMA MEMBRANES (BY SIMILARITY).
PTM: PHOSPHORYLATION OF THIS PROTEIN BY A PROTEIN KINASE C IS
SPECIFICALLY CORRELATED WITH CERTAIN FORMS OF SYNAPTIC PLASTICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      954
                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuromodulin (Axonal membrane protein GAP-43) (PP46) (B-50) (Protein FI) (Calmodulin-binding protein P-57) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNAPEKLALRNEERAIDELKKQ-----AIEDK--EATTAIEAASSDALEALADQTDALQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: THIS PROTEIN IS ASSOCIATED WITH NERVE GROWTH. IT IS A MAJOR COMPONETO OF THE MOTILE "GROWTH CONES" THAT FORM THE TIPS OF ELONGATING AXONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: BINDS CALMODULIN WITH A GREATER AFFINITY IN THE ABSENCE OF CA++ THAN IN ITS PRESENCE.
SIMILARITY: BELONGS TO THE NEUROMODULIN FAMILY.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
Serinus canaria (Canary).
Wararyota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Fringillidae;
Carduelinae; Serinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayton D.F., Jin H., Siepka S.M., Mello C.V., George J.M.; "Developmental regulation of GAP43 mRNA in the avian song control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF GROWTH CONE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurone; Phosphorylation; Membrane; Growth regulation; Calmodulin-binding; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY PKC)
986F846E27449AE0 CRC64;
                                                                                                                                                                                                                          241 AA
                                                                 124 PIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE 156
                                                                                                           ---- DLKKLEEKATTVMNECKEAECSLPEVQEQ 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSO0412; NEUROMODULIN_1; PARTIAL. PSO0413; NEUROMODULIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000048; IQ.
InterPro; IPR001422; Neuromodulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25018 MW;
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                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00612; IQ; 1.
SMART; SM00015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WASSERSCHLAGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                       NEUM_SERCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                    GAP43.
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Adams M.D., Celniker ScE., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Hichards S., Ashburner W., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Balzej R.G., Champe M., Pfeiffer B.D.,
An K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Brits K.C., Busam D.A., butler H., Cadleu E., Center A., Chandra I.,
A Brits K.C., Busam D.A., butler H., Cadleu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A dooson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Brosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Muttei B.E., McOltosh T.C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nixon K., Nusskern D.R., Pacleb J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92097547; PubMed-1756734;
Cerini C., Kerjan P., Astier M., Gratecos D., Mirande M., Semeriva M.;
A component of the multisynthetase complex is a multifunctional
aminoacy1-tRNA synthetase.";
EMBO J. 10:4267-4277(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                             74 SEEAAVVKADNAASDALEALADQ--TDALQSEEAEVVQSDNAASDAWEKAATPIALDVKK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerini C., Semeriva M., Gratecos D.;
"Evolution of the aminoacyl-tRNA synthetase family and the organization of the Drosophila glutamyl-prolyl-tRNA synthetase gene. Intron/exon structure of the gene, control of expression of the two manas, selective advantage of the multienzyme complex.";

Bur. J. Blochem. 244:176-185(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P28668; Q9VCF5;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase (EC 6.1.1.77) (Glutamate--tRNA ligase); Prolyl-tRNA AATS-GLUPRO OR CG5394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1714 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                         132 TKDTKPVVKKEERQN 146
                                                                                                                                                                                                                                                            151 STDNSPSLKADEAQD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Schert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Kflamos I., Simpson M., Strong R. Ber.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Stirskas R., Woodage T., Wolgeleton M., Weissenbach J.,
RA Williams S.M., Woodage T., Wolly K.C., Wu D., Yang S., Yao Q.A.,
RA Steng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
CATALYIC ACTIVIT: ATP + L-glutamate + tRNA(Glu) = AMP +
Glbbosphate + L-glutamyl-tRNA(Glu).
CC -I-CATALYIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
Glbbosphate + L-prolyl-tRNA(Glu).
CC -I-CATALYIC COMPONENT OF THE WILTISYMTHETASE COMPLEX WHICH IS
COMPOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMIL-PROLYL-TRNA SYNTHETASE AS WELL AS THREE AUXILIARY
CC -I-SUMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CLASS-I
AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -I-SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-I
AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -I-SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-I
AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -I-SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-I
AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -I-SIMILARITY: IN THE C-TERMINAL.
CC -I-SIMILARITY: CONTAINS G WHELE AS TOWN STANDARD STANDARD STANDARD STANDARD STANDARD STAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0987; TRNASYNTHGLU.
PRINTS; PR01046; TRNASYNTHGLU.
PROSTTE; PS00178; AA_TRNA_LIGASE_I: 1.
PROSTTE; PS00139; AA_TRNA_LIGASE_II_1; FALSE_NEG.
PROSTTE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
PROSTTE; PS00762; WHEP_TRS_; 6.
Aminoacyl_tRNA synthetase; Protein blosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUTAMYL-TRNA SYNTHETASE
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PROLYL-TRNA SYNTHETASE.
"HIGH" REGION.
"KMSKS" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M74104; AAA28594.1; --
EMBL; U59921; AAC47469.1; --
EMBL; AE003745; AAF56211.1; --
FIR; S18644; S1864.
HSSP; P00962; 1GTR.
FIYBASE; FBGN0005674; AALS-Glupro.
Interpro; IPR002106; AA_tRNA_ligase_II.
Interpro; IPR004046; GST_C.
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WHEP-TRS 3.
WHEP-TRS 4.
WHEP-TRS 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR004154; HGTP_anticodon.
Interpro; IPR000138; WHEP-TRS.
Interpro; IPR000924; tRNA-synt_IC.
INTERPRO; IPR001412; tRNA-synt_IC.
INTERPRO; IPR001412; tRNA-synt_I.
INTERPRO; IPR001316; tRNA-synt_I.
INTERPRO; IPR001316; tRNA-synt_Pro.
FRam; PF000443; GST_C; 1.
Pfam; PF00149; tRNA-synt_IC; 1.
Pfam; PP00149; tRNA-synt_IC; 1.
Pfam; PP00149; tRNA-synt_IC; 1.
Pfam; PP001469; WHEP-TRS; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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1080 LALKGEYKTLSGKDWTPDAKSEPAVVKKEASPV--SMASPAKDELTQEINA-QGEKVRAA 1136
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            28 LALRNEERAI------DELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-90037002: PubMed-2553724;
Maki M., Bagci H., Hamaguchi K., Ueda M., Murachi T., Hatanaka M.;
"Inhibition of calpain by a synthetic oligopeptide corresponding to
an exon of the human calpastatin gene.";
J. Biol. Chem. 264:18866-18869(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee W.J., Ma H., Takano E., Yang H.O., Hatanaka M., Maki M.;
"Molecular diversity in amino-terminal domains of human calpastatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-91124109; PubMed-2577276;
Asada K., Ishino Y., Shimada M., Shimojo T., Endo M., Kimizuka F.,
Asato I., Maki M., Hatanaka M., Murachi T.;
"CDNA cloning of human calpastatin: sequence homology among human,
pig, and rabbit calpastatins.";
J. Enzym. Inhib. 3:49-56(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Buteleostoml,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uemori T., Shimojo T., Asada K., Asano T., Kimizuka F., Kato I.,
Maki M., Hatanaka M., Murachi T., Hanzawa H., Arata Y.;
                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1714;
ATP (BY SIMILARITY).
TSPLP -> DKSIA (IN REF. 3).
VC -> AF (IN REF. 3).
NTACA -> KYCVR (IN REF. 3).
L -> A (IN REF. 3).
T -> S (IN REF. 3).
T -> S (IN REF. 3).
T -> S (IN REF. 3).
F -> T (IN REF. 3).
F -> P - T (IN REF. 3).
F -> P - T (IN REF. 3).
G -> V (IN REF. 3).
MISSING (IN REF. 3).
MISSING (IN REF. 3).
G -> V (IN REF. 3).
MISSING (IN REF. 3).
G -> V (IN REF. 3).
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Matches 39; Conservative 27; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calpain inhibitor (Calpastatin) (Sperm BS-17 component).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-283 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: | |||: | | |||: | 1197 VK----KEPADASGAVKKOTRLG---LEATKEDNLP 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 IALDVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                12.4%; Score 96; 25.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by exon skipping.";
J. Biol. Chem. 267:8437-8442(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92235069; PubMed=1569094;
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                                                                                                                                                                                                                                                                                                       189197 MW;
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       441
106
234
345
583
583
692
753
802
873
1201
1201
1587
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                                                                                                                  692 65
753 77
802 88
873 8
873 8
1201 1201
1461 1461
1587 156
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P20810;
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RNFC_ECOLI
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                                                                                                                                                                                                                                                                                                                                                  'Phosphorylation and subcellular distribution of calpastatin in human
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95221646; PubMed-7706496; Despres N., Talbot G., Plouffe B., Boire G., Menard H.A.; Despres N., Talbot G., Plouffe B., Boire G., Menard H.A.; Despres N., Talbot G., Plouffe B., Boire G., Menard H.A.; Detection and expression of a cDNA clone that encodes a polypeptide containing two inhibitory domains of human calpastatin and its recognition by rheumatoid arthritis sera."; J. Clin. Invest. 95:1891-1896(1995).
                                                                                                                                                                                                                                                                                                                  MEDLINE=91139699; PubMed=1995645;
Adachi Y., Ishida-Takahashi A., Takahashi C., Takano E., Murachi T.,
"Characterization of a functional domain of human calpastatin.";
                              SEQUENCE OF 153-708 FROM N.A. (SHORT ISOFORM), AND REVISIONS.
                                                                                                                                                                                                                                                                 El-Amine M., Talbot G., Despres N., Asselin C., Boire G.,
                                                  Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00748; Calpain_inhib; 4. Repeat; Thiol protease inhibitor; Alternative splicing;
                                                                                                       S.S.;
         Biochem. Biophys. Res. Commun. 166:1485-1493(1990)
                                                                                                     Wang L.F., Wel S.G., Miao S.Y., Liu Q.Y., Kolde "Calpastatin gene in human testis.";
Blochem. Mol. Biol. Int. 33:245-252(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001259; Calpain_inhib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA52066.1; JOINED.
AAA52066.1; JOINED.
AAA52066.1; JOINED.
AAA52066.1; JOINED.
AAA52206.1; -.
                                                                                            MEDLINE-95038502; Pubmed-7951045;
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                                                                       SEQUENCE OF 523-708 FROM N.A.
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                                                                                                                                               SEQUENCE OF 425-708 FROM N.A.
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                                                                                                                                                           TISSUE-Placenta;
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                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION
                                                                                  TISSUE-Testis;
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                                                                                                                                                                                                                                                                            Menard H.A.;
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                                          Wang L.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 LLPEPEEKPKPRSESELIDELSEDFDRSECKEKPSKPTEKTEESKAAAPAPVSEAVSRTS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 --ALQS--EEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKA---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 LLGNAPEKLALRNEERAIDEL-----KKQAIEDKEATTAIEAASSDALEALADQTD 70
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--- COFACTOR: Binds 2 4FE-4S clusters (Potential).
--- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC, rnfD, rnfE and rnfG (By similarity).
--- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 708;
L.
INHIBITORY DOMAIN 1.
INHIBITORY DOMAIN 2.
INHIBITORY DOMAIN 3.
INHIBITORY DOMAIN 4.
MISSING (IN SHORT ISOFORM).
G -> E.
FTId-VAR_005298.
R -> L. (IN REF. 5).
VKD -> GKE (IN REF. 5).
VKD -> GKE (IN REF. 5).
WKD -> GKE (IN REF. 8).
MISSING (IN REF. 8).
MISSING (IN REF. 8).
WR. CACD759C9284E3EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                             64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 EKLGEKEETIPPDYRLEEVKDKDGKPLLPKESKEQ---LPPMSED 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Electron transport complex protein rnfc.
                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 17;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Score 95.5;
                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                         76484 MW;
                                                                                                                                                                                                                                                                                                                                                                              12.3%; 27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                               467
486
486
543
562
708 AA;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNFC OR B1629
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                     VARSPLIC
                                                                                                                                                        VARIANT
                                                                                                                                                                                                                  CONFLICT
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Proc. Natl. Acad. Sci. U.S.A. 95:12625-12630(1998).
                                                                                                                                                                                                                                                                     Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                     7;
 -!- SIMILARITY: BELONGS TO THE 4FE4S BACTERIAL-TYPE FERREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QSEEAAVVKA----DN----AASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLALRNEERAIDELK-----KQAIEDKEATTAIEAASSDALEALADQTDAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Menozzi F.D., Bischoff R., Fort E., Brennan M.J., Locht C., "Molecular characterization of the mycobacterial heparin-binding hemagglutinin, a mycobacterial adhesin.";
                                                                                                                                                                                                                                                                             IRON-SULFUR (4FE-4S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                                                                          PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
Electron transport; Iron-sulfur; 4Fe-4S; Inner membrane;
Complete proteome. 377 IRON-SULFUR (4FE-4S) (POTEN
METAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMA_MYCTU STANDARD; PRT; 198 AA. 01142.2 085733; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Heparin-binding hemagolutinin (Adhesin). Heparin tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-M.tubercolosis, and M.bovis;
STRAIN-H37Rv, H37Ra, and BCG / Paris 1173 P2;
MEDLINE-98445421; PubMed-9770536;
                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                             Score 95.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATPIALDVKKTKDTKPVVKKEERQNVNTLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 RKTAVEAAIARAK-----ARKLEQQQANAEP 580
                                                                                                                                                                       HSSP; P00198; 1FCA.
EcoGene; E013935; rnfC.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001949; Complex1_51K.
Pfam; PF01512; Complex1_51K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria;
                                                                                                                             EMBL; AE000258; AAC74701.1; -.
                                                                                                                                                                                                                                                                                                                                                                      80171 MW;
                                                                                                                                       D90806; BAA15384.1; -. D90807; BAA15391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             12.3%;
26.5%;
                                                                                                                                                            D90808; BAA15414.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                    40; Conservative
                                                                                                                                                                                                                                fer4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                     740 AA;
          RNFC SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                   383
387
416
419
422
426
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                              METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
HBHA_MYCTU
                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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ADMERRENCE TO ENTIRELY ATTRADILMONARY DISSEMINATION. MEDIATES

CLYCOCONJUGATES PRESENT AT THE SUBRACE OF THESE CELLS. BINDS

CLYCOCONJUGATES PRESENT AT THE SUBRACE OF THESE CELLS. BINDS

CLYCOCONJUGATES PRESENT AT THE SUBRACE OF THESE CELLS. BINDS

HEPARIN, DEXTRAM SULFATE, FUCCIDAN AND CHONDROITIN SULFATE.

PROMOTES MEMAGGLUTINATION OF ERYTHMCKYTES OF CERTAIN HOST SPECIES.

INDUCES MYCOBACTERIAL AGGREGATION.

C. IS UBCELLULAR LOCATION. SUBFACE ASSOCIATED.

C. IS UBCELLULAR LOCATION. SUBFACE ASSOCIATED.

C. ID DOMAIN OF HBHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL END

DIMINISH THE AFFINITY FOR HEPARIN.

C. INTRODUCTION OF HEMARIN.

C. INTROUCTION OF 
                           SPECISS-W. tuberculosis, STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
Cole S. T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Nurphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: SERUM FROM PATIENTS DIAGNOSED WITH ACTIVE TUBERCULOSIS THAT HAD NOT BEEN VACCINATED CONTAINS ANTIBODIES THAT RECOGNIZE HBHA, WHEREAS SERUM FROM HEALTHY INDIVIDUALS DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DoeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The heparin-binding haemagglutinin of M. tuberculosis is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUGGESTS THAT THE CARBOHYDRATE MOIETY MAY BE LOCATED WITHIN THE C-
TERMINAL DOMAIN OF HBHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole genome comparison of Mycobacterium tuberculosis clinical and
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Menozzi F.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-M.tuberculosis, and M.bovis;
STRAIN=H37Ra, and BCG / Paris 1173 P2;
MEDLINE-97188915; Pubmed-9064359;
Menozzi F.D., Rouse J.H., Alavi M., Laude-Sharp M., Muller J.,
Bischoff R., Brennan M.J., Locht C.;
"Identification of a heparin-binding hemagglutinin present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-M.tuberculosis; STRAIN-CDC 1551 / Oshkosh;
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MEDLINE-21342355; PubMed-11449276;
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J. Exp. Med. 184:993-1001(1996).
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SEQUENCE FROM N.A.
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us-09-847-539a-6.std.rsp

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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                               POTENTIAL.
PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 95; 30.9%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein, serotype 6 precursor.
                                                                                                                                                                                                                                                                                                                                                              39831 MW;
                                                                                            EMBL; U32722; AAC22041.1; -. EMBL; U32470; AAC44596.1; -. HSSP; P04002; 1ATF.
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                      323
333
372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1314;
                                                                                                                                TIGR; HI0383; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 ERQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 EAE 213
                                                                                                                                                                                                                                                                                                                                                                                                            38;
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P08089;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                               58 SSDALEALADQTDALQSEEAAVVKADNAASDALE-----ALADQTDALQSEEAEVVQS 110
                                                                                                                                                                                                                                                                               MEDLINE-95350630; PubMed-7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Felischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterpack T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                  3 SPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTA----IEAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sen K., Sikkema D.J., Murphy T.F.; "Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA and tolB genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY). SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                         TIGR; MT0493; -.
TubercuList; Rv0475; -.
Cell adhesion; Heparin-binding; Hemagglutinin; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                  12.2%; Score 95; DB 1; Length 198; 28.9%; Pred. No. 4.9;
                                                                                                                                                                                          70; Indels
                                                                                                                               R -> P (IN REF. 1).
513760F6F1EB6042 CRC64;
                                                                                                                                                                                                                                                                                                              111 DNAASDAWEKAATPI--ALDVKKTKDTKPVVKKEERQNV 147
                                                                                                                                                                                                                                                                                                                                      157 ЕГРККААРАККААРАККААРАККАРАККАРАККА
                                                                                                                                                                                                                                                                                                                                                                                               TOLA_HAEIN STANDARD; PRT; 372 AA. P44678; P94810; 01-NOV-1995 (Rel. 32, Created) 1-NOV-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                          19; Mismatches
                                                                                                                     ALA/LYS-RICH.
or send an email to license@isb-sib.ch).
                                              EMBL; AE006951; AAK44716.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=1479;
MEDLINE=97080550; PubMed=8921895;
                       EMBL; AF074390; AAC26052.1; -.
                                                                                                                                            21403 MW;
                                                                                             Virulence; Complete proteome. INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
                                                                                                                                                                                          46; Conservative
                                                                                                                    193
                                    CAB00936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tolR, tolA and tolB Gene 178:75-81(1996)
                                                                                                                                          .198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tola protein.
Tola OR HI0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus
                                                                                                                                            SEQUENCE
                                                                                                                                                                  Query Match
                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                    TOLA_HAEIN
                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 EELKROOEOOROOEIKKOO-----EQAROEALEKOKOAEEAKAKOAAEAAKLKAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALE--ALADQTDALQSEEAAVVKAD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V -> A (IN STRAIN 1479).
K -> R (IN STRAIN 1479).
A -> P (IN STRAIN 1479).
A -> R (IN STRAIN 1479).
V -> A (IN STRAIN 1479).
D -> A (IN STRAIN 1479).
A -> ARAABAKAKA (IN STRAIN 1479).
I -> A (IN STRAIN 1479).
I -> A (IN STRAIN 1479).
I -> V (IN STRAIN 1479).
I -> V (IN STRAIN 1479).
N -> S (IN STRAIN 1479).
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MEDLINE-85166224; PubMed-3885219;
Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Indels
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-> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
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STRAIN 1479)
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NCBI_TaxID=1314;
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DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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6
                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).

10 x 7 AA TANDEM REPEATS.

4.5 x 25 AA TANDEM REPEATS.

TWO DIRECTLY REPEATED 27 AMINO ACID BLOCKS SEPARATED BY 15 AMINO ACIDS. HYDROPHILE.

GLYPRO-RICH (CELL WALL-SPANNING).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOTDALQSEEAAVVKAD-NAASDAL-EALADQTDALQSEEAEVVQSDNAASDAWE---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 EESKKLTEKEKAELQAKLEAEAKALKEQLAKQAEELAKLRAGKA-SDSQTPDAKPGNKVV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LANLTAELDKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKLAALEKLNKEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LGNAPEKLALRNEERAIDELKKQAIE------DKEATTAIEAASSD--ALEAL---A 66
                                        OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                       Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02770; M; 9.
PRINTS; PR00015; GPOSANCHOR:
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Virulence; Phagocytosis; Cell wall; Repeat; Antigen; Transmembrane; Colled coll; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
                                                                            -i- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
-i- SIMILARITY: TO OTHER W PROTEINS.
-i- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 95; DB 1; Length 483; 29.6%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Indels
                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS.
68F87F28DB53A448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 --KAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 PGKGQAPQA--GTKPNQNKAPMKETKRQ----LPSTGETANP 458
                                                                                                                                                                                                                                                                                                                                                                                PROTEIN, SEROTYPE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
M protein, serotype 12 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 AA
                                                                                                                                                                                                                                                    PIR; A26297; A26297.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 16, Created)
(Rel. 16, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53472 MW;
                                                                                                                                                                                                                                         EMBL; M11338; AAA26920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                483
457
477
483
138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               69
157
279
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01-NOV-1990 (
16-OCT-2001 (
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P19401;
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DOMAIN
TRANSMEM
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M12_STRPY
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                                                                                                                            STRIN-CS24 / Serotype M12;
MEDLINE-88058777; Bubmed-2445730;
Robbins J.C., Spanler J.C., Jones S.J., Simpson W.J., Cleary P.P.,;
"Streptococcus pyogenes type 12 M protein gene regulation by upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
GLY/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 LANLTAELDKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKLAALEKLNKDL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 DOTDALQSEEAAVVKAD-NAASDAL, EALADQTDALQSEEAEVVQSDNAASDAWE---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: | :: | ::| | ::| | 457 EESKKLTEKEKAELQAKLEAEAKALKEQLAKQAEELAKLRAGKA-SDSQTPDAKPGNKAV 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LGNAPEKLALRNEERAIDELKKQAIE------DKEATTAIEAASSD--ALEAL---A 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00746; Gram_pos_anchor; 1.
Parai; PS00343; 9.
PROSITE; PS00143; GRAM_POS_ANCHORING; 1.
Virulence; Phagocytosis; Cell wall; Repeat; Antigen; Transmembrane;
                                                                                                                                                                                                                                                                                       SUBCELLUIAR LOCATION: Type I membrane protein. Gell wall. SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2%; Score 95; DB 1; Length 564; 29.6%; Pred. No. 15; 1ve 22; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62904 MW; SF1549DACAA77B46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN, SEROTYPE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 -- KAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 PGKGQAPQA--GTKPNQNKAPMKETKRQ----LPSTGETANP 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1077 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A60115; A60115.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M18269; AAA88573.1; -.
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550
>564
505
541
547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 AA;
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SEQUENCE FROM N.A.
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01-FEB-1994 (Rel.
Hairless protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                           h. Dev. 38:143-156(1992).
FUNCTION: IS A POTENT ANTAGONIST OF NEUROCENIC GENE ACTIVITY
BURNCTION: IS A POTENT ANTAGONIST OF NEUROSESION OF DISTINCT CELL
BURING SENSORY ORGAN DEVELOPMENT. THE EXPRESSION OF DISTINCT CELL
FATES BY THE TRICHGEN (SHAFT) / TORMOGEN (SOCKET) SISTER CELL
PAIR DEPENDS ON THE LEVEL OF H ACTIVITY. A CERTAIN THRESHOLD LEVEL
OF H ACTIVITY IS REQUIRED, BELOW WHICH BOTH SISTER CELLS ADOPT THE
                                                                                                                               controls alternative cell fates in adult sensory organ development."; Genes Dev. 6:1752-1769(1992).
               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 DOPWKOSR--PRRGISKELSLFFHRPRNSTLGRAALRTAARKRRPHEPLTTSEDQQPIF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALAD-QTDALQSEEAEVVQ 109
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=93041287; Pubmed=1419850;
Maler D., Stumm G., Kuhn K., Preiss A.;
"Hairless, a Drosophila gene involved in neural development, encodes a novel, serine rich protein.";
Mech. Dev. 38:143-156(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSPIEQPRIIPNGCTLTNL------LGNAPEKLALRNEERAIDELKKQAIEDKEA 50
                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: OVARY, EMBRYOS, LARVAL AND PUPAL IMAGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 ATAIKAENGD------DTLKAEAAEAVEIENV-----AVADTTTNEIKIEKPDTIK
                                                                                                   Bang A.G., Posakony J.W.; "The Drosophila gene Hairless encodes a novel basic protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEDDA-ERLEKEPKKAVSDDSESKEASPGQQVEPQPKDETVDVEMKMNTSEDEEP 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDNAASDAWEKAATPIALDVKKTKDTKPVVK-----KEERQNVNTLPTTGEESNP 159
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1077;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN REF. 2).
W; A94BF1A27579E2F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S -> A (IN REF. 2).

QH -> LL (IN REF. 2).

A -> R (IN REF. 2).

AAVA -> RLLP (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 32;
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%; Score 94.5;
                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS A "PRD MOTIF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M95192; AAA28607.1; ALT_INIT.
EMBL; X67239; CAA47664.1; -.
                                                                                     MEDLINE-92387549; PubMed-1516831;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
702
702
891
864
974
974
977 AA;
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                   TORMOGEN FATE.
                           Ephydroidea; Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP: P04002:
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CONFLICT
SEQUENCE
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RESULT 33

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 ALADQTDALQSEEAEVVQSDNAAS-----DAWEKAATPIALDVKKTKDTKPVVKKE--- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 QIAEHSEQVQTQEEKISWLENQVMAMASNLQMMQEAVTALTVSQSLTPEPSPVPAVEVEA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 IDELKKQAIEDKEATTAIEAAS--SDALEALADQTDALQSEEAAVVKADNAAS---DALE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecium (Streptococcus faecium).
Bacteria: Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                           Bamford J.K.H., Haenninen A.-L., Pakula T.M., Ojala P.M.,
Kalkkinen N., Frilander M., Bamford D.H.;
Genome organization of membrane-containing bacteriophage PRD1.";
Virology 183:658-676(1991).
-i- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Tectlviridae; Tectivirus.
NCBI_TaxID=10658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuerst P., Moesch H.-U., Solioz M.;
Fuerst P., Moesch H.-U., Solioz M.;
"A protein of unusual composition from Enterococcus faecium.";
Nucleic Acids Res. 17:6724-6724(1989).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL-WALL.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 AA; 17573 MW; DC6D2DBE282195DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                 (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.0%; Score 93.5; DB Best Local Similarity 24.6%; Pred. No. 5; Matches 35; Conservative 32; Mismatches
     166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-6.
MEDLINE-91306449; Pubmed-1853567;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89385998; PubMed-2780297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 -- ERONVATLPTTG--- EESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 MPEAVTVEILPESAGDQQEAEP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M69077; AAA32462.1; -. PIR; H40477; WMBPP6.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P54 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                 Bacteriophage PRD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-1352;
                                                 01-AUG-1992 (
01-AUG-1992 (
01-DEC-1992 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus
VP06_BPPRD
P27379;
                                                                                                                               Protein P6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P54_ENTFC
P13692;
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOES_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 36
MOES_MOUSE
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entitles and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 ENEAKOKELADNOAALESQKGDLLAKQADLNVLKTSLAAEQATAEDKKADLNRKKAEAEA 226
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 EQARIREQARLAEQA ---- RQQAAQEKA EKE AREQAAAQAAQTQAL - SSASTTTESSSAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSPIEQPRIIPNGGTLTNLLGNAPEKLALRN-----EERAIDELKKQAIEDKEATTAI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasm and cortical cytoskeleton. MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H. Imamura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.: "Isolation and characterization of a novel actin filament-binding protein from Saccharomyces cerevisiae.";
Oncogene 16:121-130(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.; "Sequence and analysis of a 26.9 kb fragment from chromosome XV the yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1- FUNCTION: Binds F-actin and shows weak F-actin crosslinking
                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                    Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                 POTENTIAL.
402ECAA439846D26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 QSSSEESKAP---ESSTITEESTSTESSTITENSSTGSSSTESSS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 SDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABPX_YEAST STANDARD; PRT; 627 AA. 008641; 008644; 16-0CT-2001 (Rel. 40, Created) 116-0CT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 17;
; Mismatches
                                                                                                                                                                                                                                                    POTENTIAL.
P54 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                  12.0%; Score 93.5; 25.0%; Pred. No. 17
                                                                                                               EMBL; X16421; CAA34442.1; ALT_INIT.
PIR; S05542; S05542.
MEROPS; C40.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE-97127829; PubMed-8972580;
                                                                                                                                                                                                                                                    1 27 PO
28 516 P55
429 429 PO
516 AA; 54596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                   InterPro; IPR000064; NLPC_P60.
Pfam; PF00877; NLPC_P60; 1.
Signal; Cell wall. 27 P
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actin-binding protein ABP140.
ABP140 OR YOR239W/YOR240W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR LEU-276 AND GLY-277.
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast 12:1575-1586(1996).
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                 ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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AD ABPX_YI
AD ABPX_YI
AD ABPX_YI
AD ABPX_YI
AD 116-0CT
DT 16-0CT
DT 01-1AAR
DE ACLINAR
D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 QSEEAAVVKADNAASDALEALADQTDA--LQSEEAEVVQSDNAASDAWEKAATPIALDVK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 KNDESEEESANNASEPAEEYSQSEEDADIEQSNGKETENAENASQQA-NDGSTSTTTSKN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato N., Funayama N., Nagafuchi A., Yonemura S., Tsukita S., Tsukita S.;
"A gene family consisting of ezrin, radixin and moesin. Its specific localization at actin filament/plasma membrane association sites.";
J. Cell Sci. 103:131-143(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 KLALRNEERAIDELKKQAIEDKEATTAIEAAS----SDAL-EALADQTDAL------ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                           12.0%; Score 93.5; DB 1; Length 627; 28.1%; Pred. No. 21; ive 23; Mismatches 60; Indels 1
                                                                                                                                                                                                                                                                                                                                                                  627 AA; 71354 MW; D4E55F9485412F39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Moesin (Membrane-organizing extension splike protein).
                                                                                                                                 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93055012; PubMed-1429901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S47577; AAA11762.1; -. EMBL; M86390; AAA39728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 KTKDTKPVVKKEERQNVNT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKKKNKKKNKKKRNGNVNT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 11-576 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.0%
Best Local Similarity 28.1%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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us-09-847-539a-6.std.rsp

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SEQUENCE OF 9-1278 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alstrom syndrome.";
Genomics 53:359-364(1998).
                                                                                                                                                                              somerase; Rotamase
                                                                                                                                                                                                SEQUENCE 361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
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                                                                                                                                                                                                                                                                                        71 ALQSEEAAVVKADNAASDALEAL---ADQ---TDALQSEEAEVV------OSDNA 113
                                                                                                                                                                                                                                 20 LLGNAPEKLAL-----RNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTD 70
                                                                                                                                                                                                                                                                                                                                                                                                        074191; 090TU5;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
878.06 binding protein 39 kDa (Peptidyl-prolyl cis-trans isomerase)
(PPiase) (EC 5.2.1.8).
FKBP39 OR SPBC1347.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Himukai R., Kuzuhara T., Horikoshi M.;
"Structural classification of FKBP-type peptidyl prolỳl cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           38
                                                                                                                                                                                                                                                                                                                      114 ASDAWEKAATPIALDVKKTKD------TKPVVKKEERQNVNTLPTTGE 155
                                                                                                                                                                                                                                                                                                                                  : |:: | : |::|| : | : | : | 440 EAVEWQQKAQMVQEDLEKTRAELKTAMSTPHVAEPAENEHDEQDENGAEASAE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of GFP-gene fusion library of fission
                                                                                                                                                                                       DB 1; Length 576;
                                                                                                                                                                                                           65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                               BAND 4.1-LIKE.
EL -> DV (IN REF. 2).
RA -> SP (IN REF. 2).
5E0F455552E9145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                              12.0%; Sco. 23.7%; Pred. No. 20. . . . . . . 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                361 AA
                                                                                                                      BY SIMILARITY.
MGD; MGI:97167; Msn.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ezrin_radixin_moesin.
                              Fram: PF00333; Band_41; 1.
Fram: PF00769; ERM: 1.
FRINTS: PR00935; BAND41.
SMART; SM00295; B41; 1.
FROSITE: PS00660; BAND_41.1; 1.
PROSITE: PS00661; BAND_41.2; 1.
PROSITE: PS500657; BAND_41.2; 1.
Structural protein; Cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                 67635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-145 FROM N.A.
STRAIN-968 H90;
                                                                                                                                                                                                Local Similarity 23.7 tes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isomerases (PPIase).
                                                                                                                              57 2
330 3
370 3
576 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-JY741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                FKB4_SCHPO
                                                                                                                                                     CONFLICT
                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYNA_BUMAN STANDARD; PRT; 1278 AA.
014203; 095296; 09UIU2;
01-NOV-1997 (Rel. 36, Created)
16-OCT-2001 (Rel. 36, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Dynactin 1 (150 kDa dyncin-associated polypeptide) (DP-150) (DAP-150)
0CT-100-91ued) (p135).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 OSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 SGDATIHLSGN-----FLVDEE----DEEEEESDEDYD----LSPTEEDLVETVSGDEESE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 NGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDAL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97009557; Pubmed-8856662;
Tokito M.K., Howland D.S., Lee V.M.-Y., Holzbaur E.L.F.;
"Functionally distinct isoforms of dynactin are expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJINE-99017972; PubMed-9799602;
Collin G.B., Nishina P.M., Marshall J.D., Naggert J.K.;
"Human DCTN1: genomic structure and evaluation as a candidate for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
11.9%; Score 92.5; DB 1; Length 361;
Best Local Similarity 22.4%; Pred. No. 13;
Matches 36; Conservative 33; Mismatches 51; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 9-1278 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FA44DF1D12622A82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 K------DTKPVVKKEERQNVNTLPTT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 KVEGTPVKEKKVAFAEKLEQGPTGPAAKKEKQQASSNAPSS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holzbaur E.L.F., Tokito M.K.;
"Localization of the DCTNI gene encoding pl
2p13 by fluorescence in situ hybridization.
Genomics 31:398-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00453; FKBP_PPIASE_1; 1. PROSITE; PS00454; FKBP_PPIASE_2; 1. PROSITE; PS50059; FKBP_PPIASE_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96435441; PubMed-8838327;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001179; FKBP_PPlase, Pfam; PF00254; FKBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 PC
39301 MW;
                                                                                                                                                                                                                                              EMBL, AF017990; AAC29477.1; -. EMBL, AL035648; CAB37433.1; -. EMBL, AB027991; BAA87295.1; -. HSSP; P20071; 1BKF.
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/FTId=VAR_001373

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Complete proteome.
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                     CONFLICT
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SEQUENCE
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TRANSMEM
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                                                                                                                                MAOSKRHVYSKTPSGSRMSAEASARPLRVGSRVEVIGKGHR
GTVAYVGATLEATGKWGVILDEAKGKNDGTVGGRKYFTCD
EGGGIFVYROSOIQVFEDGADTTSPETPDSSASKVLKREGTD
TTAKTSKL -> MMRQ (IN ISOFORM P135)
                                                                                                                                                                                                                                                                                                                                - SUBCELLULAR LOCATION: CYtoplasmic.
- SUBCELLULAR LOCATION: Cytoplasmic.
- ALTERRATIVE PRODUCTS: 2 ISOFORMS; P150 (SHOWN HERE) AND P135;
- ARE PRODUCED BY ALTERNATIVE SPLICING.
- ITSSUE SPECIFICITY: BRAIN.
- PTM: PHOSPHORYLATED.
- SIMILARITY: CONTAINS 1 CAP-GLY DOMAIN.
                                                                                     Tokito M.K., Holzbaur E.L.F.; The genomic structure of DCTN1, a candidate gene for limb-girdle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01302 CAP_GLY.
PROSITE; PS00845; CAP_GLY_1.
PROSITE; PS50245; CAP_GLY_2; 1.
MOTOT proteln; Microtubules; Dynain; Colled coll; Cytoskeleton;
Alternative splicing; Phosphorylation.
DOMAIN
CAP-GLY.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SER-RICH
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EMBL, AF064203; AAD55811.1; JOINED.
EMBL, AF064204; AAD55811.1; JOINED.
EMBL, X98801; CAA67333.1; -.
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                     [4]
SEQUENCE OF 18-1278 FROM N.A.
MEDLINE-99023772; Pubmed-9805007;
Biol. Cell 7:1167-1180(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000938; CAP-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF086947; AAD03694.1;
EMBL; AF086927; AAD03694.1;
EMBL; AF086928; AAD03694.1;
EMBL; AF086929; AAD03694.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF086930; AAD03694.1;
AF086931; AAD03694.1;
AF086932; AAD03694.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF086933; AAD03694.1;
AF086934; AAD03694.1;
AF086935; AAD03694.1;
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EMBL; AF086937; AAD03694.1;
EMBL; AF086938; AAD03694.1;
EMBL; AF086939; AAD03694.1;
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1049
1211
131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF086930; FEMBL; AF086931; FEMBL; AF086932; FEMBL; AF086932; FEMBL; AF086932; FEMBL; FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF086944;
EMBL; AF086945;
EMBL; AF086946;
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MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MA GW.V., Konnedy S.P., Mahairas G.G., Berquist B., Pan M.,
A Swartzell S., Weil D., Hall J., Dahl T.A., Welti, R., Goo Y.A.,
Leithauser B., Keiler K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitasa T., Hou S., Danklas G.J., Dennis P.P., Omer A.D.,
Alam M., Freitasa T., Hou S., Danklas G.J., Dennis P.P., Omer A.D.,
Agan M., Freitasa T., Hou S., Danklas G.J., Dennis P.P., Omer A.D.,
Agan M., Freitasa T., Hou S., Danklas G.J., Dennis P.P., Omer A.D.,
Agan M., Freitasa T., Hou S., Danklas G.J., Dennis P.P., Omer A.D.,
Agan M., Freitasa T., Hou S., Danklas G.J., Dennis P.P., Omer A.D.,
The Concord M., Constant M., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Tenvor. Natl. Acad. Sci. U.S. A. 97:12176-121812000).
The CONTION: TRANSDUCES SIGNALES FROM THE PHOTOTAXIS RECEPTOR SENSORY
C. I. FUNCTION: TRANSDUCES SIGNALES FROM THE PHOTOTAXIS TO LIGHT
                                                                                                                                                                                                                                                               943 LKLEDRETVIKELKKSLKIKGEELSEANVRLSLLEKKLDSAAKDADERIEKVQTRLEETQ 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis protein II) (MPP-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
                                                                                                                    11.9%; Score 92.5; DB 1; Length 1278;
28.3%; Pred. No. 52;
:ive 21; Mismatches 39; Indels 11; Gaps
                                                                                                                                                                                                                16
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                                                                                                                                                                                                                   LALRNEERAIDELKKQ-AIEDKEATTA-----IEAASSDALEALADQTDALQSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
S -> N (IN REF. 2 AND 3).
MISSING (IN REF. 2 AND 3).
D -> V (IN REF. 2 AND 3).
MW; 6DCEA5E67856E4BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Methylation;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                     77 AAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAAS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           763 AA
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InterPro; IPR003606; HAMP.
Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCP8ignal; 1.
                                                                      1278 AA; 141694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE005080; AAG19989.1; -
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SMART; SM00283; MA; 1.
Transducer; Photoreceptor;
                                                                                                                                            Best Local Similarity 28.39
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Last Sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
protein II) (MPP-II).
HTR2 OR HTRII.
Halobacterium salinarium.
Archaea; Euryarchaeota; Halobacteriales; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAINFLXIS;
MEDLINE-96323203; PubMed-8710852;
MEDLINE-96323203; PubMed-8710852;
Among W., Broom A., Mueller M.F., Alam M.;
The primary structures of the Archaeon Halobacterium salinarium blue light receptor sensory rhodopsin II and its transducer, a methylaccepting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PICOC. NATIL ACAD. SCI. U.S.A. 93:8230-8235(1996).
-!- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR
SENSORY RHODOPSIN II (SR.II) TO THE FLACELLAR WOTOR. RESPONDS TO
LIGHT CHANGES THROUGH THE VARATION OF THE LEVEL OF METHYLATION.
-!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
                                                                                                                                                                                                        97 TDALQSEEAEVVQSDNAASDAWEKA---ATPIALDVKKT---KDTKPVVKKEERQNVNTL 150
                                                                                              Gaps
                                                                                                                        37 IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQ 96
                                                                                            17;
                                                            11.8%; Score 91.5; DB 1; Length 763; 29.1%; Pred. No. 35;
                                                                           29.1%; Pred. No. 30;
tive 20; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
W: 1E0D784E460FC588 CRC64;
                CYTOPLASMIC (POTENTIAL).
CF7A8FF04DFF309A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         764 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004089; Chemotaxis_transducer.
   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
                              78911 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U62676; AAC44369.1; -. HSSP; P02942; 1QU7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
Transducer; Photoreceptor;
                                                                            Best Local Similarity 29.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
278
298
763 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                151 PTTGEES 157
                                                                                                                                                                                                                                                                            613 KTLAEES 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-2242;
                                                                                                                                                                                                                                                                                                                                                        HTR2_HALSA
P71410;
                 DOMAIN
SEQUENCE
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TRANSMEM
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   TRANSMEM
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                                                                                                                                                                                                                                                                                                                        RESULT 40
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

 protein search, using sw model OM protein October 13, 2002, 04:38:53; Search time 43.3636 Seconds (without alignments) 352.328 Million cell updates/sec Run on:

US-09-847-539A-6 777 score:

1 VDSPIEQPRIIPNGGTLTNL.......KKEERQNVNTLPTTGEESNP 159 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	IqG-binding protei	protein G precurso	multiple ligand-bi	albumin-binding pr	S-antigen precurso	probable tail fibe	probable tail comp	sea 1	probable tail fibe	probable tail fibe		hypothetical prote	plasma protein rec	fcrA protein precu	extracellular matr	hypothetical prote		surface exclusion	probable tail fibe	tail		membrane spanning	Spann	probable tail fibe	tolA protein - Esc	hypothetical prote	O	centrosome-associa	fcrA 15 protein -
	ID	A24496	800128	567921	A44801	YAZON7	D90734	F85584	151116	H90854	B90835	C85693	T46231	S55890	S35760	T31110	OXBP1L	141024	S22452	G90907	E90968	E85816	F90725	G85576	690898	JV0057	T10699	A33939	T13802	S52536
	DB	~	~	7	7	-	~	~	~	~	ď	~	a	ď	~	~	Н	~	~	7	~	~	7	~	~	ď	ď	N	ď	C)
	Length	448	593	439	323	309	438	440	1110	437	971	973	166	413	415	2055	401	490	890	407	437	439	394	394	271	421	159	405	1096	388
ap (Query	24.2	24.1	19.5	•	16.9	16.5	16.5	15.8	15.4	15.4	15.4	14.9	14.7	14.3	14.3	14.2	14.2	14.2	14.1	14.1	14.1	14.0	14.0	14.0			13.9		13.8
	Score	188	187	151.5	138.5	131.5	128.5	128.5	122.5	119.5	119.5	119.5	116	114.5	111	111	110.5	110	110	109.5	109.5	109.5	109	109	108.5	108.5	108	108	108	107
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	probable tail fibe	hypothetical prote	probable tail fibe	fcrA protein precu	Mrp4 protein - Str	streptococcal surf	probable tail fibe	surface exclusion	EF protein - Strep	130K surface exclu	FmtB protein (impo		ATPase ScII, chrom	phage-related prot	tolA protein [impo
548385	E90996	G85631	G64887	S57834	A46173	S42574	C90169	S72375	533441	G41662	D90011	н89960	A54817	C97038	AG0592
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1679	437	375	1122	387	388	664	439	843	1822	891	2481	2186	1189	2052	376
13.8	13.7	13.6	13.6	13.5	13.5	13.5	13.4	13.4	13.4	13.4	13.4	13.3	13.3	13.2	13.1
107	106.5	105.5	105.5	105	105	105	104.5	104.5	104.5	104	104	103.5	103	102.5	102
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Streptococus sp.
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 17-Mar-2000
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 17-Mar-2000
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 17-Mar-2000
C;Accession: Askapader, P.; Nagle, J.; Filpula, D.
J; Bacteriol. 167, 870-880, 1986
J; Bacteriol. 167, 870-880, 1986
A;Title: Gene for an immunoglobulin-binding protein from a group G Streptococcus.
A;Reference number: A24496; MUID:86304178
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-448_cKBA1>
A; Crogs=references: 6B:M13825; NID:9153822; PIDN:AAA03664.1; PID:9153823
A; Crogs=references: GB:M13825; NID:9153822; PIDN:AAA03664.1; PID:9153823
R; Sjocbring, U.; Bjoerck, L.; Kästern, W.
A; BloL. Chem. 266, 399-405, 1991
A; Title: Streptococcal protein G. Gene structure and protein binding properties.
A; Reference number: A39041; MUID:91093154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.2%; Score 188; DB 2; Best Local Similarity 38.9%; Pred. No. 1.5e-05; Matches 61; Conservative 20; Mismatches 60;
IgG-binding protein - Streptococcus sp. (group G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 34-42,'N',45-48;62-76;186-200 <SJO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: spg
C;Superfamily: M5 protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A39041
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Gaps EAASSD 60 34 VDSPIEDTPIIRNGGELTNLIGNSETTLALRNEESATADLTAAAVADTVAAAAARNAGAA 93 16; 1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTA 60; Indels δ

9

61 ALEALADOTDALOSEEAAVVKADN--AASDALEAL---ADOTDALOSEEAEVVOSDNAA- 114 엄 δ g

115 -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE 142 à

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 19-May-2000 C;Accession: S00128; A94504; A26314 protein G precursor - Streptococcus sp. (Streptococcus G148)
N;Alternate names: albumin-binding protein; cell wall-bound/protein
C;Species: Streptococcus sp.
A;Variety: Streptococcus (3148
C;Date: 30-Jun-1969 #sequence_revision 30-Jun-1989 #text_change 19-M

Tue Oct 15 08:27:08 2002

10;

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of a group C streptococcal protein that binds to fibrinogen, album $67921; MUID:96202013
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C;Cacession: A44801
R;Sjobring, U.
Infect: Immun. 60, 3601-3608, 1992
A;Title: Isolation and molecular characterization of a novel albumin-binding protein A;Title: Isolation and molecular characterization of a novel albumin-binding protein A;Title: Isolation and molecular characterization of a novel albumin-binding protein A;Title: Isolation and molecular characterization of a novel albumin-binding protein A;Accession: A44801; MUID:92363555
A;Accession: A44801
A;Accession:
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           A;Title: Structure of a group C streptococcal protein that binds to fibrinoge A;Reference number: S67921; MUID:96202013
A;Accassion: S67921; MUID:96202013
A;Actatus: preliminary
A;Molecule type: DNA
A;Residues: 1-439 < TAL>
A;Residues: 1-439 < TAL>
A;Residues: 1-439 < TAL>
A;Residues: Li-439 < TAL>
A;Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ATPIALDVKKTKDTKPV-----VKKEERQNVNTLPTTGEESNP 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 151.5; DB 2; 27.2%; Pred. No. 0.004; ive 25; Mismatches 46;
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Matches 6
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A Molecule type: DNA
A Molecule to the cell wall structure of group G streptococci and is cova
C Molecule to the cell wall structure of group G streptococci and is cova
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C Molecule to the cell wall structure to the cell wall 
     R:Olsson, A.; Ellasson, M.; Guss, B.; Nilsson, B.; Hellman, U.; Lindberg, M.; Uhlen, M. Bur. J. Blochem. 168, 319-324, 1987
A.7Hile: Structure and evolution of the repetitive gene encoding streptococcal protein GA:Reference number: 800128; MUID:88023445
A.Accession: 800128; MUID:88023445
A.Accession: 800128
A.Molecule type: DNA
A.Residues: 1-593 < CLS>
A.Molecule type: DNA
A.Residues: 1-593 < CLS>
A.Note: par of this sequence, Emblay as Streptococcus G148
A.Note: part of this sequence, including the amino end of the mature protein, was confir R.Sjoebring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.
J. Immunol. 140, 1595-1599, 1988
A.7Hile: Isolation and characterization of a 14-kDa albumin-binding fragment of streptoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 62-101 <5J0>
R;Guss, B.; Ellasson, M.; Olsson, A.; Uhlen, M.; Frej, A.K.; Jornvall, H.; Flock, J.I.;
EMBO J. 5, 1567-1575, 1986
A;Title: Structure of the IgG-binding regions of streptococcal protein G.
A;Reference number: A26314; MUID:86300657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-Apr-1997 #text_change 20-Jun-2000
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A;Variety: serotype C20
C;Date: 19 Mar-1997 #sequence_revision 25-Ap
C;Accession: S67921
R;Talay, S.R.: Grammel, M.P.; Chhatwal, G.S.
Biochem. J. 315, 577-582, 1996
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F;216-266/Region: B
F;267-290/Region: A repeat
F;303-497/Domain: IgG binding
F;303-357/Region: C repeat
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F;428-442/Region: D
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Best Local S:
Matches 61,
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Query Match 15.8%
Best Local Similarity 29.4%
Matches 37; Conservative
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Matches 49; Conservative
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NF-180 - sea lamprey
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                                                                                                                                                                                                                                                                                                                          A; Gene: 20982
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A;Title: Conserved sequences flank variable tandem repeats in two S-antigen gnes of Plas
A;Reference number: A90863; MUID:85176931
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A; Residues: 1-309 < COM>
A; Experimental source: clone NF7.S
A; Note: the intact NF7 S-antigen contains about 35 more of the 8-residue repeats
A; Note: the intact NF7 S-antigen contains about 35 more of the 8-residue repeats
C; Comment: The S-antigen is secreted by the parasite.
C; Superfamily: plasmodlum S-antigen
C; Superfamily: plasmodlum S-antigen; tandem repeat
C; Superfamily: signal sequence #status predicted < SIG>
F; 1-23/Domain: signal sequence #status predicted < CIG>
F; 24-309/Product: S-antigen #status predicted < CMT>
F; 27-256/Region: 8-residue repeats (S-D-E-A-E-A-L/R-K)
F; 257-271, 272-286/Region: 15-residue repeats
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                          26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEA-LADQTDALQSEEAAVVKADN 84
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                                                                                                                                                                                                                                                                       ch 16.9%; Score 131.5; DB 1 Similarity 34.1%; Pred. No. 0.059; 43; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Sco. 7. 26.0%; Pred. No. v.. 26.0%; Pred. No. v.. 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 128.5; Di
Pred. No. 0.14;
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Best Local Similarity
Matches 43; Conserva
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-438 <HAY>
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                                      A; Accession: B22011
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C. Species: Petromyzon marinus (sea lamprey)
C. Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
R. Jacobs, A. J.; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
A. Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation
A. Reference number: 151116
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRM
A. Molecule type: mRM
A. Residues: 1-1110 c.JAC>
A. Residues: 1-1110 c.JAC>
A. Cross-references: EMBL:U19361; NID:g632549; PIDN:AAA80106.1; PID:g632549
C. Superfamily: neurofilament triplet H protein
                                       C; Species: Escherichia coli propring of 1978. Species: Escherichia coli propring of 1978. Species: Escherichia coli propring of 1978. Species: Escherichia coli forbate: 16. Feb-2001 #text_change 14. Sep-2001 · C; Accession: F85584 · S.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 · A; Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551 · A; Reference number: A8584 · A; Status: preliminary A; Molecule type: DNA A; Residues: 1-440 < STO> A; R
probable tail component of prophage CP-933K Z0982 [imported] - Escherichia coli (stra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ----ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 128.5; DB 26.6%; Pred. No. 0.14;
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29.4%; Pred. No. 1;
tive 28; Mismatches
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probable membrane protein of prophage CP-933X Z1918 [imported] - Escherichia coli (st Crobable membrane protein of prophage CP-933X Z1918 [imported] - Escherichia coli (st Crobable membrane soli coli et col
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C; Species: Arabidopsis thallana (mouse-ear cress)
C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C; Accession: T46231
R; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemck aubmitted to the Protein Sequence Database, December 1999
A; Reference number: 223026
A; Reference number: 223026
A; Reference number: 233026
A; Reference number: 233026
A; Residues: 1-166 < RIE>
A; Residues: 1-166 < RIE>
A; Residues: 1-166 < RIE>
A; Resperimental source: cultivar Columbia; BAC clone T9C5
C; Genetics:
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DQTDALQSEEAAVVKADNAASDALEALADQ-TDALQSEEAEVVQSDNAASDAWEKAATPI 125
                             67 DQTDALQSEEAAVVKADNAASDALEALADQ-TDALQSEEAEVVQSDNAASDAWEKAATPI 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GTLTNLLGNAPE----KLALRNEERAIDELKKQAIEDKEATTAIEAASSD----ALEALA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 PNGGTLTNLLGNAP----EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%; Score 119.5;
30.4%; Pred. No. 1.4;
live 21; Mismatches
                                                                                             126 ALDVKKTKDTKPVVKKEERQNVNTLPTT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 ALDVKKTKDTKPVVKKEERQNVNTLPTT 153
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                                                                                                                                  SAGAAKTSETNAAVSQQSAATSASTATT 227
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es 41; Conserv
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A; Introns: 32/3
A; Note: T9C5.130
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C85693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEER-----QNVNTLPTT----GE 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 119.5; D
Pred. No. 1.4;
1; Mismatches
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Conservative 21;
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Best Local Similarity
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Best Local Similarity
    FPEDEP 823
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OY 67 DQTDALQSE	C; Superfamily: M5 protein Query Match Query Match Best Local Similarity 29.0%; Pred. No. 1.9; Matches 54; Conservative 18; Mismatches 60; Indels 54; Gaps 10; Qy 16 TLTNLLGNA
RESULT 13 S55890 Julia Protein receptor MAG precursor - Streptococcus dysgalactiae C; Species: Streptococcus dysgalactiae C; Species: Streptococcus dysgalactiae C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000 C; Accession: S55890 R; Jonsson, H.: Frykberg, L.; Rantamaeki, L.; Guss, B. Gene 143, 85-89, 1994 A; Title: MAG, a novel plasma protein receptor from Streptococccus dysgalactiae. A; Reference number: S55890; MUID: 94259307 A; Reference number: S55890 A; Reterence number: S55890 A; Residue: preliminary A; Molecule type: DNA A; Residues: 1-413 c,JON> A; Residues: 1-413 c,JON> A; Residues: 1-413 c,JON> A; Residues: BMB: L27798; NID: 9475117; PIDN: AAA26921.1; PID: 9475118	
Ouery Match Query Match Query Match 14.7%; Score 114.5; DB 2; Length 413; Best Local Similarity 26.2%; Pred. No. 1.1; Matches 49; Conservative 15; Mismatches 56; Indels 67; Gaps 6; Qy 36 AIDELKKOAIED	extracellular matrix binding protein - Abiotrophia defectiva (fragment) C;Species: Abiotrophia defectiva C;Species: Abiotrophia defectiva C;Species: Abiotrophia defectiva C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Accession: 731110 R;Manganelli, R.; van de Rijn, I. Infect. Immun. 67, 50-56, 1999 A;Title: Cloning and characterization of emb, a gene encoding the major adhesin of St A;Accession: 73110 A;Title: Dannaber: 220988; MUID:99081722 A;Accession: 73110 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-2055 <
322 PTEPKKPEASIPLVPLTPATPIAKDDAKKDDTKKEDAKKPEAKKEEAKKAATLPT 153 TGESNP 159 111 11	Query Match 14.3%; Score 111; DB 2; Length 2055; Best Local Similarity 25.6%; Pred. No. 12; Matches 43; Conservative 28; Mismatches 61; Indels 36; Gaps 6; OY 18 TNLIGNAPERLALRNEERALDEKKQAIED
RESULT 14 S35760 forA protein precursor - Streptococcus pyogenes C; Species: Streptococcus pyogenes C; Species: Streptococcus pyogenes C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999 C; Accession: S35760; A42711 S; Podbielski, A. Submitted to the EMBL Data Library, November 1992 A; Reference number: S35760	HAAKAAVEQAADA TDALQSEEA I : : : : : : : : :
A.Accession: 353760 A.Accession: 353760 A.Status: preliminary A.Holecule type: DNA A.Residues: 1-415 <pod> A.Cross references: EMBL:X69324; NID:g311759; PIDN:CAA49165.1; PID:g311760 A.Greences: E.J.; Heath, D.G.; Cleary, P.P. J. Bacteriol: 174, 4967-4976, 1992 A.Title: Architecture of the vir regulons of group A streptococci parallels opacity fact A.Reference number: A42711; MUID:92332431 A.Accession: A42711 A.Status: preliminary A.Molecule type: DNA A.Residues: 343-415 <haa> A.Residues: 343-415 <haa> A.Cross-references: GB:M86806; NID:g153630; PIDN:AAA26887.1; PID:g153631 A.Rexperimental source: strain CS101, OF+ A.Note: sequence extracted from NCBI backbone (NCBIN:108942, NCBIP:108945)</haa></haa></pod>	RESULT 16 QXBPLL hypothetical protein 401 - phage lambda N;Alternate names: orf401; orf401 C;Species: phage lambda C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999 C;Accession: G43010; D43016; A04389 R;Daniels, D. Submitted to the Nucleic Acid Sequence Database, September 1982 A;Reference number: A94614 A;Accession: G43010 A;Molecule type: DNA A;Residues: 1-401 < CDAN> R;Sanger, F; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B. J. Mol. Biol. 162, 729-773, 1982

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probable tail fiber protein (imported] - Escherichia coli (strain O157:H7, substrain C15Species: Escherichia coli (C15Decies: 18-101-2001 (C15Decies: 18-101-2001) (C15Decies: 18-101-2001) (C15Decies: 10. 1-20, 2001) (C15Decies: 1. 1-22, 2001) (C15Decies:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 ----ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
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A;Reference number: S22451; MUID:92293110
A;Accession: S22452
A;Accession: S22452
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-890 < WEI>
A;Cross-references: EMBL:X62658; NID:g49019; PIDN:CAA44526.1; PID:g49021
A;Genet: seal
A;Genee: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTT----GEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 OPKTPENSST-----EQPIVKATQTTEGAITE-KQQOVTEKQAIVDGKQQVADTAKKEK
                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
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                                                                                                                                                                                                                                                                                                                                      71; Indels
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                                                                                                                                                                                                                                                                         14.2%; Score 110; DB 29.1%; Pred. No. 5.4; tive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%; Score 109.5; C
27.0%; Pred. No. 2.4;
ive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 ALDVKKTKDTKPVVKKEERQNVNTLPTTGEE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 ATDTQAVDDQQKVV-DQAQTDVNQQQAVVEE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 27.0
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            44;
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Cispecies: Bscherichia coli

Cispecies: Bscherichia coli

Cipate: 24-May-1996 #sequence_revision 24-May-1996 #text_change 26-Aug-1999

CiAccession: 141024

Mirobiol. 16, 57-67, 1995

A.Title: Novel colicin 10: assignment of four domains to TonB- and TolC-dependent uptake

A:Reference number: 141024

A:Reference number: 141024

A:Residues: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-490 <RES>

A:Cross-references: EMBL:X82682; NID:g807875; PIDN:CAA57998.1; PID:g807876
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                                                                                                :Molecule type: DNA
:Residues: 1-401 <SAN>
:Cross-references: GB:J02459; GB:M17233; GB:W24325; GB:V00636; GB:X00906; NID:g215104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface exclusion protein seal precursor - Enterococcus faecalis plasmid pAD1 C; Species: Enterococcus faecalis C; Date: 04-Dec:1992 *Sequence_revision 04-Dec-1992 *text_change 15-Oct-1999 C; Accession: 222452; S22069 K; Weidlich, G.; Wirth, R.; Galli, D. Mol. Gen. Genet. 233, 161-168, 1992 Mol. Gen. Genet. 233, 161-168, 1992 A; Title: Sex pheromone plasmid pAD1-encoded surface exclusion protein of Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKT--KDTKPVVKK 141
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                                                                                                                                                                                                                                                                                                                                                                                                                       48; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 APEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKAD 83
                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                           Length 401;
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                                                                                                                                                                                                                                                                                                                                                                    Indels
A:Title: Nucleotide sequence of bacteriophage lambda DNA. A:Reference number: A92891; MUID:83189071
A:Accession: D43016
A:Molecule type: DNA
A:Residues: 1401 <SAN>
A:Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:VCGenetics:
A:Map position: 40.51-42.99
C:Superfamily: phage lambda hypothetical protein 401
                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                     ; Score 110.5; 1; Pred. No. 2; 18; Mismatches
                                                                                                                                                                                                                                                                                                     14.28; 27.48;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.4%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 ERQNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 ---NARSSETAAERS 291
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262 LERQ 265
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RESULT 21
E85816
                                  membrane spanning protein TolA [imported] -
C;Specles: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Ju
C;Accession: F90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable tail fiber protein of prophage CP-933U Z3074 [imported] - Escheric
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C:Genetics:
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.;
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimale
Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-437 <HAY>
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A; Accession: E90968
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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1, T.; Maximaga, N.; Yasunaga, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AESAAGNAARDA--TTATEKARESAESAQSAEQSRIAAEEAVNRIPTVVGPPGPKGEP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTT----GEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAANADTSAGDASESARQAAESAAAAKQSEEASSSSASAAAQKASESSQSAADAELSKKT 203
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                                                                                                                                                                                                                                      EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTT----GEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                      GTLTNLLGNAPE----KLALRNEERAIDELKKQAIEDKE----------
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                                                                                                                                                                                                                                                                          SAANADTSAGDASESARQAAESAAAAKQSEEASSSSASAAAQKASESSQSAADAELSKKT
                                                                                                                                                                                                                                                                                                            ----ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
                                                                                                                                                                                                                                                                                                                                                  GTLNDFLGAMSEDDVRPEALRRFELMVEEAARHAEEAKKNAGEAETSARNAGISASQAEE 145
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                      Makino, K.; Ohnishi, M.;
Yasunaga, T.; Kuhara, S.;
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llarity 27.0%;
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Pred. No. 2.6;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                         18-Jul-2001 #text_change
                      Kurokawa, K.; Ishii, K.; Yokoyama, K.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                               Escherichia coli
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anta, E.; Potamousis,
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                                                                                                                                                                                                      261
                                                                                                               O157:H7,
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C;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change C;Accession: G85576 C;Accession: G85576 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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G85576
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A; Residues: 1-394 <STO>
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A; Residues: 1-394 <HAY>
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A;Experimental source: strain 0157:H7, substrain
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Best Local
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EKAAADKKAAAEKAAADKK 247
                                  PIALDVKKTKDTKPVVKKE 142
                                                                   KKAEAEAAKAAAEAQKKAEAAAAALKKKAEAAEAAAAEARKKAAAEKAAADKKAAEKAAA
                                                                                                   QSEEAAVVKA------DNAASDALEALADQTDALQSEEAEVVQSDNAASD--AWEKAAT 123
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42; Conser
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Pred. No. 2.5;
23; Mismatches
                                                                                                                                                                                                                           Score 109;
Pred. No. 2.
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probable tail fiber protein [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18 C;Accession: G90898 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Sh

Kurokawa, K.; Ishii, K.; Yokoyama, Shiba, T.; Hattori, M.; Shinagawa,

Han,

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18-Jul-2001

O157:H7, substrain

RESULT G90898

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A; Residues: 1-421 KLEV
A; Cross-references: GB:M28232; NID:g148018; PIDN:AAA246B3.1; PID:g148019
A; Experimental source: strain JM105
A; Rote: the authors translated the initiation codon GTG for residue 1 as Val
A; Rote: the authors translated the initiation codon GTG for residue 1 as Val
A; Rote: the authors translated the initiation codon GTG for residue 1 as Val
A; Rote: the plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
.A.; Rose, D.J; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Rittle: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Reference number: A64720; MUID:97426617
A; Reference number: A64720; MUID:97426617
A; Recession: B64810
A; Residues: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-421 GBLAT>
A; Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A; Experimental source: strain K-12, substrain MG1655
C; Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach to G; Genetics:
A; Genetics:
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C;Date: 07-Sep-1990 #sequence_revision 07-Se
C;Accession: JV0057; B64810
R:Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tola an
A;Reference number: JV0057; MUID:90078104
A;Accession: JV0057
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A; Accession: G90898
A; Status: preliminary
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
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A; Residues: 1-421 <LEV>
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A; Residues: 1-271 <HAY>
                                                                                                                                                                                                               F;355-362/Region: nucleotide-binding motif A (P-loop)
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Best Local :
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  ERLAAQEQKKQAEEAAKQAELKQKQAEEAAAKAAADA-KAKA-EADAKAAEEA----
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                                                   EKLALRNEERAIDELKKQA-IEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADN 84
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                                                                                                                                   Similarity
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                                                                                                                                   Score 108.5;
Pred. No. 2.9
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2; Mismatches
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Pred. No. 1.
                                                                                                          Mismatches
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     -AKK 162
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hypothetical protein - common buckwheat
C;Species: Fagopyrum esculentum (common buckwheat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C;Accession: T10699
R;Fujino, K.; Funatsuki, H.; Inada, M.; Shimono, Y.
submitted to the EMBL Data Library, September 1996
- parameter and common and parameter and logic of
                                                                                                                                                                                                                   A;Cross-references: GB:M22532; NID:g153628; C;Superfamily: M5 protein C;Keywords: immunoglobulin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A33939
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-405 <HEA>
                                                                                                                                                                                                                                                                                                                                               R:Heath, D.G.; Cleary, P.P.
Proc. Natl. Acad. Sci. U.S.A. 86, 4741-4745, 1989
A;Title: For-receptor and M-protein genes of group
A;Reference number: A33939; MUID:89282846
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptococcus sp.
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990
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A;Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc gamma (IgG) receptor II precursor - Streptococcus sp. (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-159 < FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
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Best Local (
                                                                       218
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                                   40
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                                KEATTAIEAASSDALE----ALADQTDALQSEEA---AVVKADNAASDALE----ALADQ 96
                                                                       EIAKLQSEAATLENLLGSAKRELTDLQAKLDTATAEKAKLESQVTTLENLLGSAKRELTD
LOAKLDAANAEKEKLOSOAAALEKOLEATKKELADLOAKLAATNOEKEKLEAEAKALKEO 337
                                                                                                         EQPRIIPNGGTLTNLLGNA----
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se: cv. Kitayuki; immature seed; 14 days
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                                                                                                                                             Score 108; DB Pred. No. 3; 25; Mismatches
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Pred. No. 1;
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ice analysis of
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                                                                                                                                             48;
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C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C:Accession: T13802 R:Whitfield, W.G.F.: Chaplin, M.A.: Oegema, K.: Parry, H.; Glover, D.M. J. Cell Sci. 108, 3377-3387, 1995 A:Title: The 190 Kba centroscome-associated protein of Drosophila melanogasta. A:Reference number: Z17765; MUID:96154790 A:Accession: T13802
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 29
S52536
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A; Residues: 1-386 < KATS
A; Cross-references: GB:S75411; NID:g914107; PIDN:AAB33261.1;
C; Superfamily: M5 protein
                                                                                                                                                                                                                               A;Title: Sequencing of genes within the vir A;Reference number: S52535; MUID:95147851 A;Accession: S52536
                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                   fcrA 15 protein - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 23-Aug-1995 *sequence_revision 19-Oct-1995 *text_change 28-May-1999
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A;Residues: 1-1096 <WHI>
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                                   TLTNLLGNAPE------KLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQ 68
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 TLENLLGSAKRELTDLQAKLDAANAEKA -- KLQSQA --
                                                                                                                                                                                                                                                                                       Genet.
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                                                                                                                                                                                                                                                                                                                        S52536
                                                                                          Similarity
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t. 245, 78-85, 1994
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                                                                        Conservative
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Pred. No. 9.2;
42; Mismatches 6:
                                                                      Score 107; DB Pred. No. 3.3; L8; Mismatches
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AALEKQLEATKKE
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hypothetical protein YIL149c
C;Species: Saccharomyces cer
C;Date: 02-Dec-1994 #sequenc
C;Accession: S48385
R;Churcher, C.
submitted to the EMBL Data L
                                                                                                                                                                                                                       A; Dactus: r--- DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-437 <HAY>
A; Residues: 1-437 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB36364.1; PID:gl3362410; GSPDB:GN00154
A: Evnerimental source: Strain O157:H7, Substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 31
E90996
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S48385
                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A99629; A; Accession: E90996
                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Hayashi, T.; Makino, K.; Ohnishi, M.;
gasawara, N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 18-Jul-2001 #sequence_revision C;Accession: E90996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable tail fiber protein [imported] -
C:Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:Z47047; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S48310
A; Accession: S48385
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                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: MIPS:YIL149c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1679 <
                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1261 LTNEISDLKGKLSSAENANADLENKFNRLKKQAHEKLDASKKQQAALTNELNELKAIKDK 1320
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                    62
                                                              84
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                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity es 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AASDAWEKAATPIALDVKKTKD-----TKPVVKK-EERQNVNT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKPGNKEVPTRPSQTRTNTNKAPMAQTKRQLPSTGEETTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQS----EEAAVVKAD------NAASDALEALADQTDALQSEEAEVVQSDN 112
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LEALADQT--DALQS-----EEAAVVK-ADNAASDALEALADQTDALQSEEAEVVQSDNA 113
                                                            GTLNDFLGAMSEDDVRPEALRRFELMVEEAARHAEEAKKNAGEAETSARNAGISASQAEE 143
                                                                                                   GTLTNLLGNAPE----KLALRNEERAIDELKKQAIEDK----EATTA-----IEAASSDA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEQDLHFENAKVIDLDTKLKAHELQSEDVSRDHEKDTYRTLMEEIESLK-KELQIFKTAN 1379
                                                                                                                                      l Similarity
47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      Yasunaga,
1-22, 2001
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26.8%;
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                                                                                                                                          24;
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Pred. No. 17;
32; Mismatches
                                                                                                                                    Pred. No. 4.1;
4; Mismatches
                                                                                                                                                           Score 106.5;
Pred. No. 4.1;
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Shiba, T.; Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli (strain 0157:H7, substrain
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                                                                                                                                          27;
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Shinagawa,
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RESULT 32
(88563)
(88563)
hypothetical protein z1382 [imported] - Escherichia
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: G85631
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau,
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau,
                                                                               moto, Y.; Horiuchi, T.
DNA Res. 3, 363-377, 1996
A;Title: A 570-kb DNA sequence of the Escherichia coli
A;Reference number: Z16603; MUID:97251357
A;Accession: T09189
                                                                                                                                                                               R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Reference number: A64887
A;Reference number: A64887
A;Reference nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1122 <BLAT>
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636; A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; FID:g1787636; A;Experimental source: strain K-12, substrain MG1655
R;Aiba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Kasai, H.; Motomura, K.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; Saito,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
G64887
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                         A; Molecule type: DNA
A; Residues: 3-1122 <AIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable tail fiber protein GP37 - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: G64887; T09189
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C;Genetics:
A;Gene: Z1382
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A;Molecule type: DNA
A;Residues: 1-375 <STO
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A:Reference number: A8548
A:Accession: G85631
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      A; Cross-references:
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                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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      GB: AE000234;
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80; MUID:21074935; PMID:11206551
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    GB:U00096;
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Pred. No. 4;
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    NID:g1787633;
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    PIDN: AAC74454.1;
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    PID:g1787636
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C; Date: 28-Oct-19
C; Accession: S578
R; Boyle, M.D.P.;
A; Molecule type: nucleic
A; Residues: 1-388 <01T>
A; Note: sequence extracte
C; Superfamily: M5 proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: DNA
A;Residues: 1-387 <BOY>
A;Cross-references: EMBI
C;Superfamily: M5 prote
                                                                                                                                       R;O'Toole, P.; Stenberg, L.; Rissler, M.; Lindahl, Proc. Natl. Acad. Sci. U.S.A. 89, 8661-8665, 1992 A;Title: Two major classes in the M protein family A;Reference number: A46173; MUID:92409576
                                                                                                                                                                                                                           C;Species: Streptococcus sp.
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change
C;Accession: A46173
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Infect. Immun. 62, 1336-1347, 1994
A;Title: Analysis of genes encoding two unique
A;Reference number: S57834; MUID:94178942
                                                                                                                         A; Contents: group
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Note: sequence extracted Superfamily: M5 protein
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                                                                                                                                                                                                                                                                                                                                                                                            RELPSTGEETTNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   -TLPTTGEE-SNP
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-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
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27.5%;
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Pred. No. 4.
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Pred. No. 14;
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                    backbone (NCBIN:114063, NCBIP:114064)
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C:Accession: S42574
R;Jonsson, H.; Mueller, H.P.
Eur. J. Biochem. 220, 819-826, 1994
A;Fitle: The type-III Fc receptor from Streptococcus
A;Reference number: S42574; MUID:94192673
A;Accession: S42574
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$42574
$42574

Streptococcal surface protein - Streptococcus dysgalactiae
C;Species: Streptococcus dysgalactiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_cl
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                            A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: C90769
                                                                         R;Hayashi, T.; Makino, K.; Ohnishi, M.; gasawara, N.; Yasunaga, T.; Kuhara, S.; DNA Res. 8, 11-22, 2001
                                                                                                                        probable tail fiber protein [imported] C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision C;Accession: C90769
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A; Residues: 1-664 <JON>
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Similarity 23.9%;
54; Conservative :
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26.9%;
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                                                                                           Kurokawa, K.; Ishii,
Shiba, T.; Hattori, 
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                                                                                          M.; Shinagawa,
                                                                                                         K.; Yokoyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
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                                                                         EF protein - Streptococcus suis
C;Species: Streptococcus suis
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S33441
R;Smith, H.E.; Reek, F.H.; Vecht, U.; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
S72375
                                                        R;Smith, H.E.; Reek, F.H.; Vecht, U
submitted to the EMBL Data Library,
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             A; Reference number: S33441
A; Accession: S33441
                                             A; Description:
                                                                                                                                                         S33441
                                                                                                                                                                        RESULT 39
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Repeats in an

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Smits,

Reek, F.H.; Vecht, U.; Gielkens, A.L.J.;

06-Jan-1995

#text_change 15-Oct-1999

May

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A;Residues: 1-439 <HAY>
A;Cross-references: GB:B#
A;Experimental source: st
C;GenetLcs:
A;Gene: ECs1123
                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Gen. Genet. 252, 640-647, 1996
A;Title: Comparative analysis of 18 sex pheromone
A;Reference number: S72375; MUID:97074879
A;Accession: S72375
A;Molecule +---
                                                                                                                                                                                                                                                                    A:Genome: plasmid PUI
F:1-30/Domain: signal sequence #status predicted
p:31-843/Product: surface exclusion protein #stat
                                                                                                                                                                                                                                                                                                                                 A;Gene: sep1
                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface exclusion protein sep1 precursor - Enterocc C;Species: Enterococcus facealis C;Date: 12-reb-1998 *sequence_revision 13-Mar-1998 C;Accession: S72375
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X96976; NID:g1272652; A;Experimental source: strain OG1X
                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-843 <HIR>
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                              Matches
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                                                                                                                                                                    QPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTLNDFLGAMSEDDVRPEALRRFELMVEEAARHAEEAKKNAGEAETSARNAGISASQAEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AESAAGNAARDA--TTATEKARESAESAQSAEQSRIAAEEAVNRIPTVVGPPGPKGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTLTNLLGNAPE----KLALRNEERAIDELKKQAIEDKE----
                                                                                                                                       QPK-----TPENASSEQPTVKATQTTEQAITEKQQQVIE-KQAIVDQKQQVADTAKKEK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTT----GEESNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAANADTSAGDASESARQAAESAAAAKQSEEASSSSASAAAQKASESSQSAAEAELSRKT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
ATDTQAVDDQQKVVEQAQ
                                ALDVKKTKDTKPVVKKEE
                                                                     DTIDQSVKDQQAVVDQNKDALVQSQQAVTDQ-QAVVDEAKKVV--DEATPSAIEKAKEQV 141
                                                                                                      DQTD-ALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
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                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%;
26.4%;
                                                                                                                                                                                                                            13.4%; Score 104.5; 28.3%; Pred. No. 12;
 159
                                  143
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Pred. No. 5.6;
                                                                                                                                                                                                            Pred. No. 12;
7; Mismatches
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                                                                                                                                                                                                                                                                                                  <SIG>
                                                                                                                                                                                                            61;
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                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid
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Search completed: October 13, 2002, 04:49:16 Job time: 47.3636 secs
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A;Accession: G41662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-891 <KAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Residues: 1-1822 <SMI>
A; Cross-references: EMBL:X71880; NID:g298031; PIDN:CAA50714.1; PID:g298032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GB:M64978; NID:g150552; PIDN:AAA65847.1; PID:g150554
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.4%; Score 104; DB 2; Length 891; Best Local Similarity 26.9%; Pred. No. 14; Matches 42; Conservative 27; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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                                                                                                                                                                                                   142 ATDTQAVDEQQKVVDQAQTDVNQQQAVVDEKAKETN 177
                                                                                                                                                                                                                                                                                               126 ALDVKKTKDTKPVVKKEE----RONVNTLPTTGEESN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 KDTKPVVKKEERQNVNTLPTTGE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 QSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 OPKTPENSST-----EOPTVKATQTTEQAITE-KQQQVTEKQAIVDQKQQVADTAKKEK 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 QPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQTDALQSEEAAVVKADNAASD-ALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPI 125
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-MODEL-frame+_p2n.model -DEV*x1h
-Q-/cgn2_1/USPTO_spool/US9847539/runat_10102002_093106_5020/app_query.fasta_1.526
-Q-/cgn2_1/USPTO_spool/US9847539/runat_10102002_093106_5020/app_query.fasta_1.526
-DB-Issued_Patents_NA -QFMT-fastap -SUFFIX*std.rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-40
-MODE-LOCAL -CUTEMT-pto -NORM-ext -HEAPSIZE*=500 -MINLEN-0 -MAXLEN-200000000
-USER-US0847539_eGGN_1 _1 _13 _erunat_10102002_093106_5020 -NCPU-6 -ICPU-3
-NO_KLPXY -NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
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                                                            C
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      110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB seq
                                                                                                                    105
104.5
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length: 2000000000
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X9apop 10.0 , X9apext
Y9apop 10.0 , Y9apext
F9apop 6.0 , F9apext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6
777
                                                                                                                                                                                           Match
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                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
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                                                                                                                                                                                                          Query
   14.7
13.6
13.5
13.4
13.4
13.0
13.0
12.5
12.4
12.4
12.4
112.4
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-08-669-408B-9
US-08-6171-517B-5
US-08-619-408B-1
US-08-119-125A-2
US-08-630-822A-61
US-08-678-614-1
US-08-936-165A-224
US-08-936-165A-224
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ALIGNMENTS

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Sequence 9, Applic Patent No. 6100055
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                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCI
APPLICATION DATA:
06-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,408B
FILING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RANTAMAKI, Liisa K.
APPLICATION NUMBER: SE 9302855-3 FILING DATE: 06-SEP-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08669408B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANTAMAKI, LIISA K.

VENTION: METHOD AND MEANS FOR PRODUCING

VENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
SERGTH: 1555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                          1431
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)872-5300
TELEPHONE: (202)672-5309
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TELLEFAX: 904136
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                         ACTGGTGAAGGAAGCAACCCA 1451
                                                           ThrGlyGluGluSerAsnPro 159
                                                                                                                                                                                                                                                                             GATGATGCGACTAAGACCTTTACTGTAACTGAAATGGTTACTGAAGTTCCTGGTGATGCA 1250
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                                                                                                 GATGCTAAAAAAACCAGAAGCTAAGAAAGAAGAAGCTAAGAAAGCTGCAACTCTTCCTACA
                                                                                                                                                          ProIleAlaLeuAspValLysLysThrLysAspThr -----
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Conservative:
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CURRENT APPLICATION NUMBER: US/09/171,517B
CURRENT FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: PCT/CA97/00265
PRIOR FILING DATE: 1997-04-23
PRIOR APPLICATION NUMBER: 60/015,999
PRIOR APPLICATION NUMBER: 1996-04-23
VINDER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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; NAME/KEY: CDS
; LOCATION: (31)..(975)
US-09-171-517B-5
                   RESULT
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APPLICANT: Finlay, B. Brett
APPLICANT: Kenny, Brendan
APPLICANT: Stein, Markus
TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN
FILE REFERENCE: 07422/019001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application Patent No. 6355254
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                                                       760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ProlleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsn
                                                                                        ThrGlyGluGluSer 157
                                                                                                                                                 LysAspThrLysProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThr 152
                                                                                                                                                                                                                                                                            AGCGTGATGCAGCAAGCGATGACTACAGCAACGAGAGCGGCCAGCCGTACATCCGACGTT 582
                                                                                                                                                                                                                                                                                                                                                                                                                            GCGACTAAAACGTTGACTAAGGCAACGGAAAGCGTTGCTGATGCTGTTGAAGATGCATCC 522
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                                                       ACGGTATCTGAATCA
                                                                                                                              GGCTCTACACCATTTATTGCCGTTACCAGTCTTGCCGAAGGCACGAAGACATTGCCAACA
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                                                                                                                                                                                                                                                                                                               ThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAsp 116
                                                                                                                                                                                                                                                                                                                                                                                        AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln
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Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PRIOR APPLICATION NUMBER: WO PCT/SE94/00826
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 61743/102
TELECOMMUNICATION: THOORMATION:
TELEPHONE: (202)672-5300
TELEZEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SECURENCE CHARACTERISTICS:
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                                                                                                                                                US-09-847-539A-6 (1-159) x US-08-669-408B-1 (1-2526)
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD AND MEANS TITLE OF INVENTION: PLASMAPROTEINASE NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RANTAMAKI, Liisa K.
                                                                           1772
1832 ACTTTCTCA------GGCGAAACAACTACTAAAGCAGTA-----GACGCAGAAACT 1876
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/669,408B FILING DATE: 03-JUL-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 K Strate: Washington STATE: D.C.
                                16 ThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArg 35
                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                ATTGACGCACCTGAACTACTCCAGCCTTGACTACTTACAAACTTATTGTTAAAGGTAAC
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506..2497
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506..2497
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13.51%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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	PPLICATION NUMBER: ILING DATE: 21-MAR-	
	APPLICATION NUMBER: PCT/NL92/00054 FILING DATE: 19-MAR-1992	
	SSIFICATION: 514	
	CATION NUMBER	
	fect v. 6. DATA:	
	8	
	MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage	
	EADABLE FORM:	
	COUNTRY: The Netherlands ZIP: NL-8219	
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	PH Lelystad	
	ADDRESSEE: C	٠.
	CORRESPONDENCE ADDRESS:	٠. ٠.
ß,	OF INVENTION: protection against infection by S. suis in	٠.
thereof for the di	INVENTION: Characteristics of Streptococcus suis and INVENTION: antibodies derived therefrom and the use	
-	OF INVENTION: DNA Sequences which code for Virulence	٠. ٠
	APPLICANT: SMITH, Hilda Elizabeth APPLICANT: VECHT, Uri	
	AL I	
	:08-119-125A-2 Sequence 2, Application US/08119125A Patent No. 5610011	S. S.
		RE
	2405 GGTGAAGGAACCCA 2422	망
	154 GlyGluGluSerAsnPro 159	Qy
2404	2345 GCTAAGAAAGAAGAAGCTAAGAAAGAAGCTAAGAAAGCTGCAACTCTTCCTACAACT	д
153	139ValLysLysGluGluArgGlnAsnValAsnThrLeuProThrThr	Qy
2344	Ã	В
138	130 LysLysThrLysAspThrLysProVal	Qy
2284	2225 CCAGAAGCAAGTATCCCTCTTGTTCCGTTAACTCCTGCAACTCCAATTGCTAAAGATGAC	рь
129	121 ·····-AlaAlaThrProIleAlaLeuAspVal	Qy
2224	2165 TTTACGGTAACTGAAATGGTTACTGAAGTTCCTGGTGATGCACCAACTGAACCAGAAAAG	Ъ
120	119	Qy
2164	2105 CAATACGCTAACGAAAACGGTGTTGGATGGTGTTTGGACTTACGATGATGCGACTAAGACC	Ъ
118	107 ValValGlnSerAspAlaAlaSerAspAlaTrp	Qy
2104	AACAACTACTAAAGCAGTAGACGCAGAAACTGCAGAAAAAGCCTTC	Db
106	88 ASPALaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGlu	Qy
2044	GGTAAAA	Db
87	68 GlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSer	Qy
1996	1937 GACGATGCAACTAAAACCTTTACAGTTACTGAAAAACCAGCAGTGATTGACGCACCTGAA	Dр
67	AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLe	Qy
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Best Local Similarity:
                                                                                                                                                                                                                                                                            score:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
    4108
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                                                                                                                 ### 1000 AGCTTGACAGACACAGGTAAAGAAGCTAGAGATGCAGTTGAATTGGCTAAGGATAAA----
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TELECOMMUNICATION INFORMATION:
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LOCATION:
LOCATION:
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                                                                                                                                             16 ThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArg
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TYPE: Nucleic acid with corresponding amino acids
STRANDEDNESS: single stranded
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GTAGAGAAACTTGCAGAAGATACGCGCAAAGCTATCGAGGACAATCCAAACTTGTCAGAT 4167
                                                                          AlaIleAspGluLeuLysLysGlnAlaIle-----GluAspLysGluAlaThrThrAla
                            IleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAsp---AlaLeu 72
                                                        -----GAATTAGCTAAGGAAGCAATCCGAACAGAAGAAGAAGAAGCTACTAAAATA 4107
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from
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from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 start of repetitive units R1-R11 bp 2869, 3097, 3292, 3520, 4087, 4381, 4609, 4837, 5065, 5293, 5521:
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bp 361 to 498
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24.48%
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Conservative:
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Percent Similarity:
Best Local Similarity:
 Query Match:
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                                                                                         Alignment Scores:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
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                                                                                                                                             NAME/KEY:
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Color
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US-09-005-069-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/09005069 Patent No. 5932470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TITLE OF INVENTION: AND APPARATUS
TOTAL OF SPONENCES: 107
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
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                                 APPLICATION NUMBER: 08/6:
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                          CLASSIFICATION:
                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                         FILING DATE:
                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGAAGTAGCATCTCTCCAAGGCAAACTTTCTCAAGAGGAGGAGCTCTAGATCACAGGCT
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FRANK, GLENN R.
FUNTER, SHIRLEY WU
WALLENFELS, LYNDA
WALLENFELS, LYNDA
WALLENFELS, LYNDA
WARNION: NOVEL ECTOPARASITE SALIVA PROTEINS
WYRNION: NOVEL PROTEINS
                                                                                                                                                                                                                                                                                                                                                   1700 Lincoln Street, Suite
                                                                                                                                                                                                                                                                                                   U.S.A.
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                                                                                                  Sequence 1, Application US/08678614 Patent No. 6013507 GENERAL INFORMATION:
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TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 61:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LENGTH: 2706 base pair:
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Indels:
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE 4248 base pairs
SEGUENCE 1-2 acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/678,614
FILING DATE: 10-JUL-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                               2430
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MEDIUM TYPE: Floppy
                                                               2490 CCTTTAAATCCTGATACAACAAATGAAGAAGTAGCGGAAGCTATTGAACGTATTAATGCA
                                                                                                                                                                                              2370 GTAGAAGCCATTAAAACAAAAGCAATCAATGATATTAATCAAACTACACCTGCTACAACA 2429
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                             114 AlaSerAspAlaTrpGluLysAla....-AlaThrProIleAlaLeuAspValLysLys 131
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LOCATION:
                                                                                                94
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                                                                                                                                                                 74
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-139
                                                                                                                                                                                                                             54 IlcGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 73
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GCTAAAGTTTCTGGTGTTAAAGCAATTGAAGCGACAACGACTGCACAAGATTTAGAAAGA 2609
                                                                                            AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAla 113
                                                                                                                             GCTAAAGCAGCAGCTCTTGAAGAATTTGACGAAGTTGTTCAAGCACAAATTGATCAAGCA 2489
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Percent Similarity:
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Query Match:
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                                                                                                                       Score:
                                                                                                                                                          Pred. No.:
                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                    US-08-936-165A-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANI. AVERAGE AND APPLICANIA TO APPLICANIA APPLICANIA WATCH JUDITH APPLICANIA WATCH JUDITH WATCH JUDITH WATCH AND APPLICANIA WATCH WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glami, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0:
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2730 TCAAATGCAACAAATGAAGAA 2750
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                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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nucleic acid
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Rosenberg, Martin
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Lonetto, Michael
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47.50%
25.83%
12.42%
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                                                             Length:
Matches:
Conservative:
Mismatches:
Gaps:
                         Indels:
      31
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RESULT 9
US-08-158-353-1
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Percent Similarity:
Best Local Similarity:
                                     Score:
                                                         Pred. No.:
                                                                           Alignment Scores:
                                                                                                                US-08-158-353-1
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                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 824 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                 TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lyme
TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1203 CAGGCTGCTGTT-----AATCAAATCACTCAACTTAAAGATCAAGCAATTAATCAA 1153
                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 ProValValLysGluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGlu 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Mil
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/158,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAsp 116
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                                                                                                                                DNA (genomic)
0.016
96.00
46.34%
28.66%
                                                                                                                                                                                                                                                                                                                            UCT93-05
                                     Length:
Matches:
Conservative: Mismatches:
824
47
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58
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У	us-09-8	Alignment Pred. No.: Score: Percent S: Best Local Query Mato DB:	ESULT 10 S-08-821-6 Sequence Patent N GEMERAL 1 APPLICAN CURRENT CURREN	ъ 7	Y 1		Y 1		Сп		л	4	4	ω	w	-09-8	Query M DB:
14 G1 	47-53	Sc. Sc.	SULT 10 -08-821-872- OR -08-1872- Sequence 1. Patent No. 6 Patent No. 6 Patent No. 6 Patent Properties Applicant: Applicant TITLE OF IN OUR TITLE SECURT OF IN SECURT OF IN ORGANISM: ORGANISM: ORGANISM:	50 GC	54 Gly	90 GAT	37 Pr	117 Al 	∞ –	7 7	77 AL	65 80 GG	47 Asp ::: 20 AAT	30 Leu ::: 60 GTG	14 G1 11 00 GG	47-539A	Match:
LyG1yT	9A-6	ores: larit imila	872-1 1. Applicat 0. 6204004 INFORMATION: NIT: Kaper, J NIT: Jarvis, F INVENTION: F INVENTION: F INVENTION: F INVENTION F INVENTION D INVENTION E: Patentin O 1 0 1 0 37 DNA SM: Escheric SM: Escheric	ე::	GluG	ପ	roValVal	aTrpG1	ନ୍ଦ =	rAspAl	LaAlaVa	AGCCTA	pLysG1 : TTTGAT	LeuArgAs :::::: GTGAAAGA	lyGlyThrLeu GGCCTAATCTT	9A-6 (
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 	s-08-8)282 50 31% 49%	+ U 6 6 a 8			CTTGAA	GluAr	ChrPro	GTC	G .	AS	Le :: GAGCCTACGTAATATCAACCCTAAT	hrThrAlaIleGluAl ::: AAAATGGTTTAAATGC	тестт	LeuLeuG ::: NTAAGTA	-08-1	de .
yas 	21-87		872A 0Stic ion 40044			G	Arg	IleAl	 ATGCGGAJ	AlaGl	nAlaAla	uAl : AGC	GluAla AATGC	ArgAlaIleA ::: TTGCATCTATAG	GlyAsnAl AAAAAAAT	58-353	0.11
nAlaPr	2-1 (1	Length: Matches: Conserval Mismatche Indels: Gaps:	rest Re			::: TTATTTGAA	Gln	aLeuAs	ACTCGG	Val	Ser	ASPG1 ::::: \GAAAA	luAlaAlaSerSerA ::::: ATGCCGGTGCTAATC	gAlaIleAspG ::: ATCTATAGATG)AlaPr \ATTAC	-1 (1	Indels Gaps:
roGluLys	-937)	: s: vative ches:	for En			:::: ATCAGT	nAsnVa	pvally: ::: -ATTTT.	ΤA	lGlnSe	AspAlaLeuGluAlaLeuAlaAspGln 	aAspGlnThrAspAlaLeu ::::: AGAAAAATTAGATGGATTG	rSerAs :::: TAATCA	SPGluLe :: ATGAAGT	uLeuGlyAsnAlaProGluLys	-824)	
/sLeuAla/ 		93 46 67 23	teroh 9JK			TAAAAA	lAsnThr	SLYST AAAA	GAATG	SerAspAs	uGluA :::	SPALAL	spAl :: AAAACGGATC	luLeuLysLys ::: AAGTTGCTAAG	'S		30 8
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aLeuArgAsnG] :::			gic			CAAAA	roThr	PThr TACT	g=	Maser	AlaAsp		euGl - TGTT	laII CTAT	LeuAl BTTCTCGC		
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US-08-795-475-5
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                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
                              FEATURE:
                                                                                                                                                                                TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bjvrck, Lars APPLICANT: Sjvbring, Ul:
                                           HYPOTHETICAL:
                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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NAME/KEY:
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                                                                                      STRANDEDNESS:
                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                             REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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DEDNESS: double
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                                                                                                                     1332 base pairs
                                                                                                                                                  (206) 682-6031
(706) 70 NO: 5:
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WENTION: PROTEIN L AND
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08216894 Patent No. 5876734
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
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FILING DATE: ATTORNEY/AGENT
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                               STREET: 3000 K Street, CITY: Washington, D.C.
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                                                                                                                                                                   COUNTRY:
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              24-MAR-1994
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NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768

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                                                                                                                                   Sequence 9, Application US/09115746 Patent No. 6228601
     GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 85:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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LOCATION:
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ADDRESSEE:
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                                                                                                                                                                                                                                                       LysAspThrLysProValValLysLysGluGluArgGln 145
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                                                                                                                                                                                                                                                                                                                            AspAlaTrpGluLysAla-----AlaThrProIleAla---LeuAspValLysLysThr 132
                                                                                                                                                                                                                                                                                                                                                                GCCACGAAGGTTGCCGAAGCGGAGAAGCAGAAGGCAGCTGAAGCCACGAAGGTTGCCGAA 1011
                                                                                                                                                                                                                                                                                                                                                                                                GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSer 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO . .
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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TELEX: 904136
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: doub
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GCGGAGAAGCAGAAGGCAGCTGAAGCCACGAAGGTTGCCGAAGCGGAGAAGCAGAAGGCA 1071
                                                                                                                               AAGCAAAAGGCAGCTGAGGCCACGAAGGTTGCCGGAGACGAGAAGCAGAAGGCAGCTGAA
                                                                                                                                                                                                                                                                                                                                  GAAGCGGAGAAGCAGAAGCCTGAAGCCACGAAGGTTGCCGAAGCCGGAGAAGCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                 SerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeuLeuGly 22
                               AspAlaTrpGluLysAla-----AlaThrProIleAla---LeuAspValLysLysThr 132
                                                                                             GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSer 115
                                                                                                                                                                                               GTTGCCGAAGCGGAGAAGCAGAGGGCA----GCTGAAGCCACGAAGGTTGCCGAAGCGGAG
                                                                                                                                                                                                                            AlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu
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                                                                                                                                                                                                                                                                                                AlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGlu
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-446-137B-1
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NAME/KEY: exon
LOCATION: 103..3186
IDENTIFICATION METHOD:
OTHER INFORMATION: /cod
OTHER INFORMATION: /pro
OTHER INFORMATION: /pro
OTHER INFORMATION: /oun
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPUTER: DAY PC COMPUTER: DAY PC CODS/MS-DOS OPTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,13 FILING DATE: 22-MAY-1995
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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MEDIUM TYPE: Floppy disk
 FEATURE:
NAME/KEY:
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ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
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ADDRESSEE: SEED and BERRY LLP
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                                                                                                                      NAME/KEY: CDS
LOCATION: 103..3186
OTHER INFORMATION: OTHER INFORMATION:
                                OTHER INFORMATION: OTHER INFORMATION:
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STRAIN: 1018
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STRANDEDNESS: doub
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    /evidence= EXPERIMENTAL
    /number= 1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
              COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS v.6.0
SOFTWARE: WOR'DEFICE v. 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,12
FILING DATE: 20-SEP-1993
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ADDRESSEE: Centraal Diergeneeskundig Instituut
STREET: Edelhertweg 15
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APPLICANT:
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                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch,
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                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AGCACACAAAATGCAGAATTCAAAGGAACATTCGCAAAAGCAGTATCAGATGCT 1065
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                                                                                                                                                                                  RY: The Netherlands NL-8219
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92.50
41.408
26.758
11.908
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                                                                                                                                                                                                                                                                                                                                           DNA Sequences which code for Virulence Characteristics of Streptococcus suis and parts thereof, antibodies derived therefrom and the use thereof for the protection against infection by S. suis in mammals, inclu
                                      US/08/119,125#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LysLysThrLysAspThrLysProVal 138
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Matches:
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PRIOR APPLICATION DATA:

NL 9100510 PCT/NL92/00054

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; LOCATION:
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; NAME/KEY:
; LOCATION:
US-08-119-125A-1
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                       Alignment Scores:
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TELEPAX: (203) 838-8794
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4376 base pairs
TYPE: Nucleic acid with corresponding amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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NAME/KEY:
LOCATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Handal, Anthony H.
REGISTRATION NUMBER: 26275
REFERENCE/DOCKET NUMBER: SMITHHEll9125
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 838-8589
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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                                                         2889
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NAME/KEY:
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2931 GATGCTAAGAATAAGATTGCTAAAGAATCCGACGCTGCTAAGTCAGCCATTGACGCGAAT 2990
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NAME/KEY:
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LOCATION:
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LOCATION:
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LOCATION:
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FILING DATE: 19-MAR-1992
APPLICATION NUMBER: NL 9
FILING DATE: 21-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                        IleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 73
               SerGluGluAlaAlaYalLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeu 93
                                                       GTAGGTTCAATCGCCCAAGATGTTCTTGACGCA--
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bp 66 to 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribosome binding site bp 350 to 356
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bp 176 to 181
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bp 89 to 94
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bp 361 to 498
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bp 153 to 158
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92.50
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26.57%
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Matches:
Conservative:
Mismatches:
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March Non	TELEPHOI TELEFAX INFORMATION SEQUENCE (LENGTH: TYPE: TYPE: STRANDE: STRANDE: TOPOLOG: MOLECULE: FEATURE: NAME/KE: LOCATION 08-968-751-	ZIP: COMPUTER MEDIUM COMPUT OPERAT SOFTWA CURRENT: APPLIC. AITORNEY: NAME: REGIST REFERE TELECOMM	ESULT 16 S-08-968-75 Sequence 3 Sequence 3 Patent No. GENERAL 1 APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA CORRESP CORRESP CORRESP CORRESP TITY: COUNT	157 3213	137 3168	126 3111	113 3051	94 2991
Scores : !milari ! Simil	TELEPHONE: (TELEPHONE: (TELEPAX: (51) STRMATION FOR SQUENCE CHARAC LENGTH: 3256 TYPAE: nuclei stranded type: (1) TOPOLOGY: 11 STRURE: ATTURE: NAME/KEY: CD LOCATION: 34	ZIP: 94806 COMPUTER READABLY MEDIUM TYPE: COMPUTER: IBM OPERATING SYST SOFTWARE: PAT CURRENT APPLICATION NU FILING DATE: CLASSIFICATION ATTORNEY/AGENT IN REGISTRATION N REGISTRATION N REFERENCE/DOCK TELECOMMUNICATIO	3, 7 3, 7 3, 7 3, 7 3, 7 3, 7 1, 7 1, 7 1, 7 1, 7 1, 7 1, 7 1, 7 1	SerAsnPro	Prova:	AAAGG	AlaAlaS :	AlaAsı :: CCAAA
: ty: arity	ONE: (510) 262- XX: (510) 222-97 XX: (510) 222-97 XX: SEQ ID NO: CHARACTERISTICS : 3256 base pai nucleic acid EDNESS: double 3Y: linear TYPE: CDNA EY: CDS ON: 342541	COMPUTER: 94806 COMPUTER: FLOPPY di COMPUTER: IBM PC compa OPERATING SYSTEM: PC-L SOFTWARE: PATENTION DATA: APPLICATION NUMBER: US FILING DATE: CLASSIFICATION: 435 ATFORNEY AGENT INFORMATIC NAME: Giotta, Gregory REGISTRATION NUMBER: US REFERENCE/DOCKET NUMBER TELECOMMUNICATION INFORMATIC NAME: GIOTTON INFORMATIC NAME: GIOTTON INFORMATIC NAME: GIOTTON INFORMATIC NAME: GIOTTON INFORMATIC NEGROUP SOME STANDARD SOME SOME SOME SOME SOME SOME SOME SOME	3, Application 3, Application 5948643 INFORMATION: ANT: Rubinfel ANT: Ligenfel ANT: Ligenfel ANT: Ligenfel OF INVENTION: OF SEQUENCES: PONDENCE ADDRE ESSEE: ONYX PET: 3031 Rese E: Richmond E: CA		LValLy ;;; 3ATTGC	CTAGG	aSerAs ::: GACAGA	oGlnTh: : TTGAC
0.3 91 42 : 23	N 0200000000000000000000000000000000000	FORMSERS	expex, fight:	159 3221	sLysGlu TAAAGAG	CGCCAT	PAlaTr GCAAT	rAspAl AGATGC
316 .50 .148 .278	262-8710 2-9758 NO: 3: TICS: pairs d ble ble	ਹਿਲ ਦੇ ਜ਼ਿੰਦੇ ਚੋਲ	US/0896875 d, Bonnee Paul G. ter, Carol erilyn T. MODULATORS 6 SS: harmaceutic arch Drive		uGluAr GGCAG <i>I</i>	CGCCA	pGluLy ;;; TGATGC	aLeuGl :: AGAGAA
	0	e S-DO #1. 968, 968,	on US/08968751 sld, Bonnee , Paul G. lter, Carol Terilyn T. Terilyn T. BOULATORS OF BESS: Pharmaceuticals Pharmaceuticals		gglnAs ATCCG	AGACA	'SALAAI ::: TTCAAC	nSerG] ; ; ;GGAATO
Length: Matches: Conservati Mismatches Indels:		0, Vers 751	F BRCA1		snValA: : CTAAGT	laLeuAsp TCTTGAT	erAspAlaTrpGluLysAlaAlaThrProI :: cagaTgCaATTGATGCTTCAACAAGTCCAG	luGluA CAGCTA
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256 7 0 3					ThrThr	ThrLys ::: CAA	CAATCG	lnSer ::: hTGCA
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                                                                                                                                                                                 CLASSTTEE: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Vt CURRENT APPLICATION DATA:

FILING DATE:
CLASSTTEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08591079 Patent No. 5972899 GENERAL INFORMATION:
                                            TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 7:
                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 1566
TELECOMMUNICATION INFORMATION:
TELEPIONE: (202) 887-1500
              SEQUENCE CHARACTERISTICS:
LENGTH: 3622 base pair:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis Induced by Shigella
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                           (202) 887-0764
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acid
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; NAME/KEY: CDS; LOCATION: 575..2356; OTHER INFORMATION: , OTHER INFORMATION: , US-08-591-079-7
                                                                                                                                                                                                                                                                                                                                                                 RESULT 18
US-08-591-079-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6 (1-159) x US-08-591-079-7 (1-3622)
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                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08591079 Patent No. 5972899
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOMPHTER: IBM PC compatible
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
                                                                                                                                                                                                     TITLE OF INVENTION: AF NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                           1250 ATTCTGACC 1258
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                                                                                                                                               STREET: 2000 Pennsylvania Avenue, CITY: Washington
                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 LeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGlu---AspLys 48
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                                                                                                                                                                                       MORRISON & FOERSTER
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/gene= "si
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Indels:
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Matches:
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CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: FILING DATE:

US/08/591,079

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Best Local Similarity:
RESULT 19
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REFERENCE/DOCKET NUMBER: 1566
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: CDS
LOCATION: 543..2324
OTHER INFORMATION:
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: li
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                                   ATTCTGACC 1226
                                                                ValAsnThr 149
                                                                                                   ACGGATGCGACGGTTAAAGCAGGCACAGACGCCAAAGCCGAAAGCCGAGAAAGCGGATAAC
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
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Patent No. 5948677
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 654-
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                        1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
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1189 GAGGCGGCGGAGAAGGCGCGCGCCGAGGCG----GAGGCGGCGGCGGAGGAGCAGAAGGCG 1245
                                                        1132
                                                                                                                                                                                                                                                                                           892 CGCGTGGTGGACAAGCTGGTGGAGGACGCGGCGGCGCGCTGGCAGCCAATCGCAGCACC
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                           82
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                                                                                                                                                                                                                                                            45 IleGluAspLysGluAlaThrThrAla-----
                                                                                                                                                                                                                                                                                                                    35 ArgAlaIleAspGluLeuLysLysGlnAla------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/762,106 FILING DATE: 09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                               GAGCTGACGGCG----CAGGCGGAGGAGGCGGCCAACGCCAAGTGGGAGGCGGACAAGGCG 1188
                                                                                                                                                                        CTGGCGGACAAGGCCGCCAGCAGCGCCGCCGGTGGACGCCTGGGCGGAGCGGCAGGCC 1011
                                                                                  GlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys----
                          ----AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAla
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FRAME INDEPENDENT EPITOPE
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1548 base pairs
LENGTH: 1548 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER;
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Roleman "."
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REGISTRATION NUMBER: 3
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US-08-762-106-6
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                                                                                       MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pair
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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US-09-320-774-6
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Patent No. 6265545
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan
TITLE OF INVENTION: READING
TITLE OF INVENTION: TAGGING
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                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                           APPLICATION NUMBER: FILING DATE:
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Conservative:
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US-08-106-981-1
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Best Local Similarity:
                                                                                            Sequence 1, Application US/08106981 Patent No. 5731419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
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CORRESPONDENCE ADDRESS:
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27.17%
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US-09-847-539A-6 (1-159) x US-09-320-774-6 (1-1581)
GENERAL INFORMATION:
APPLICANT: SARHAN, Fathey
APPLICANT: HOUDE, Mario
APPLICANT: LALIBERT, Jean-Francis
TITLE OF INVENTION: DNA MOLECULES ENCODING FREEZING
TITLE OF INVENTION: TOLERANCE PROTEINS IN GRAMINEAE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                  1384 GTGGAGGCTGAGGTGGCCAAGGCGGTGGAGGCTGTGCCC 1422
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Conservative:
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RESULT 24
US-08-072-070-1
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Best Local Similarity:
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GENERAL INFORMATION: APPLICANT: Briles
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TELEX: 200797 NIN UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORREY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TYPE: Nucleic acid
TYPE: Nucleic acid
Double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
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                                                                                                          GCACAGGGCATCACGGACAAAGTCGCCGCCGCGCCCAAAAAGGAAGCT
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Conservative:
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Best Local Similarity:
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                                                                                                                                                                                                                                                   Score:
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TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                     CLONE: JY2
FEATURE:
NAME/KEY:
LOCATION:
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APPLICATION NUMBER: US
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TELEFAX: (703) 521-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/835,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
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LENGTH: 2085 base pairs
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MEDIUM TYPE: Floppy disk
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                                694 AAAGCTACTGAAGCCAAACAAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATC 753
                                                                                           634 GCACCAGAACTTACTAAAAAACTAGAAGAAGCTAAAGCAAAATTAGAAGAGGCTGAGAAA 693
                                                                                                                                                                                                                                                                                                                             LOCATION:
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OPERATING SYSTEM:
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STATE: Virginia
63
                                                                                                                  24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAla---IleAspGluLeuLysLys 42
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                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal----
                                                           GlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeu
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McDaniel, Larry
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SYSTEM: PC-DOS/MS-DOS
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..2025, 2029..2031, 2035..2085)
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Lte 1203, 2001 Jefferson Davis Highway
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US-08-465-746-1
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                                                                                                                       TELEPHONE: (703) 111-0378
TELEFAX: (703) 521-0378
TELEEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
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APPLICANT: Briles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yother, Janes L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: EPITOPIC REGIONS OF PNEUMOCOCCAL SURFACE
                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/835,698 FILING DATE: 12-FEB-1992 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1054
ORIGINAL SOURCE: ORGANISM: Str
                                                                                                                                                                                                                                                                                                         FILING DATE: 15-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
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                                     ANTI-SENSE:
                                                    HYPOTHETICAL:
                                                                       MOLECULE TYPE:
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STATE: Virginia
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                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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OPERATING SYSTEM:
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                                                                                                            STRANDEDNESS:
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Yother, Janet L
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-214-164-1
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                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08214164 Patent No. 5728387
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: BRILES, DAVID E.
APPLICANT: YOTHER, JANET L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
                             ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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IMMEDIATE SOURCE:
CLONE: JY4313
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CORRESPONDENCE ADDRESS:
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                                                                                                   STREET: Suite 120
CITY: Arlington
STATE: Virginia
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LOCATION:
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LOCATION: 1..2085
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COMPUTER: IBM PC OPERATING SYSTEM:
                                                                       COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                           ADDRESSEE:
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                                                                                                                                          SE: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Dav
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Best Local Similarity:
Query Match:
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US-08-214-164-1
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TELEFAX: (703) 521-0813
TELEX: LUXPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
1054 GAAGCTGACCTTAAGAAAGCAGTTAATGAGCCAGAAAAA 1092
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APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/0
FILING DATE: 17-MAR-1994
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REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAla---IleAspGluLeuLysLys
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STRANDEDNESS: doub
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                            Lys---AspThrLysProValValLysLysGluGluArg 144
                                                             TACTTTAAAGAAGGTTTAGAGAAAAACTATTGCTGCTAAAAAAGCTGAATTAGAAAAAACT 1053
                                                                                           -----SerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThr 132
                                                                                                                            GAAATTGCAAAACTTGAAGATCAACTTAAAGCTGCTGAAGAAAACAATAATGTAGAAGAC
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US-09-847-539A-6 (1-159) x US-08-469-434-1 (1-2085)
                                                              Percent Similarity:
Best Local Similarity:
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US-08-469-434-1
                                                                                                                                Alignment Scores:
                                                                                                                                                                   US-08-469-434-1
                                                                                                   Score:
                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Applic Patent No. 5753463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
[INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-100
TELFCOMMUNICATION NUMBER: US/07/656,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/072,065
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite 120
CITY: Arlington
STATE: Virginia
                                                                                                                                                                               NAME/KEY:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                   NAME/KEY:
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(703) 52
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90.00
39.22%
24.18%
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                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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n Davis Highway
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US-08-214-222-1
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GENERAL INFORMATION:
                                                                                                                                                                                                  FILING DATE: 12-FEB-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEFAX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
   HYPOTHETICAL:
                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
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CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 22202-0286
                                                         TOPOLOGY:
                                                                                 STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAGCTAAACTATCAAAACTTGAAGAGTTAAGTGATAAGATTGATGAGTTAGACGCT 933
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                            linear
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ite 1203, 2001 Jefferson Davis Highway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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                                                                                                                                                                                                                                                                                                                                                                              US-08-467-852A-1
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                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08467852A Patent No. 5856170
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                 APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
APPLICANT: WOTHER, Janet L.
APPLICANT: MCDANIEL, LAITY S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
COMMERCE ADDRESS:
COMMER
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IMMEDIATE SOURCE:
CLONE: JY2008
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                           CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer 102
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                                                      745 Fifth Avenue
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                      DB:
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INFORMATION FOR SEQ ID NO: 1:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-588-0800
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   934
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GAAATTGCAAAACTTGAAGATCAACTTAAAGCTGCTGAAGAAAACAATAATGTAGAAGAC 993
                            GluGluAlaGluValValGlnSerAspAsnAlaAla-----
                                                          AAAAAAGCTAAACTATCAAAACTTGAAGAGTTAAGTGATAAGATTGATGAGTTAGACGCT
                                                                                      AspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer 102
                                                                                                                                                                                                                                             AAAGCTACTGAAGCCAAACAAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATC
                                                                                                                                                                                                                                                                      GlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeu
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Matches:
Conservative:
Mismatches:
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Alignment Scores:
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US-08-468-718-1
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US-08-468-718-1
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                                                                                                                                                                                STRAIN: Rx1
IMMEDIATE SOURCE:
CLONE: JY2008
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,068
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pair
                                                                                                                    FEATURE
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CORRESPONDENCE ADDRESS:
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                                                                                   LOCATION:
                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 15-FE
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CITY: Arlington
STATE: Virginia
                                                                                                                                    LOCATION:
                                                                                                                                                    NAME/KEY:
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Suite 1203, 2001 Jefferson Davis Highway
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Yother, Janet L
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Best Local Similarity:
Query Match:
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US-08-246-636-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08246636 Patent No. 5965141
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Briles
APPLICANT: Yother
                                       SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,636
FILING DATE: 20-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EPITOPIC REGIONS OF PNEUMOCOCCAL SURFACE TITLE OF INVENTION: PROTEIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1054 GAAGCTGACCTTAAGAAAGCAGTTAATGAGCCAGAAAAA 1092
             FILING DATE: 15-FEB-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B74 AAAAAAGCTAAACTATCAAAACTTGAAGAGTTAAGTGATGAGTTAGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 Lys---AspThrLysProValValLysLysGluGluArg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          994 TACTTTAAAGAAGGTTTAGAGAAAACTATTGCTGCTAAAAAAGCTGAATTAGAAAAAACT
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                                                                                                                                                                                                                                                               STREET: Suite 12
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     STATE: Virginia COUNTRY: U.S.A.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Yother, Janet L
McDaniel, Larry S
Wu, Hong-Yin
NVENTION
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Suite 1203, 2001 Jefferson Davis Highway
                            15-FEB-1991
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US 07/835,698
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                                                                                                                                         Version #1.25
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US-09-847-539A-6 (1-159) x US-08-246-636-1 (1-2085)
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RESULT 32
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TELEFAX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICATION NUMBER: 1
FILING DATE: 20-APR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-APR-1993 TELECOMMUNICATION INFORMATION:
                                 1054
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                               GAAGCTGACCTTAAGAAAGCAGTTAATGAGCCAGAAAAA 1092
                                                                   Lys --- AspThrLysProValValLysLysGluGluArg 144
                                                                                                                                                                           GAAATTGCAAAACTTGAAGATCAACTTAAAGCTGCTGAAGAAAACAATAATGTAGAAGAC 993
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                                                                                                                                                                                                                                                                                    AspasnalaalaSeraspalaLeuGluAlaLeuAlaAspGlnThrAspalaLeuGlnSer 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGCTACTGAAGCCAAACAAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATC 753
                                                                                                      TACTTTAAAGAAGGTTTAGAGAAAACTATTGCTGCTAAAAAAAGCTGAATTAGAAAAAACT 1053
                                                                                                                                                                                                                                                                                                                                                                                             GCTGAATTGGAAAATCAAGTTCATAGACTAGAACAAGAGCTCAAAGAGATTGATGAGTCT 813
                                                                                                                                        -----SerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThr 132
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Matches:
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Indels:
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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US-08-247-491A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 1:
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FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: YOTHER, Janet L.

TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN MUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEF: FROM THE PROTEIN FROM THE PROTE
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Streptococcus IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO . . .
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                                                                 694 AAAGCTACTGAAGCCAAACAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATC
                                                                                                                                                                                                   634 GCACCAGAACTTACTAAAAAACTAGAAGAAGCTAAAGCAAAATTAGAAGAGGCTGAGAAA
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                                                                                                                                                                                                                                                             24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAla---IleAspGluLeuLysLys 42
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STATE: NY
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GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal------
                                                                                                                              GlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeu 62
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US-08-319-795-1
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                                                                                                    TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Briles, Larry S
APPLICANT: Yother, Janet L.
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: Epitopic R
TOTAL OF TOTAL PROCEIN A
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              FILING DATE: 12-FEB-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,896
FILING DATE: 20-APR-1993
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 HYPOTHETICAL:
                     MOLECULE TYPE:
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OPERATING SYSTEM:
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STREET: Davis Highway
CITY: Arlington
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                                      TOPOLOGY:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-468-985-1
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Patent No. 5997882
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                                                                                                               APPLICANT: Briles, David E.
APPLICANT: Yother, Janet L.
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: Epitopic Regions
TITLE OF INVENTION: Protein A
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CLONE: JY4313
                                                                               CORRESPONDENCE ADDRESS:
                                                                                                 NUMBER OF SEQUENCES:
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STREET:
CITY: AI
STATE: V
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LOCATION:
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Arlington
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                                 Davis Highway
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                                              E: Sheomaker and Mattare, Ltd.
1203 Crystal Plaza Bldg. 1, 2001 Jefferson
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US-08-468-985-1
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ZIP: 22202-UZGC
ZIP: 22202-UZGC
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THE PC-DOS/MS-DOS
COMPUTER: COMPUTEM: PC-DOS/MS-DOS
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IMMEDIATE SOURCE:
TYPNE: JY4313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/048,896 FILING DATE: 20-APR-1993 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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LENGTH: 2085 base pairs
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                                754 GCTGAATTGGAAAATCAAGTTCATAGACTAGAACAAGAGCTCAAAGAGATTGATGAGTCT 813
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                                                                                                                    GlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeu 62
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                                                                GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal-----
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                                                                                                                                                                           Alignment Scores:
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                                                                                                                            Percent Similarity:
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APPLICANT: Briles, David E.
APPLICANT: Wu, Hong-Yin
TITLE OF INVENTION: MUCOSAL ADMINISTRATION
TITLE OF INVENTION: PNEUMOCOCCAL ANTIGENS
                                                                                                                                                                                                                                                                 TELEFAX: (212) 840-0712
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2086 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45*
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 30-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: New York
STATE: New York
COUNTRY: United
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30-SEP-1994
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                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus pneumoniae US-08-446-201-2
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CURRENT FILING DATE: 1995-05-19
EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-05-20
EARLIER APPLICATION NUMBER: 08/048,896
EARLIER APPLICATION NUMBER: 07/835,698
EARLIER APPLICATION NUMBER: 07/835,698
EARLIER APPLICATION NUMBER: 07/835,698
EARLIER FILING DATE: 1992-02-12
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SEQ ID NO 2
LENGTH: 2086
TYPE: DNA
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Patent NO. 6042838
GEMERAL INFORMATION:
APPLICANT: BRILES, David E.
APPLICANT: WU, Hong-Yin
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA)
FILE REFERENCE: 454312-2018
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Matches:
Conservative:
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RESULT 37
US-08-937-271-9
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Patent No. 6063386
                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dale, James B.

APPLICANT: Lederer, James W.

TITLE OF INVENTION: RECOMBINANT MULTIVALENT M
TITLE OF INVENTION: VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                      MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1054 GAAGCTGACCTTAAGAAAGCAGTTAATGAGCCAGAAAAA 1092
                 HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     934
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            NAME: Rosenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 481112.405C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: doub
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   ORGANISM:
                                                                                               TOPOLOGY:
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Streptococcus pyogenes
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; LOCATION:
US-08-937-271-9
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US-07-813-584A-1
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                       APPLICANT: Fischetti, Vincent A. APPLICANT: Bessen, Debra E. TITLE OF INVENTION: No. 5352588e
                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                   838
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                                                                          ADDRESSEE: Kittie Murray
STREET: 98 Cutter Mill Road
CITY: Great Neck
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                                ZIP:
                                                               STATE:
                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCA 840
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Matches:
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Indels:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Release #1.0,

Version

#1.25

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RESULT 39
US-08-330-515-1
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
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Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Relei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19911224
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
FEATURE:
                                                              1287
                                                                                                                          1236
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LENGTH: 1560 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MUTTBY, KITLIE
REGISTRATION NUMBER: 30,246
REFERENCE/DOCKET NUMBER: RU-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Murray, Kittle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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                                                            GCTAACCCA 1295
                                                                                          SerAsnPro 159
                                                                                                                          CCTAGCCAAAATAAAGGAATGAGA-----
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                                                                                                                                                     ProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGlu 156
 Application US/08330515
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: RU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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FILING DATE: 24-DEC-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Bessen, Debra E.
TITLE OF INVENTION: No. 5556944el Immunoglobulin A Binding Protein
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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STRANDEDNESS: single
TOPOLOGY: unknown
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                                                                                                                                                                                                                                               17 LeuThrAsnLeuLeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAla
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                                                                                                                                                                         37 IleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAla
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                             AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln 96
                                                                                       AlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGlu
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2421 N.W. 41st Street, Suite
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FRIGHT: 1771 base pairs
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                                                                                                                                                              FEATURE:
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                ProArgIleIleProAsnGlyGlyThrLeuThr-AsnLeuLeuGlyAsnAlaProGluLy
CCGCGTCCAGGCCCTCGAGGAGGCAGCGCGCGTCTCCGCGCGGAGCTGGAGGCGGCCGAGGA
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-O-/Ggn2_1/USPTO_spool/US09847539/runat_10102002_093105_4982/app_query.fasta_1.526
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-NO_KLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDENT=0.5 -FGAPDP=6 -FGAPEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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ALIGNMENTS

RESULT 1 AAD00560 standard; DNA; Streptococcus pyogenes strain SF370 GRAB protein coding region. 29-AUG-2000 AAD00560; immune response; (first entry) Streptococcus ВP pyogenes

GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; Streptococcus pyogenes. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding full-length GRAB protein from S. pyogenes strain SF370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
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                                                                                                GCCTTAGAAGCATTAGCGGATCAAACAGACGCTTTACAATCAGAAGAAGCTGCGGTTGTT
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                                                                                                           New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
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The patent discloses a new family of proteins termed GRAB (protein related alpha2M binding protein) from Streptococcus pyogenes which the ability to bind alpha2-macroglobulin (alpha2M) and show homolog

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    related alpha2M binding protein) from Streptococcus pyogenes which has the ability to bind alpha2-macroglobulin (alpha2M) and show homology protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective
                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New alpha2M binding protein for generating to group A streptococcus and purifying the
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DB; AAY71046.
            AlaAlaThrProIleAlaLeuAspValLysLysThrLysAspThrLysProValValLys
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                                                                                                                                                                                 The patent discloses a new family of proteins termed GRAB (protein Greiated alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus progenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain API.
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                                                                                                                                                                                                                                                                                                                              New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein -
                                                                                                                                                                                                                                                                                                                                                                                                Bjorck LH,
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                                                                                                                                                                                                                                                                                            GRAB protein; protein G related alpha2M binding protein; vaccalpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                        Bjorck
                                                                                                                                          02-NOV-1998;
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The patent discloses a new family of proteins termed GRAB (protein related alpha2M binding protein) from Streptococcus pyogenes which the ability to bind alpha2-macroglobulin (alpha2M) and show homolog

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Claim 13;

Page 64; 67pp; English.

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            ValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnValAsn
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ValAspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu

(1-777)

US-09-847-539A-6 (1-159) x AAD00561

Alignment Pred. No.

Scores:

No.:

Percent Similarity: Best Local Similarity:

1.83e-65 692.00 64.02% 64.02% 89.06%

Matches:
Conservative:
Mismatches:
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                                                                             related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequencis a DNA encoding partial GRAB protein from S. pyogenes strain KTL9. The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAB protein;
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                                                                                                                                                                                                                                                                                                                                       The patent discloses a new family of proteins termed GRAB (protein
                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 63-64; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
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/product= "GRAB protein"
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23-APR-1986;
17-FEB-1987;
19-JUN-1987;
1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1949 BP; 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments and variants of the sequence are claimed esp. incorporated into a non-pathogenic host eg. E.coli, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-297491/39
P-PSDB; AAR07013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at high levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8a-c; 48pp; English
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                                                                                                                                                                                                                                                                                                                                        GTTGATTCACCAATCGAAGATACCCCCAATTATTCGTAATGGTGGTGAATTAACTAATCTT
ACTIGTTAAATCAATTGAATTAGCTGAAGCTAAAGTCTTAGCTAACAGAGAA
             AspValLysLysThrLys-----AspThrLysProValValLysLysGlu
                                             ATTTCAGAAGCAACAGATGCCTTATCTGATTTCTTGAAATCGCAAACACCTGCTGAAGAT
                                                                                                           AAAGAATTCAACAATATGGAGTAAGTGACTATTACAAGAATCTAATCAACAATGCCAAA
                                                                                                                                                            LysAlaAspAsn-----AlaAlaSerAspAlaLeuGluAlaLeu------AlaAsp
                                                                                                                                                                                                                                                              LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scores:
                                                                     ---SerAspAlaTrpGlu-----
                                                                                              ACTGTTGAAGGCATAAAAGACCTTCAAGCACAAGTTGTTGAATCAGCGAAGAAAGCGCGT
                                                                                                                                                                                            GCTTGGGAAGCAGCGGCA----GCAGCAGATGCTCTAGCAAAAGCCAAAGCAGATGCCCTT
                                                                                                                                                                                                                 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
                                                                                                                                                                                                                                            ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCAGCGGCAGCTGAAAATGCTGGGGCAGCA
                                                                                                                                                                                                                                                                                          CTGGGGAATTCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGATTTG
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86US-0854887.
87WO-US00329.
87US-0063959.
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-35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloned protein G variant genes - expressing proteins having immunoglobulin-binding properties protein G and derived from Streptococcus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene encodes protein G of non-pathogenic streptococcus sp. allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones and treatment of disease.
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DB; AAP95030.
                                                                                                         LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
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                                       LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                 CTGGGGAATTCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGATTTG
                                                                                                                                                                  GTTGATTCACCAATCGAAGATACCCCCAATTATTCGTAATGGTGGTGAATTAACTAATCTT
ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCAGCGGCAGCTGAAAAATGCTGGGGCAGCA 856
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487..492
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-35_signal
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                Gene encodes protein G of non-pathogenic streptococcus sp. allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones and treatment of disease.
                                                                                       Cloned protein G variant genes - expressing proteins having immunoglobulin-binding protein G and derived from Streptococcus sp.
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P-PSDB; AAP95030.
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                                                                      Disclosure; ; 116pp; English.
                                                                                                                                                                  Fahnestock SR
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Pred. No.:
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                    23-APR-1986;
17-FEB-1987;
19-JUN-1987;
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                                                    20-JUN-1988;
14-FEB-1986;
                                                                                                          11-SEP-1990
                                                                                                                               US4956296-A
                                                                                                                                                                                               Streptococcus
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(GENE-) GENEX
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                                                                                                                                                                                                                                                                                                                                                                     AspValLysLysThrLys-----AspThrLysProValValLysLysGlu 142
                                                                                                                                                                                                                                                                                                                                                                                            ATTTCAGAAGCAACAGATGGCTTATCTGATTTCTTGAAATCGCAAACACCTGCTGAAGAT
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 CORP
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                    88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                    88US-0209236
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          Sequecne encoding Streptococcus
                                                                                         AAQ10001 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant Protein G variants - obtd, using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
                                                               AAQ10001;
                                                                                                                                                                                                 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The variants have a higher binding efficiency and capacity immunoglobulin, and may be used for purifying, detecting an isolating antibodies.
                                      13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1950 BP; 706 A; 323 C;
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                                                                                                                                             ACTGTTAAATCAATTGAATTAGCTGAAGCTAAAGTCTTAGCTAACAGAGAA 1144
                                                                                                                                                           AspValLysLysThrLys-----AspThrLysProValValLysLysGlu
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                                                                                                                                                                                                                                                                                                                       LysAlaAspAsn-----AlaAlaSerAspAlaLeuGluAlaLeu------AlaAsp
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DB; AAR07012.
                                                                                                                                                                                                 ATTTCAGAAGCAACAGATGGCTTATCTGATTTCTTGAAATCGCAAACACCTGCTGAAGAT
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                                                                                                                                                                                                                                                    ACTGTTGAAGGCATAAAAGACCTTCAAGCACAAGTTGTTGAATCAGCGAAGAAAGCGCGT
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Best Local Similarity:
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19-JUN-1987;
20-JUN-1988;
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CDS
                                                                                                                                                                                                                                                                                                                                               Protein G gene product may be modified allowing the va
imobilised and exhibit different binding profiles. The
protein is useful in purification and detection of Igs
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23-APR-1986;
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and purificn. immunoglobulin(s) and in
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          GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla---
                                                  LysAlaAspAsn-----AlaAlaSerAspAlaLeuGluAlaLeu------AlaAsp
                                                                                                                                                                                          1991-006758/01.
ACTGTTGAAGGCATAAAAGACCTTCAAGCACAAGTTGTTGAATCAGCGAAGAAAGCGCGT
                                                                          GCTTGGGAAGCAGCGGCA----GCAGCAGATGCTCTAGCAAAAGCCAAAGCAGATGCCCTT
                                                                                            AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
                                                                                                                 ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCAGCGGCAGCTGAAAATGCTGGGGCAGCA
                                                                                                                            LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                                                                                     CTGGGGAATTCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGATTTG
                                     AAAGAATTCAACAAATATGGAGTAAGTGACTATTACAAGAATCTAATCAACAATGCCAAA
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86US-0829354.
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87WO-US00329.
87US-0063959.
88US-0209236.
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Matches:
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RESULT 12
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20-JUN-1988;
19-JUN-1990;
21-APR-1992;
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                                                                                       A 1.9kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7809. The Protein G 1gG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domain the structure of the streptococcal protein G variants.
                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                                                              Sequence 1950
                                                                                 are claimed.
                                                                                                                                     Example
                                                                                                                                                     New recombinant streptococcal protein G antibody detection and purification and
                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                             Fahnestock SR;
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immunoglobulin; Lancefield Group G; bacterial
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                                                                                                                                                                                            1994-159179/19
                                            Scores:
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                                                                                                                                                                                                                                               86US-0854887.
87US-0063959.
88US-0209236.
90US-0540169.
92US-0871539.
                                                               B₽;
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Conservative:
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for therapy
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Query Match:

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                                                                    20-JUN-1988;
14-FEB-1986;
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                   WPI; 1990-297491/39.
                                                                                                                                                                                   CDS
         P-PSDB; AAR07014.
                                    Fahnestock SR;
                                                                                                                                                                                                            Streptococcus
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                                                                                                                                                                                                                                             encoding Protein
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                                                     CORP
                                                                                                                                                                                                          sp. Lancefield Group
                                                                    86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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                          Streptococcus
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                                                                                             AAQ10002;
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                                          Immunoglobulins;
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                                                          encoding Streptococcus
                                                                           (first entry)
                        sp GX7805.
Location/Qualifiers 577..2355
                                         Ig;
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187.00
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Disclosure; Fig 9; 48pp; English
                                                                                                                                    Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
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Fragments and variants of the sequence are claimed incorporated into a non-pathogenic host eg. E.coli, at high levels. The variants have a higher binding efficiency and capacity immunoglobulin, and may be used for purifying, detecting an esp.

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411 ç 479 <u>ი</u> 626 •∃ `` 0 other

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Length:
Matches:
Conservative:
Mismatches:
Gaps:
       Indels:
2383
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(1-2383)

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40
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CTGGGGAATTCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGATTTG LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 795

ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCAGCGGCAGCTGAAAATGCTGGGGCAGCA LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp 855 60

GCTTGGGAAGCAGCGGCA---GCAGCAGATGCTCTAGCAAAAGCCAAAAGCAGATGCCCTT 912

AAAGAATTCAACAAATATGGAGTAAGTGACTATTACAAGAATCTAATCAACAATGCCAAA 972 LysAlaAspAsn-----AlaAlaSerAspAlaLeuGluAlaLeu-------AlaAsp 95

GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla--- 114
::: :::::: :::::: ACTGTTGAAGGCGTAAAAGACCTTCAAGCACAAGTTGTTGAATCAGCGAAGAAAGCGCGT 1032

---SerAspAlaTrpGlu------------LysAlaAlaThrProIleAlaLeu ATTTCAGAAGCAACAGATGGCTTATCTGATTTCTTGAAATCACAAACACCTGCTGAAGAT 1092 127

AspValLysLysThrLys-----AspThrLysProValValLysLysGlu 142 ACTGTTAAATCAATTGAATTAGCTGAAGCTAAAGTCTTAGCTAACAGAGAA 1143

GX7805 protein

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14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
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and purificn. immunoglobulin(s) and ir
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                                                                                                                                                                                                                                                                                                                                        otein G gene product may be modified allowing the variant to imobilised and exhibit different binding profiles. The bound otein is useful in purification and detection of Igs and frame
                                                                                                                                                                                                                        ValAspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu
                                                                                                                                                            LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
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ATTTCAGAAGCAACAGATGGCTTATCTGAATTCTTGAAATCACAAAACACCTGCTGAAGAT
                                                      ACTGTTGAAGGCGTAAAAGACCTTCAAGCACAAGTTGTTGAATCAGCGAAGAAAGCGCGT
                                                                     GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla---
                                                                                     AAAGAATTCAACAAATATGGAGTAAGTGACTATTACAAGAATCTAATCAACAATGCCAAA
                                                                                                    LysAlaAspAsn-----AlaAlaSerAspAlaLeuGluAlaLeu-----
                                                                                                                    GCTTGGGAAGCAGCGGCA---GCAGCAGATGCTCTAGCAAAAGCCAAAGCAGATGCCCTT
                                                                                                                                 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
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86US-0829354.
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                                                              Percent Similarity:
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RESULT 15
AAQ75036
                                                 Alignment
Pred No:
Score:
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23 - APR-1986;
19 - JUN-1987;
20 - JUN-1988;
19 - JUN-1990;
21 - APR-1992;
                                                                                                                                    A 2.4kb HindIII fragment containing the entire coding sequence for protein G was isolated from Streptococcus GX7805 using the 1.9kb Protein G coding sequence from Streptococcus GX7809. The Protein has IgG-binding activity which has been localised to the B repeat structure. Streptococcal Protein G variants comprising the B domastructure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
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                                                                                                                                                                                                                                      New recombinant streptococcal protein G antibody detection and purification and
                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                  Sequence
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87US-0063959.
88US-0209236.
90US-0540169.
92US-0871539.
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577..2358
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/transl_except=
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38.85%
24.07%
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G; bacterial
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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aa:Leu
aa:Gly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
                                                                                                                                                                                                                                                                              Streptococcus strain G 148; protein G'; protein G primer; liposome; liposomal delivery complex; connecting molety; antibody; Fc region; diagnosis; therapeutic agent; antibiotic; antidepressant; antiviral; antitumourigenic; cytokine; hormone; imaging agent; neurotransmitter; stimulant; cytotoxic agent; malignant cell; ss.
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          Lau JR;
                                                                                 19-MAY-1999;
                                                                                                         25-NOV-1999
                                                                                                                                                                                                                                                        Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                               10-MAR-2000
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                                  (SDGS-) SDG INC
                                                          20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
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                                                          98US-0086347
                                                                                 99WO-US11177
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705..1262
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/product= "protein G'"
/transi_except= (pos:7
                                                                                                                                                                                                                   Location/Qualifiers 292..603
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or antibody fragment to a liposome. The construct comprises protein G'
CC and a linking molety for connecting the protein G' to the liposome.
Also described are: (1) a liposomal delivery vehicle comprising: (a) a
CC liposome; and (b) a connecting molety connected to the liposome, which
specifically binds the Fc region of an antibody, for connecting the
CC aptibody to the liposoma; and (2) forming a liposomal carrier comprising:
CC (a) providing liposomal components having binding moleties, for forming
CC connecting molety bound together; and (c) combining the liposomal
CC connecting molety bound together; and (c) combining the liposomal
CC connecting molety bound together; and (c) combining the liposomal
CC connecting molety bound together; and (c) combining to that the
CC binding moleties are exposed on a surface of the liposome, for binding to
C the linking molety, and to facilitate the binding between them. The
CC agents. The liposomes may contain or may be associated with a diagnostic
CC artitumpuridenics, antivirals, cytokines, hormones, imaging agents.
                                                                                                                   antitumourigenics, antivirals, cytokines, hormones, imaging agents, neurotransmitters, or stimulants. They can be used particularly for the delivery of cytotoxic agents to malignant cells. The protein G' connecting molety provides a liposomal delivery complex having improved targeting efficiency. As a result of the binding between Protein G' and the Ec region of antibodies, protein G' shields the Ec regions of the
                                            attached antibodies from non-specific binding to cell-surproteins, and anatomical structures. The present sequence an unidentified protein and protein \mathbf{G}'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New liposome constructs comprising a liposome connected to an antibody, used, e.g. for delivery of cytotoxic agents to malignant cells \,\cdot\,
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P-PSDB; AAY57610, AAY57611.
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or antibody
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                                                                                                   to cell-surfaces,
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s protein G'
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Sequence 1576 ВP; 572 ۶. 270 ü 330 <u>ი</u> 404 .. 0

US-09-847-539A-6 (1-159) x AAZ47931 (1-1576)	DB: 21 Gaps: 7	19.95% Indels:	imilarity: 22.19%	25.75% Conservative:	Score: 155.00 Matches: 81	07 Length:	
	7	210	62	13	81	1576	

800	741 GCTACTGCAGAAAAAGTCTTCAAACAATACGGTAACGACAACGGTGTTGACGGTGAATGG 800	dd.
101	101	Qy
740	681 AAATTAATCCTTAATGGTAAAACATTGAAAGGCGAAACAACTACTGAAGCTGTTGATGCT 740	ф
101	101 Gln	Qy
680	627 AAAGAATTCAACATAGATGAAATTTTTAGCTGCATTACCTAAGACTGACACTTAC	Db
100	81 LysalaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 100	Qy
626	570 GCTTGGGAAGCAGCGGCAGCAGCAGATGCTCTAGCAAAAGCCAAAGCAGATGCCCTT	Db
80	61 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal	Qy
569	511 ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCAGCAGCAGCTGAAAATGCTGGGCAGCA- 569	Db
60	41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp 60	οy
510	451 CTGGGGAATTCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGATTTG	DЬ
40	21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu	Qy
450	391 GTTGACTCACCAATCGAAGATACCCCCAATTATTCGTAATGGTGGAATTAACTAATCTT	Db
20	1 ValaspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu	Qy

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             (GENE-) GENEX
                                                                 20-JUN-1988;
                                                                                            29-DEC-1988
                                                                                                                      W08810306-A
                                                                                                                                                                          Protein G; immunoglobulin;
                                                                                                                                                                                                     Protein G
                                                                                                                                                                                                                                 04-JUL-1990
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                                        19-JUN-1987;
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                                                                                                                                                                                                     gene variant
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                                                                 88WO-US02084
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene encodes protein G variant of non-pathogenic streptococcus allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 83; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAP94785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln-----SerGluGluAla 77
LysLysGluGluArgGlnAsnValAsnThr 149
                                                                                                                                                                                                                                                                                              GAAGTGATCGATGCGTCTGAATTAACACCAGCCGTGACAACTTACAAACTTGTTATTAAT
                                                                                                                                                                                                                                                                                                                        AlavalValLysAlaAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrAlaIleGluAlaAlaSerSerAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGACTGACACTTACAAATTAATCCTTAATGGTAAAACATTGAAAGGCGAAACAACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGGGTACCCATTACCT
                          GCTAAAGATGACGCTAAGAAAGACGATACTAAGAAAGAAGATGCTAAAAAAACCAGAAGCT
                                                                           GAACCAGAAAAACCAGAAGCAAGTATCCCTCTTGTTCCGTTAACTCCTGCAACTCCAATT
                                                                                                                                                                                                                Ala---GluValValGlnSerAspAsnAlaAlaSerAspAlaTrp----
                                                                                                                                                                                                                                                                                                                                                      GTTGACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAAAAAACCA 399
                                                                                                                                                                                                                                                                                                                                                                                                          GAAGCTGTTGATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGT
                                              AlaLeuAspValLysLysThrLysAspThr------
                                                                                                        -----GluLys----
                                                                                                                                   ACTAAGACCTTTACGGTAACTGAAATGGTTACAGAGGTTCCTCGAGGTGATGCACCAACT
                                                                                                                                                                                       GCCTTCAAACAATACGCTAACGACAACGGTGTTGATGGTGTTTTGGACTTATGATGATGCG
                                                                                                                                                                                                                                            GGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACTGCAGAAAAA
                                                                                                                                                                                                                                                                    AlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGlu
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Matches:
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17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 199
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence may be incorporated into a non-pathogenic host eg. E.coli, where they may be expressed at high levels. The proteins have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Protein G variants - obtd. encoding Protein G from Streptococcus immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 798 BP; 277 A; 161 C; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Column 47; 48pp; English.
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                                                                                                                                AlaProGluLysLeuAlaLeuArgAsmGluGluArgAlaIleAspGlu--------
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DB; AARO7004.
                  ThrAlaIleGluAlaAlaSerSerAsp---
                                               AAGACTGACACTTACAAATTAATCCTTAATGGTAAAACATTGAAAGGCGAAACAACTACT
                                                                                                          TCAGAGACAACACTGGCTTTGCCGTAATGAAGAGAGTGCTACAGCTGGGTACCCATTACCT
                                                                                                                                                                         CCAATCGAAGATACCCCAATTATTCGTAATGGTGGTGAATTAACTAATCTTCTGGGGAAT
SR;
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87WO-US00329.
87US-0063959.
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Indels:
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14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
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                Disclosure; Column
                                                                                            WPI; 1991-006758/01.
P-PSDB; AAR10011.
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                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
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86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                          Lee
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             52pp; English
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Immobilised protein G variants - used for detection, isolatiand purificn. immunoglobulin(s) and immunoglobulin fragments
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protein is useful
IgG-binding Streptococcus Protein G variant coding sequence
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                                                                                                                                                   GCTAAAGATGACGCTAAGAAAGACGATACTAAGAAAGAAGATGCTAAAAAAACCAGAAGCT
                                                                                                                                                                    AlaLeuAspValLysLysThrLysAspThr----
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23-APR-1986;
19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
21-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus Protein
                                                                                                                                                                                                                                                                              Protein G isolated from Streptococcus has IgG-binding activity which has been localised to the B repeating structure (see AAR53290).

The nucleotide sequence AAO64648 codes for a claimed Streptococcal protein G variant comprising the B domain active site and retaining
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-159179/19.
P-PSDB; AAR53294.
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                                                                                                                                                                                                                                                  Sequence 798 BP;
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                                                                                                                                                                                                                                                                                                                                                New recombinant streptococcal protein G variants - antibody detection and purification and for therapy
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                                                                           TCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGGGTACCCATTACCT
                                                                                   AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGlu---
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                 ThralaIleGluAlaAlaSerSerAsp----
                                     AAGACTGACACTTACAAATTAATCCTTAATGGTAAAACATTGAAAGGCGAAACAACTACT
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87US-0063959.
88US-0209236.
90US-0540169.
92US-0871539.
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                                                  dysgalactiae
                                 gene;
                                                                                                                                               GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSer
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                                                                                                                                     GAACCAGTAAAAGCTGAGGCTGAACCAGTAAAGGAGGAGAGTAAACAA
                                                                                                                                                                                AspAsnAlaAlaSerAspAlaTrpGluLysAla---AlaThrProIleAlaLeuAspVal
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                                                                                                                                                                                                                                                                           GAAACAACTCCTGCTGTTCAACCAGAGGTTGCAGCCGTCGAAGAGTCTTCTTCTGCTGAT
                                                                                                                                                                                                                                                                                   AspGlnThrAspAlaLeuGlnSerGlu-----::: ||| ||| ||| |||
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                         SS.
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        dysgalactiae
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                                 albumin binding
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Mismatches:
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Gaps:
                                 protein stabilization;
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                                                                                                                                                                A phage lambda EMBL3 library of S. dysgalactiae 8215 DNA was analyzed for alpha-2-macroglobulin, BSA- and IgG-binding activity. Clone lambda-SD1, which expressed all 3 activities, was analyzed to obtain DNA encoding the SA-binding protein, MAG. The mag gene (given in Q86080) encoded a 44 kDa MAG protein (R71670).

Recombinant, immobilized MAG was used for serum albumin affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
promoter
                                                                                                                                                                                                                                    DNA encoding a serum albumin binding protein - used to obtain prods. for sepns., detection, quantification, protein stabilisation or vaccine development
                                                                                                                                                                                                                     Disclosure; Page 29-30; 38pp; English.
                                                                                                                                             Sequence 1555
                                                                                                                                                                                                                                                                                          Guss
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                                                                                                                                                           purification,
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(JONS/) JONSSON H.
(LIND/) LINDBERG M.
                                                                                                                                                                                                                                                                                                                                       06-SEP-1993;
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       963
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      GGTAAAACTGCAGAAGGTGTGACTGCTCTTAAAGATGAAATTTTAGCTTCAAAACCAGCA 1022
                                   AlaIleAspGluLeuLysLysGlnAlaIleGluAsp------
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                    -----LysGluAlaThrThrAlaIleGlu-----AlaAlaSerSerAspAla
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/note= "putative;
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390..1524
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288..1527
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/note= "putative promoter sequence"
230..235
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/note- "putative promoter sequence"
276..281
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34.22%
26.20%
14.74%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ89197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1131 GCAGAAAAAGCCTTCAAACAATACGCTAACGAAAACGGTGTTGATGGTGTTTGGACTTAC 1190
16-MAR-1995
                                  W09507296-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fast alpha-2-macroglobulin binding protein; FAM;
na proteinase-inhibitor binding protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGCTAAAAAACCAGAAGCTAAGAAAGAAGGAAGCTAAGAAAGCTGCAACTCTTCCTACA 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGATGCGACTAAGACCTTTACTGTAACTGAAATGGTTACTGAAGTTCCTGGTGATGCA 1250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProTleAlaLeuAspValLysLysThrLysAspThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerGluGluAla---GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGlu--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGATTGACGCACCTGAATTAACACCAGCTTTGACAACCTACAAACTTGTTATC-----
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230..235
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276..281
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06-SEP-1994;

94WO-SE00826

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                                                                                                                                                                                                                                                                                                                                                                                                         A phage lambda EMBL library of S. dysgalactiae 8215 DNA was analyzed for fast-acting alpha-2-macroglobulin (FAM). BSA- and IgG-binding activity. Clone lambda-SD1, which expressed all 3 activities, was analyzed to obtain DNA encoding the FAM-binding protein, MAG. The mag gene (given in Q89197) encodes a 44 kDa protein (R71929).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding fast alpha 2-macro:globulin-binding proteins to obtain prods. for sepn., detection or quantification or binding inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MUEL/)
(RANT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig.4; 50pp;
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1555 BP; 583 A; 242 C; 304 G; 426 T;
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                                                                                                                                                                                                                                                     --------LysGluAlaThrThrAlaIleGlu-----AlaAlaSerSerAspAla
                                                                                                                                                                                                                                                                     CCAACTGAACCAAAAAAACCAGAAGCAAGTATCCCTCTTGTTCCGTTAACTCCTGCAACT 1310
                                                                                             GATGATGCGACTAAGACCTTTACTGTAACTGAAATGGTTACTGAAGTTCCTGGTGATGCA 1250
                                                                                                                              GCAGAAAAAGCCTTCAAACAATACGCTAACGAAAAACGGTGTTGATGGTGTTTGGACTTAC
                                                                                                                                               SerGluGluAla---GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGlu---
                                                                                                                                                                                AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln
                                                                                                                                                                                                  GTGATTGACGCACCTGAATTAACACCAGCTTTGACAACCTACAAACTTGTTATC-----
                                                                                                                                                                                                                  LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                          ProlleAlaLeuAspValLysLysThrLysAspThr----
                                                                                                                                                                -----AATGGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACT 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) GUSS B.
) JONSSON H.
) LINDBERG M.
) MUELLER H.
) RANTAMAKI L
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LysProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThr 152
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RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoding polypeptide possessing IgG-binding activity of protein G from Streptococcus {\tt G148}.
                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                        misc_feature
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(PHAA ) PHARMACIA AB
                    21-MAR-1986;
                                         20-MAR-1987;
                                                              24-SEP-1987
                                                                                  W08705631-A
                                                                                                                             misc_feature
                                                                                                                                                           misc_feature
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                     86SE-0001325
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/label- C1
732..776
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777..941
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81..233
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/label= C2
942..986
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/label= D2
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459..530
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567..731
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RESULT 25
ABL20337
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  Drosophila; developmental
pharmaceutical; gene; ds.
                            Drosophila melanogaster genomic polynucleotide SEQ
                                                                                                                             1360 AACCCA 1365
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                                                  26-MAR-2002
                                                                     ABL20337;
                                                                                        ABL20337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity protein G from Streptococous G148 (AAN70757) is claimed. See, for example, AAN70754, AAN70755 and AAN70756.
                                                                                                                                                                    1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example;
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                                                                                                                                                                   GAAGCTAAGAAAGAAGACGCTAAGAAAGCTGAAACTCTTCCTACAACTGGTGAAGGCAGC
                                                                                                                                                                                   ValValLysLysGluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGluSer 157
                                                                                                                                                                                                                                                                                                                                             GluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAla
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                                                                                                                                                                                                         ProlleAlaLeuAspValLysLysThrLysAspThr------LysPro 137
                                                                                                                                                                                                                                               CCAACTGAACCAGAAAAACCAGAAGCAAGTATCCCTCTTGTTCCGTTAACTCCTGCAACT
                                                                                                                                                                                                                                                                   SerAspAlaTrpGluLys-----
                                                                                                                                                                                                                                                                                      GATGCGACTAAGACCTTTACGGTAACTGAAATG---GTTACAGAGGTTCCTGGTGATGCA 1179
                                                                                                                                                                                                                                                                                                        AspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla 114
                                                                                                                                                                                                                                                                                                                           GAAAAAGCCTTCAAACAATACGCTAACGACAACGGTGTTGATGGTGTTTGGACTTATGAT 1122
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                                                                                       standard;
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          biology; cell signalling;
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          insecticide;
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US-09-847-539A-6 (1-159) x ABL20337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL040-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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AlaAlaSerAspAlaTrpGluLysAlaAla
                                                     GAGGCTCTCCTGGCTGAAGCTGCCCCCAAAAAGCAGCCGAAGAAGCTAAAGCCCTAAAA 1464
                                                                                                                                                             AAGCAGGCTGCTAAAGGCCAAAAAGGCTGCCGAGGAGGCCGCCAAAATCGCTGCCGAA 1404
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                                                                                                                                                                                                                                                                     CGTAGGGAAGAG - - - AGGGCTCTCAAGGAGGAGGGATCGCCTGACGGCTGAGGCCGAA
                                                                                                                                                                                                                                                                                                                       SerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu-----GlnSerGlu .75
                                                                                                                                                                                                                                                                                                                                                                               GACGAGGTGGAC-----TTGGAAAAGAAGCGTGCCCAGAAAGCCGATGAAGCCCAAG
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                                                                                                                      Best
                                                                                                                                                                   Alignment Scores
                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                       A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecals nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
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06-MAY-1997;
16-MAY-1997;
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LysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGlu 46
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                                              GlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsnAlaProGlu
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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01-APR-1999;
06-APR-1999;
08-APR-1999;
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23-APR-1999;
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                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL018176-ABL30511), expressed DNA sequences (ABL018737-ABB72072).
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pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 27491; 21pp +
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                          New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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P-PSDB; ABB66899.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more geness from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
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                                   Enterococcus
                                                                                                                                                                                                         1835 GACGAGAAGGAAGCC
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                                                                                                                                      standard;
 faecalis;
                               faecalis genome contig
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contig; detection; Enterococcal infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21pp + Sequence Listing; English.
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 486 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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GCAAAAAAAGTTGTG----
                                                                                                                                                                                                                                                                                          ProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAla
                              GluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThr
                                                                 GGTGCATTGGATCAAAGTCAACAAGCAGTGACTGACCAA----CAAGCGGTCGTAGACGAA
                                                                                    AlaAlaSerAsp---AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 103
                                                                                                                                    GAAAAAGACACCATTGATCAATCTGTTAAAGACCAACAAGCAGTGGTCGATCAAAACAAA 302
                                                                                                                                                       LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn
                                                                                                                                                                                                     GTAACAGAGAAACAAGCAATTGTCGATCAAAAACAACAAGTTGCTGACACTGCGAAAAAAA 362
                                                                                                                                                                                                                                       IleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAla
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97US-0044031.
97US-0046655.
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 -GATGAAGCAACACCTTCAGCCMTTGAAAAAGCCAAAAAC
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Matches:
Conservative:
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Indels:
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                                                      This sequence comprises the espB gene from a rabbit
centeropathogenic Escherichia coli (RDEC-1) strain. It codes for a
celaimed EspB virulence factor (see AAW27286). The espB and espA
celaimed EspB virulence factor (see AAW27286). The espB and espA
celaimed EspB virulence factor (see AAW27286). The espB and espA
celaimed EspB virulence factor (see AAW27286). The espB and espA
centeropathogenic E. coli. Claimed novel, isolated EspA polypeptides
centeropathogenic E. coli. Claimed novel, isolated EspA polypeptides
centeropathogenic (EPEC) or enterohaemorrhagic (EHEC) E. coli;
centeropathogenic E. coli espa probes in the diagnosis of
colisease caused by EspA-producing E. coli comprising inserting a
selectable marker nucleic acid into the espA gene. EspA
colisease caused to the espA gene. EspA
                                                                                                                                                                                                                                                                                 EspA from entero-pathogenic or entero-haemorrhagic E. coli immunise against, and treat diseases caused by EspA producing
                                                                                                                                                                                                                                                                                                                                                              Finlay BB,
                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1996;
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RBS
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                     polypeptides can be used to immunise a host susceptible caused by EspA-producing E. coli, and in a method for an disease caused by EspA-producing organisms.
                                                                                                                                                                                                                                               Example 6; Fig 4B; 62pp; English
                                                                                                                                                                                                                                                                        organisms
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Sequence 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen;
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                                                                                                                                                                                                                                                                                                                           AAW27286
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                                                                                                                                                                                                                                                                                                                                                              Kenny B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enteropathogenic E. coli; RDEC-1; virulence factor;
fection; diagnosis; therapy; vaccine; gastroenteriti
BP; 278 A; 211 C; 240 G; 260 T; 0 other;
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31..975
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Alignment Scores:

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US-09-847-539A-6 (1-159) x AAT91293 (1-989)
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WPI; 1995-106854/14
                                                                                                                                        02-MAR-1995.
                                                                                                                                                                  W09506125-A
                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                     Synthetic;
                                                                                                                                                                                                                                                                Synthetic protein G gene, MD1
                                                                                                                                                                                                                                                                                             11-OCT-1995
                                                                                                                                                                                                                                                                                                                         AAQ84886;
                                                                                                                                                                                                                                                                                                                                                     AAQ84886 standard;
                          Lee YM,
                                                                                23-AUG-1993;
                                                                                                            23-AUG-1994;
                                                                                                                                                                                                                     Synthetic; protein G; IgG; Fc recepto: lymphoma; cancer; autoimmune disease;
                                                    ( - DWMI )
                                                                                                                                                                                                                                                                                                                                                                                                                                     153 ThrGlyGluGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AlaLeuGluAlaLeuAlaAspGlnThr...-AspAlaLeuGlnSerGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 AlaIleGluAspLysGluAlaThrThr------AlaIleGluAlaAlaSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGACTAAAACGTTGACTAAGGCAACGGAAAGCGTTGCTGATGCTGTTGAAGATGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTCTACACCATTTATTGCCGTTACCAGTCTTGCCGAAGGCACGAAGACATTGCCAACA
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                                                    APPLIED
                        Okarma TB,
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                                                                                93US-0110653.
                                                                                                            94WO-US09141
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pimmune disease; ds.
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  plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide(s) which bind the comprising a nontotal portion Protein A and/or Protein G
                                                           22-SEP-1995
                                                                                                         AAQ89196
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                                   dysgalactiae
fast alpha-2-macroglobulin binding
ma proteinase-inhibitor binding prot
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                                                                                                                                                                                                   GAAGCTAAAAAAGAAGATGCTAAAAAAGCTGAAACTCTGCCGACTACTGGTGAAGGTTCT
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                                                                                                                                                                                                                                                                                                                    SerAspAlaTrpGluLys----
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                                                                                                         standard;
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the amino
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Best Local Similarity:
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                                                                                                        Query
                                                                                                                                                                                              for fast-acting alpha-2-macroglobulin (FAM)- and IgG-binding activity. One clone, which expressed both activities, was analyzed to obtain DNA encoding the FAM-binding protein, MIG (AAR71929). The mig gene is given in AAQ89196
                        1772
                                                                                                                                                                                                                                                                                 Disclosure; Page 31; 50pp;
                                                                                                                                                                                                                                                                                                                   DNA encoding fast alpha
to obtain prods. for sep
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DB; AAR71929.
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 ThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArg
                       ATTGACGCACCTGAACTAACTCCAGCCTTGACTACTTACAAACTTATTGTTAAAGGTAAC
                                             ValAspSerProIleGluGlnPro-----
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sepn., detection or quantification or
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990S-0132863 990S-0134218 990S-0134218 990S-0134219 990S-0134370 990S-0135124 990S-0135124 990S-0135629 990S-0136392 990S-0137522 990S-0137522 990S-0137522 990S-0137522 990S-0137522 990S-0139452 990S-0139452 990S-0139453 990S-0139453 990S-0139454 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139453 990S-0139461 990S-0139463 990S-0140354 990S-0140354 990S-0140354 990S-0140823 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0144085 990S-0144085 990S-0144331 990S-0144331	012871 013047 013051 013053 013064 013065 01324 01324 01324 01324 01324 01324 01324

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GAGACCACTGAAACAACTTCTGTCGAAGCTAAGGAGACATTTCCGGTCGAGCCGACCAAG
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                                                                                                                                                                                                                                                                                   CCCAAGGAATCAGACATGCAAAACGAAGAAGGCTCTGTTCCTAACAAGCCTGTCTCTGAA
                                          GAACCAGTAAAAGCTGAGGCTGAACCAGTA
                                                   LysLysThrLys---AspThrLysProVal
                                                                                          AspAsnAlaAlaSerAspAlaTrpGluLysAla---AlaThrProIleAlaLeuAspVal
                                                                                                            GAAGCAAAGGTGGAGGCGGTTGCCGTAGCTGCACCCGAAAAGGTTGAGGTT-----
                                                                                                                     GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSer
                                                                                                                                              AACGTAGTAGCCAAGGAGAACAACACAGAAAGCGGTGAGAAACAGAACCAGACAGTGGCT
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                                                                            GCAGTGGAAGCGGAGAAAAAGGCTGAAGCTGAACCAGTAAAGGCTGAGGCT
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9908-0159688

9908-0159584

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9908-0160767

9908-0160768

9908-0160814

9908-0160814

9908-016081

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Mismatches:
Indels:
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9905-0144333 9905-0144335 9905-0144335 9905-0144834 9905-014508 9905-014508 9905-014508 9905-014508 9905-014508 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-014521 9905-01472 9905-014775 9905-015133

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Alignment :
Pred. No.:
                    Qγ
                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
밁
                                                                                                                          Score:
                                                                                                                                                                                                          CC The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part CC from the printed specification, but was obtained in electronic format directly from WIPD at
                                                US-09-847-539A-6 (1-159) x
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27-NOV-2000;
22-DEC-2000;
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23-MAY-2000;
26-MAY-2000;
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Yamamoto RT,
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)B; AAU34320.
GTTGATCAAGCTGTGACAACTCAAAATCAAGCAATTGATAATACAACTGGTGCTACAACT 4209
                      ValAspSerProIle---GluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsn 19
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; antibacterial;
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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Xu HH;
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16-FEB-
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23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
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Haselbeck R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is; prokaryotic cellular proliferation gene;
antibacterial; drug design.
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Ohlsen KL,
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CC essential prokaryotic cellular proliferation form part of the printed specification, but was obtained in electronic format directly from WIPO at
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ATTCAAGCAATTGACCCAATTCAAGCATCAACAGATGTTAAAACGAATGCAAGAGCGGAA 4611
                                 GluLysAlaAlaThrProIle-----AlaLeuAspValLys----
                                                                  ANTCAMAATATTGAMAATGCACAGTCAMTCGATGATGTMAACACTGCAMAAGATAMTGCA 455:
                                                                                                                                       GCGACTACTGAAGAAAAAGAACAAGCAAATCAACAAGTAGACGCACAATTAACACAAGGT
                                                                                                                                                                       AlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer-----
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                                                                                                   AAAGCAAACGAACAAAAGCGCTTATTGCACAAACTGCA------GAT 4431
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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumonile, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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26-MAY-2000;
23-OCT-2000;
23-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
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DB; AAU34319.
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; antibacterial;
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2000US-253625P.
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DT 13-FE
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                                                                                        antibiotic;
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              27-SEP-2001
                                                               Staphylococcus aureus
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                                                                                                                                                                                                                                                          GATAATAGTCTTGATTCAACAGATAATGAG 4137
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                                                                                                                                                                                                                                                                                                                                  LeuAspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsn 146
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                                                                                      ds; prokaryotic
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Best Local Similarity:
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                                                         3691
                                                                                                                                                                  Sequence
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P-PSDB; AAU37319.
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23-MAY-2000;
                                              3751 GCAGAAGTAGACCAAGCTGCGACAGTAGCAGAGAATAATATCGATGCTGTTCAAGTTGAT 3810
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AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla---
                                                                                                         AATACTTTAAATCAAGACAGACAACAAGCTATTGAAAGTATTAAACAAGCTAACACAAAT 3750
                                                                                                                                     AspGluLeu-----
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                  US-09-847-539A-6 (1-159)
                                                                                   Alignment
Pred. No.:
                                                                         Score
                                                                                                                                     of e.g. pigs and elimination of infected and crearried out. The new diagnostic tests can distinativation and virulent strains. It may be used a vaccine. See also AAQ29470 and AAQ29472.
                                                                                                                                                The sequence is that of the extracellular factor related protein gene from Streptococcus suis type II (non-pathogenic) which allows the detection and the prevention of infections by S. suis in a more effective manner than was previously possible. It facilitates screening of e.g. plys and elimination of infected and carrier pigs can then be carried out. The new diagnostic tests can distinguish between avirulent and virulent strains. It may be used in the prodn. of
                                                                                                                                                                                                                                                         Deoxyribonucleic acid encoding virulence characteristic of
Streptococcus suis - useful for antibody and polypeptide for
diagnosing and preventing infections in pigs and humans
                                                                                                                 Sequence 6744 BP; 2402 A; 1231 C; 1535 G;
                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                     WPI; 1992-349215/42.
P-PSDB; AAR27745.
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4360 GATGGTGAG 4368
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                                                                                                     4279 -----CTAGCAGATCTTGAAAAAGCT 4299
                                                                 133 LysAspThrLysProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThr 152
                                                                                                                           113 AlaAlaSerAspAlaTrpGluLysAlaAlaThrProlleAlaLeuAspValLysLysThr 132
                    153 ThrGlyGlu 155
                                                                                                                                                                                                                                 73 GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla 92
                                                                                                                                                                                                                                                                                  54 IleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAsp---AlaLeu 72
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Search completed: October 13, 2002, 05:02:14 Job time: 240.471 secs

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Result
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Gapop 10.0 , Gapext 0.5
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2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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1: /SIDS1/gcgdata/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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     AAY71041
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AAY71046
AAY71044
AAY71044
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AAY71037
AAP70493
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273.300 Million cell updates/sec
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	AAU37320	22	2186		103.5
Staphylococcus aur	AAU34319		2076	٠	
Extracellular fact	AAR27745		1822	13.3	103.5
Staphylococcus aur	AAU37374		2478		0
Staphylococcus aur	AAU34320		2478	13.4	104
al	AAG37153		151		104.5
S. dysgalactiae MI	AAR71929		664	•	105
Synthetic protein	AAR71127		208	13.5	105
Rabbit enteropatho	AAW27286		314		105.5
Arabidopsis thalia	AAG20163		168	•	105.5
Drosophila melanog	ABB62318		. 1096		108
	AAG20162		180	٠	108.5
	AAG41390		316		109
Arabidopsis thalia	AAG41391		230	14.0	109
Arabidopsis thalia	AAG41392		191		109
Sequence of polype	AAP70468		480	14.4	112
Arabidopsis thalia	AAG38476		154	14.4	112
S. dysgalactiae MA	AAR71670		413	14.7	114.5
S. dysgalactiae MA	AAR71928		413	14.7	114.5
Streptococcus pyog	AAY71048		25	•	115
-	AAG38475	21	166	14.9	116
Streptococcus pyog	AAY71036		23	•	120
tococcus	AAY71038		28		129
IgG-binding Strept	AAR53294		265	17.9	139
Type 4 GX7809 prot	AAR10011		265		139
Protein G variant.	AAR07004		235	٠	139
rotein G vari	AAP94785	10	235	٠	139
Streptococcus stra	AAY57611	21	103		142
	AAR10005	12	594	24.1	187
coccus Pro	AAR62944	15	593	24.1	187
rotein G variant	AAR07014	11	593		187
treptococcus Pro	AAR53290	15	448	24.2	188
coccus GX	AAR10004	12	448		188
Protein G variant	AAR07013	11	448	24.2	188

ALIGNMENTS

PG X PT T GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection. Claim 5; Page 57-58; 67pp; English. New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein $\,\cdot\,$ Streptococcus 29-AUG-2000 (first entry) AAY71041 standard; peptide; WPI; 2000-365572/31. Bjorck LH, Rasmussen M; 02-NOV-1998; 02-NOV-1999; WO200026240-A2 Streptococcus pyogenes. (ACTI-) ACTINOVA LTD pyogenes strain SF370 GRAB protein fragment #5 98GB-0023975. 99WO-GB03631. 159 Å

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a fragment of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-192 and devoid of the membrane spanning region. This
                                                                                                                                                         Region
          02-NOV-1998;
                                   02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                         GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                         11-MAY-2000
                                                                                WO200026240-A2
                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                       pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                pyogenes strain SF370 mature
          98GB-0023975
                                   99WO-GB03631
                                                                                                                    /note= "consensus sequence
surface cell wall anchored
160..184
                                                                                                                                                                                   /note- "r
                                                                                                                                                                                                                      /label= R1
/note= "repeat region"
87..114
                                                                                                                                                                                                                                                             /label= alpha2-macroglobulin_binding_site
59..86
                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                      /label- Membrane_spanning_region
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e 777; DB 21;
. No. 1.2e-61;
smatches 0;
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                                                                                                                                for gram-positive proteins"
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RESULT 3
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                                                                                                                                                                                                                                           GRAB protein; protein G related alpha2M binding protein; vaccine;
alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                    Region
                                                            Region
                                                                                       Domain
                                                                                                            Binding-site
                                                                                                                                          Protein
                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365572/31
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92..11
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                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequencies a full-length GRAB protein from S. pyogenes strain SF370.
                                                           GRAB protein; protein G related alpha2M binding protein; vaccine;
alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
           WO200026240-A2
                             Streptococcus pyogenes
                                                                                        Streptococcus pyogenes strain KTL3 partial GRAB protein.
                                                                                                             29-AUG-2000
                                                                                                                                AAY71046;
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bjorck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                    AAY71046 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                      154
                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                     61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                           1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                                                                                                             AATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
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                                                                                                                                                                                                                                                                                                                          159;
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                 217
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                                                                                                            (first entry)
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surface cell wall anchored
193. 217
                                                 Streptococcus
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                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                       Score 777; DB 21;
Pred. No. 1.7e-61;
; Mismatches 0;
                                                pyogenes infection
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                                                                                                                                                                                                                                                                                                                                           Length
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Best Local
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                                                                                                                                                                     29-AUG-2000
                                                                                                                                                                                                           AAY71044 standard; Protein; 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 62-63;
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          WO200026240-A2
                                                          Misc-difference
                                                                                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          composition.
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                                                                                                          response;
                                                                                                                                                                                                                                                                                                                                                                                                                       167
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                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67pp;
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GRAB protein; protein G related alpha2M binding protein; vaccalpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequencis a partial GRAB protein from S. pyogenes strain KTL3.
                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes strain AP1 partial GRAB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a new family of proteins termed GRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE
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                                                                                              Location/Qualifiers
/note= "Thr at position 18 of GRAB protein fragment (AAY71036) from S. pyogenes strain SF370 is replaced with Ile"
                                                                                                                                                                                                                                                     Streptococcus pyogenes infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                   vaccine;
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Best Local S
Matches 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequent is a partial GRAB protein from S. pyogenes strain API.

The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 60-61;
             02-NOV-1998;
                                    02-NOV-1999;
                                                                                                                                         GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New alpha2M binding protein for generating to group A streptococcus and purifying the
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                                                          11-MAY-2000
                                                                                  WO200026240-A2
                                                                                                       Streptococcus pyogenes.
                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                      29-AUG-2000
                                                                                                                                                                                                                           AAY71045;
                                                                                                                                                                                                                                                   AAY71045 standard;
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                                                                                                                                                                                                                                                                                                                                                                          LEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 99.4
54; Conservative
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                                                                                                                                                                                                    (first entry)
                                                                                                                                                                            pyogenes strain AP49 partial GRAB protein.
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            98GB-0023975
                                    99WO-GB03631.
                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67pp; English.
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Pred. No. 2.
                                                                                                                              pyogenes
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.9e-59;
                                                                                                                                                                                                                                                                                                              155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a protective immune binding protein .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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RESULT 7
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Best Local Sin
Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2M calpha2M, and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain AP49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                               GRAB protein; protein G related alpha2M bindi alpha2-macroglobulin; group A Streptococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                         Streptococcus
                                                                                                                                                                                                29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses a new family of proteins termed GRAB (protein related alpha2M binding protein) from Streptococcus pyogenes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ACTI-) ACTINOVA LTD
             02-NOV-1999;
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                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                         AAY71043;
                                                                                                                                                                                                                                                 AAY71043 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition.
                                                               WO200026240-A2
                                                                                                                   immune
                                                                                                                                                                                                                                                                                                                   244
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                                                                                                                                                                                                                                                                                                                  VKKTKDTKPVVKKEERQNVNTLPTTGEE 156
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                                                                                                                                                                                                                                                                                                                                                                   TDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATFIALD
                                                                                                                                                                                                                                                                                                                                                                                     TDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALD 128
                                                                                                                                                                                                                                                                                                                                                                                                                       LADQTDALQSEEASVVKADNAASDALEALADQTDALQSEEASVVKADNAASDALEALADQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 61-62; 67pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                (first entry)
                                                                                         pyogenes
                                                                                                                                            protein G related alpha2M binding protein; vaccine;
                                                                                                                                                                    pyogenes strain KTL9 partial GRAB protein
             99WO-GB03631
                                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 694; DB
Pred. No. 5.5e
0; Mismatches
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                                                                                                                                                                                                                                                   ξ
                                                                                                                   infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                               GAS; antibiotic;
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RESULT 8
AAX71040
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AC AAX7
DT 29-A
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GRAE
KW GRAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective lumnume response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain KTL9.
                                                                                                                                                      GRAB protein; protein G related alpha2M binding protein; alpha2-macroglobulin; group A Streptococcus; GAS; antibidimmune response; Streptococcus pyogenes infection.
                                                                                                                                                                                                               Streptococcus pyogenes strain SF370 GRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
              02-NOV-1998;
                                           02-NOV-1999;
                                                                     11-MAY-2000
                                                                                                  WO200026240-A2
                                                                                                                           Streptococcus pyogenes
                                                                                                                                                                                                                                              29-AUG-2000
                                                                                                                                                                                                                                                                                                  AAY71040 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                              141 LADQTDALQSEEAAVVKADNAASDTLEALADQTDALQSEEAAVVKADNAASDTLEALADQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                         (first entry)
                98GB-0023975
                                           99WO-GB03631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.1%;
64.0%;
                                                                                                                                                      A Streptococcus; GAS; antibiotic; cus pyogenes infection.
                                                                                                                                                                                                                                                                                                   141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 692; DB Pred. No. 7.8e 0; Mismatches
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                                                                                                                                                                                                             protein fragment
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RESULT 9
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Best Local 9
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                                                             WPI; 2000-365572/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes strain SF370 GRAB protein fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71037;
                                                                                                                                                                                                                                                                                                    02-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                     WO200026240-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 57; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
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                                                                                                                                                                            (ACTI-) ACTINOVA LTD
                                                                                                                                                                                                                                         02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
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                                                                                                                       LH,
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                                                                                                                       Rasmussen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; 58
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New alpha2M binding protein for generating a protective immune response

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RESULT 10
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a fragment of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-91. This fragment is capable of binding alpha2M and useful in vaccine composition.
Protein G expressed by inserting the gene into an expression vector. A second vector may also be used as a cryptic helper plasmid to stably maintain the first plasmid in the host cell. Bacterial Fc receptors such as Protein G can be used to detect and purify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                        Disclosure; Fig. 3; 68pp;
                                                                                            Cloned
                                                                                                                                                                                                                                                                                                                               Active-site
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                             Protein G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP70493 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                detection
                                                                                                                   WPI; 1987-250197/35.
N-PSDB; AAN70811.
                                                                                                                                                      Fahnestock S;
                                                                                                                                                                                                              22-APR-1986;
14-FEB-1986;
                                                                                                                                                                                                                                               17-FEB-1987;
                                                                                                                                                                                                                                                                      27-AUG-1987
                                                                                                                                                                                                                                                                                             WO8705025-A
                                                                                                                                                                                                                                                                                                                                                      Active-site
                                                                                                                                                                           (FAHN/)
                                                                                                                                                                                       (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 36.7%;
Local Similarity 100.0%;
les 58; Conservative (
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                                                                                           Protein G
                                                                                                                                                                           GENEX CORP
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                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                             antibody;
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                                                                              ln G gene -
d purificn.
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                                                                                                                                                                                                                                                                                                                                                                                     Lancefield Group G strain.
                                                                                                                                                                                                            86US-0854997.
86US-0829354.
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                                                                                                                                                                                                                                                                                                                              /label=active site 298..352
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228..297
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                                                                                                                                                                                                                                                                                                                                                                                                            Fc receptor;
                                                                                used for producing of antibodies and t
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                                                         English.
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Pred. No.
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2e-18;
                                                                                treatment
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61;

Conservative

1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60

Mismatches

60;

Indels

16;

Gaps

6;

93

VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA

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33333×3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 61
Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies, and in the treatment of disease. Fo receptors are useful to purify antibodies to be used in the purific. of protein drugs and as therapeutics. High levels of Protein G can be obtd. In conditions favourable for isolation, using a non-pathogenic host. Suitable cloning vectors are lambda gtll, Ml3mp9 and pcX1066.
                                                                             Protein G
useful as
                                                                                                                                  Cloned protein G variant genes - expressing proteins having immunu protein G and derived from Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                             19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                   Protein G; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP95030;
                                             Sequence
                                                                                                              Disclosure; ;
                                                                                                                                                                                N-PSDB; AAN91093.
                                                                                                                                                                                           WPI; 1989-023848/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP95030 standard;
                                                                   screening
                                                                                                                                                                                                                Fahnestock SR,
                                                                                                                                                                                                                                                                                 20-JUN-1988;
                                                                                                                                                                                                                                                                                                        29-DEC-1988.
                                                                                                                                                                                                                                                                                                                             W08810306-A
                                                                                                                                                                                                                                     GENE-) GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWEAAA-AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALEALADQTDALQSEEAAVVKADN--AASDALEAL---ADQTDALQSEEAEVVQSDNAA- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
61; Conserv
                                                                 of non-pathogenic streptococcus and variants may be isolabacterial Fc receptors eg in purification and detection of hybridoma clones and treatment of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
                                             448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                              116pp;
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                            87US-0063959
                                                                                                                                                                                                                                                                                   88WO-US02084
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.2%;
            24.2%;
                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                         FC
                                                                                                                                              immunoglobulin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                               448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 188; DE
Pred. No. 1e-0
20; Mismatches
           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                         receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188; DB 8;
No. 1e-08;
           188; DB 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 448;
                        Length
                                                                                                                                              properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 12
AAR07013
ID AAR07
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                                                Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                           20-JUN-1988;
14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                      at high levels. The variants have a higher binding efficiency and capacity for Immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                     Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
                                                                                                                                                                                                                                                                                                                                           US4956296-A
                                                                                                                                                                                                                                                                                                                                                                   Active-site
                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR07013 standard; protein;
                                                                                                                            Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed
                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                              Fahnestock
                                                                                                                                                                                                                                                                                                           20-JUN-1988;
                                                                                                                                                                                                                                                                                                                           11-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                   Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR07013;
                                                                                Sequence
                                                                                                                                                     Disclosure; Fig 8a-c; 48pp;
                                                                                                                                                                                                                                             (GENE-) GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
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 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALEALADQTDALQSEEAAVVKADN--AASDALEAL---ADQTDALQSEEAEVVQSDNAA-
                                                                                                                                                                                                     1990-297491/39.
DB; AAQ06018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE 189
 ALEALADQTDALQSEEAAVVKADN--AASDALEAL---ADQTDALQSEEAEVVQSDNAA- 114
                                VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWEAAA - AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR
                VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA 93
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          variant with
                                                                                                                                                                                                                              SR;
                                               24.2%;
nilarity 38.9%;
Conservative 2
                                                                                448
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           sp.
                                                                                                                                                                                                                                              CORP
                                                                                                                                                                                                                                                            88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
228. 282
/label=B1
298. 352
/label=B2
                                                                                ξ,
                                                                                                                                                                                                                                                                                                           88US-0209236
                                                                                                                                                                                                                                                                                                                                                                                                          Lancefield Group G
                                                                                                                                                                                                                                                                                                                                                                                                                                           two
                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                          active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
                                                                                                                                                     English.
                                               Score 188; DB 1
Pred. No. 1e-08;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                           sites
                                                                                                                                                                                                                                                                                                                                                                                                           strain.
                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
                                                60;
                                                               Length
                                                Indels
                                                                448;
                                                16;
                                60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                6;
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AAR10004
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                                                                                      Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                   23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus GX7809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1991
                                                                                                                                                                                                            WPI; 1991-006758/01.
Q-PSDB; Q10001.
                                                                                                                                                                                                                                                                                                   19-MAY-1989;
14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                Key
Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR10004;
                                                                                                                      Sequence
                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                     Fahnestoc SR,
                                                                                                                                                                                                                                                                                                                                           11-DEC-1990
                                                                                                                                                                                                                                                                                                                                                          US4977247-A
                                                                                                                                                                                                                                                                                                                                                                                  Active-site
                                                                                                                                                                                                                                                    (GENE-) GENEX
                                                                                                                                                                                                                                                                                                                           19-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
         115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                       94
                                       61
                                                       34
-SDAWE-----
                                                                                              Similarity
                                                                                                                      448
                                                                                                                                                                   Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         дs
                                                                                                                                                                                                                                                     CORP.
                                                                                                                                                                                                                                    Lee
                                                                                                                                                                                                                                                                   89US-0354264.

86US-0829354.

86US-0854887.

87WO-US00329.

87US-0063959.

88US-0209236.
                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                          89US-0354264
                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                                  /label=
298..352
                                                                                                                                                                                                                                                                                                                                                                          /label-
                                                                                                                                                                                                                                                                                                                                                                                                                          GX7809
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig.
                                                                                                                                                                                                                                     Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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AAR10004 standard; Protein; 448
                                                                                                                                                                                                                                                                                                                                           Protein G gene product may be modified allowing the variant to imobilised and exhibit different binding profiles. The bound protein is useful in purification and detection of Igs and frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immobilised protein G variants - used for detection, isolation
and purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE 189
                                                                                                                                         VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                 ALEALADOTDALOSEEAAVVKADN--AASDALEAL---ADOTDALOSEEAEVVOSDNAA- 114
                                                             AWEAAA-AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
228..282
-KAATPIALDVKKTK--DTKPVVKKE
                                                                                                                                                                                                                                                                                                                                                                                                                             52pp; English.
                                                                                                                                                                                                                       24.2%; Score 188; DB 1
38.9%; Pred. No. 1e-08;
Live 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wroble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В2
                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                               Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolation
                                                                                                                                                                                                                                                                                                                                             fragments
                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                       þe
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
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AAR53290
                                                              В
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                                                                                                                                                   밁
                                                                                                        Query Match
Best Local S
Matches 61
                                                                                                                                                                            A 1.9kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7809. The Protein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains
                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1986;
23-APR-1986;
19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
                                                                                                                                                                       are claimed.
                                                                                                                                                                                                                                 Example 2; Fig 3 and Fig 8; 48pp; English.
                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR53290 standard;
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                     Fahnestock
                                                                                                                                                                                                                                                                                                                                         (PHAA ) PHARMACIA LKB
                                                                                                                                                                                                                                                                                                                                                               21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5312901-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Active-site
  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                     94
                                         61
                                                              34
                                                                                                        Local Similarity 38.9
                                                                                   1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                                                                                                                                                     recombinant streptococcal protein G variants - useful for ibody detection and purification and for therapy
                     AWEAAA-AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR
                                        ALEALADQTDALQSEEAAVVKADN..AASDALEAL...ADQTDALQSEEAEVVQSDNAA.
                                                              VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA
                                                                                                                                                                                                                                                                                                 1994-159179/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE 189
  -SDAWE----
                                                                                                                                                                                                                                                                                       AAQ64644.
                                                                                                                                                                                                                                                                                                                     SR
                                                                                                                                                  448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein G derived from strain GX7809
                                                                                                                                                                                                                                                                                                                                                             88US-0209236.
90US-0540169.
92US-0871539.
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                                                                                                                                                                                                                                                                                                                                                                                              86US-0854887
87US-0063959
                                                                                                                                                                                                                                                                                                                                                                                                                  86US-0829354
                                                                                                                                                                                                                                                                                                                                                                                                                                       86US-0829354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 81
283..297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- b
/note- "linking
298..352
 -KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GX7809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 448
                                                                                                                 24.2%;
                                                                                                                                                                                                                                                                                                                                         BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В2
                                                                                                        20;
                                                                                                                 Score 188; DB 1
Pred. No. 1e-08;
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region"
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                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                           DB 15;
                                                                                                        60;
                                                                                                                           Length 448;
                                                                                                        Indels
                                                                                                        16;
                                                                                                      Gaps
                                                              93
                                                                                  60
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                                                                                                                                                 RESULT 15
AAR07014
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                    Дb
                                      δÃ
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                                                                                                        Matches
                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1988;
14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                  incorporated into a non-pathogenic host eg. E.coli, and express at high levels.
The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                         Recombinant Protein G encoding Protein G fro
                                                                                                                                               Sequence
                                                                                                                                                                                                            Fragments and variants of the sequence are claimed esp. incorporated into a non-pathogenic host eg. E.coli, and
                                                                                                                                                                                                                                           Disclosure; Fig 9;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ06019
                                                                                                                                                                                                                                                                                                                   WPI: 1990-297491/39.
                                                                                                                                                                                                                                                                                                                                         Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein G variant with three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR07014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR07014 standard;
                                                                                                                                                                                                                                                                immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                            (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
 115
                    94
                                       61
                                                              34
                                                                      1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                              VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE
 -SDAWE----
                    AWEAAA-AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGVKDLQAQVVESAKKAR
                                       ALEALADQTDALQSEEAAVVKADN--AASDALEAL---ADQTDALQSEEAEVVQSDNAA- 114
                                                                                                      61;
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                             GENEX CORP.
                                                                                                                                               593
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                 88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp. Lancefield Group
                                                                                                                                               A,
                                                                                                                                                                                                                                                                                                                                                                                                                                               88US-0209236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=B1
373..427
/label=B3
443..497
/label=B2
 -KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
303..372
                                                                                                                                                                                                                                                                           G from
                                                                                                                                                                                                                                           48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                 24.1%; Score 187; DB 11; 38.9%; Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                         variants - obtd. using a cloned gene om Streptococcus sp., used for binding
                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        active sites
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                           Length 593;
                                                                                                        Indels
```

where expressed

16;

Gaps

6.

93

õ

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RESULT 16
AAR62944
  В
                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor.
                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                     кеу
                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                               Region
                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                            Active-site
                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR62944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR62944 standard; Protein;
 14-FEB-1986;
               14-FEB-1986;
                                           US5312901-A
                                                                Misc-difference
                                                                                                                                                                                                                                   Active-site
                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                               Domain
                              17-MAY-1994
                                                                              Region
                                                                                            Region
                                                                                                          Region
                                                                                                                        Region
                                                                                                                                      Region
                                                                                                                                                    Misc-difference
                                                                                                                                                                         Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                   sp. GX7805
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein G derived from strain GX7805
 86US-0829354
                                                                                                                                                                                                                                                                                                        /label- a2
/note- "linking :
254..290
               86US-0829354
                                                                                                                                                                        /label= b
/note= "linking |
443..497
                                                                              546..550
/label= C4
551..555
                                                                                                  536..540
/label= C2
541..545
/label= C3
                                                                                                                                                                                                             /note- "involved 376
                                                                /label- C5
592
                                                                                                                                                                                                                                  /label- b
/note- "linking
373..427
                                                                                                                                                                                                428..442
                                                                                                                                                          /note= "involved
                                                                                                                                                                                                     /note- "corresponds to
                                                                                                                                                                                                                                                             /label= B1
/note= "involved in
                                                                                                                                                                                                                                                                                                  /label- A3
                                                                                                                                                                                                                                                                                                                                                 /label= a1
/note= "linking
                                                                                                                                                                                                                                                                                                                                                                141..178
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                        note= "corresponds"
                                                                                                                                                                   /label= B2
                                                                                                                                                                                                                                                                                                                                                                       'label- A1
                                                                                                                                             'note= "corresponds to ACT codon"
                                                                                                                                                                                                                                                                                  note=
                                                                                                                              label- C1
                                                                                                                                                                                                                                                                                                                                     label=
                                                                                                                                      . . 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                  "corresponds to
                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                            B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593
                                                                                                                                                                                region'
                                                                                                                                                                                                                                         region"
                                                                                                                                                                                                                                                                                                                                                 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                               region"
                                                                                                                                                                                                                    'n
                                                                                                                                                         in IgG binding activity"
                                                                                                                                                                                                                   IgG
                                                                                                                                                                                                                                                             IgG
                                                          6
                                                                                                                                                                                                      CCT codon *
                                                         GAA codon"
                                                                                                                                                                                                                                                                                   GGA codon'
                                                                                                                                                                                                                  binding activity"
                                                                                                                                                                                                                                                             binding activity"
                                                                                                                                                                                             RESULT 17
AAR10005
 밁
                                                                                                                                                                                                                                       δÃ
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                                                                                                                                                                                                                                                                  Q
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1986;
19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
21-APR-1992;
                                                                                                   Key
                                                                                                                                           Streptococcus GX7805
                                                                                                                                                                        AAR10005;
                                                                                                                                                                                      AAR10005
                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant streptococcal protein G antibody detection and purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-159179/19.
N-PSDB; AAQ75036.
19-MAY-1989;
              19-MAY-1989;
                           11-DEC-1990
                                          US4977247-A
                                                              Active-site
                                                                             Active-site
                                                                                           Active-site
                                                                                                                Streptococcus
                                                                                                                             Immunoglobulins;
                                                                                                                                                          13-MAR-1991
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 9; 48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA LKB BIOTECHNOLOGY
                                                                                                                                                                                                                                        115
                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                  34 VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA 93
                                                                                                                                                                                                                                                               ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE
                                                                                                                                                                                                                                        -SDAWE----KAATPIALDVKKTK--DTKPVVKKE
                                                                                                                                                                                                                                                       AWEAAA-AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGVKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                              1 Similarity
61; Conserv
                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                          593 AA;
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                         (first entry)
                                                                                                                sp GX7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-0854887.
87US-0063959.
88US-0209236.
90US-0540169.
92US-0871539.
89US-0354264
              8905-0354264
                                                        444..498
/label- #
                                                                                           304 . .
                                                                                                 Location/Qualifiers
                                                                      /label-
                                                                                   /label-
                                                                                                                             Ig.
                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                    24.1%; 38.9%;
                                                                             .428
                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                        Active
                                                                     Active Site
                                                                                   Active
                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                       594
                                                                                                                                            G
                                                        Site
                                                                                   Site
                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑВ
                                                        В2
                                                                     B3
                                                                                   B1
                                                                                                                                                                                                                           189
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A 2.4kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7805 using the 1.9kb Protein G coding sequence from Streptococcus GX7809. The Protein G has 1gG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains
VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                            Score 187; DB 15;
Pred. No. 1.8e-08;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variants - useful for for therapy
                                                                                                                        Length 593;
                                                               Indels
                                                               16;
                                                         Gaps
                                                               6;
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RESULT 18
AAY57611
ID AAY57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                             Streptococcus strain G 148; protein G'; protein G primer; liposome; liposomal delivery complex; connecting molety; antibody; Fc region; diagnosis; therapeutic agent; antibiotic; antidepressant; antiviral; antitumourigenic; cytokine; hormone; imaging agent; neurotransmitter; stimulant; cytotoxic agent; mallgnant cell.
WPI; 2000-062383/05.
N-PSDB; AAZ47931.
                                                                                               19-MAY-1999;
                                                                                                                     25-NOV-1999
                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein G gene product may be modified allowing the variant to be imobilised and exhibit different binding profiles. The bound protein is useful in purification and detection of Igs and fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                     (SDGS-)
                                                                          20-мау-1998;
                                                                                                                                          W09959643-A2
                                                                                                                                                                                                                                                                       10-MAR-2000
                                                                                                                                                                                                                                                                                              AAY57611;
                                                                                                                                                                                                                                                                                                                AAY57611 standard; Protein; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fahnestoc SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immobilised protein G variants - use and purificn. immunoglobulin(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-1986;
23-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-)
                                                                                                                                                                                                                                                                                                                                                                       153
                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                                                                                                                                                                                                                                                                                                                                ALEALADQTDALQSEEAAVVKADN--AASDALEAL---ADQTDALQSEEAEVVQSDNAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA
                                                                                                                                                                                                                                                                                                                                                                    ISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRE 189
                                                                                                                                                                                                                                                                                                                                                                                                              AWEAAA-AADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGVKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1991-006758/01
                                                                                                                                                                                                                                                                                                                                                                                         -SDAWE-----KAATPIALDVKKTK--DTKPVVKKE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                    SDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q10002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594 AA;
                                                     INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                              gp.
                                                                                                                                                                                                                                                  strain G 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
88US-0209236.
                                                                         9805-0086347
                                                                                               99WO-US11177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wroble
                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 187;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X
                                                                                                                                                                                                                                                                                                                 A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
L.8e-08;
hes 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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cc a liposome; (b) providing a construct comprising a linking molety and a connecting molety bound together; and (c) combination so that the connecting molety bound together; and (c) combination so that the compression of the liposomal components and the construct and sonicating the combination so that the condition molety, and to facilitate the binding between them. The crossor of the linking molety, and to facilitate the binding between them. The conducts can be used for the delivery of diagnostic or therapeutic conducts can be used for the delivery of diagnostic or therapeutic agent, e.g. antibiotics, antidepressants, continuourigenics, antivirals, cytokines, hormones, imaging agents, controtransmitters, or stimulants. They can be used particularly for the connecting molety provides a liposomal delivery complex having improved cargeting efficiency. As a result of the binding between protein G and the Fc region of antibodies, protein G'shields the Fc regions of the crossor of antibodies from non-specific binding to cell-surfaces, other correcting, and anaromical structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or antibody fragment to a liposome. The construct comprises protein G and a linking molety for connecting the protein G to the liposome. Also described are: (1) a liposomal delivery vehicle comprising: (a) a liposome; and (b) a connecting molety connected to the liposome, which specifically binds the Fc region of an antibody, for connecting the antibody to the liposome; and (2) forming a liposomal correct comprising the compromed to the liposome.
                                                                    proteins, and anatomical structures. The present sequence represents an unidentified protein encoded by the same sequence which encodes
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New liposome constructs comprising a used, e.g. for delivery of cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a
                                                    ળ
103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         construct for connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liposome connected to an antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to malignant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ting the
ter comprising:
, for forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an antibody
s protein G'
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Query Match Best Local Matches 4 1 VDSPIEOPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAA 57 VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENA 33; Conserv Conservative 18.3%; ω `` Score 142; DB 21; Pred. No. 2.1e-05; 3; Mismatches 21; Length 103; Indels 0, 90 Gaps 0

В Ş

RESULT 19 Protein G variant. 04-JUL-1990 Protein G; AAP94785; AAP94785 standard; immunoglobulin; Fc receptor; (first protein; entry) 235 ₹

WPI; 1989-023848/03 Fahnestock SR; WO8810306-A Streptococcus (GENE-) GENEX CORP 19-JUN-1987; 20-JUN-1988; 29-DEC-1988 qs 87us-0063959 88WO-US02084

N-PSDB; AAN91099

Length Indels

84;

Gaps

8

51

63

84

118

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RESULT 2

AARO 7004

ID AARO 7004

AAC AAR

AC AAR

AC AAR

AC AAR

AC Imm

COX St.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SXCCCCXXXXPT
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                             23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloned protein G variant genes - expressing proteins having immuno protein G and derived from Strep
                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein G variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and treatment of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene for protein G variant of non-pathogenic streptococcus sp. allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                     Disclosure; Column
                                                                                      Recombinant Protein G variants - encoding Protein G from Streptoco
                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                    Fahnestock
                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US4956296-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR07004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR07004 standard;
                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin
                                                                   immunoglobulin.
                                                                                                                                                                                                                                                                               (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIEDTPIIRNGGELTNLLGNSETTLALRNEESATAGYPLPKTDTYKLILNGKTLKGETTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDE------LKKQAIEDKEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVTEVPRGDAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASDALEALADQTDALQSEEA-EVVQSDNAASDAW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAIEAASSD-----ALEALADOTDALQ----SEEAAVVKAD-----N
                                                                                                                                                                                        1990-297491/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPEKPEASIPLVPLTPATPIAKDDAKKDDTKKEDAKKPEAKKDDAKKAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --EK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 25.3
58; Conservative
                                                                                                                                                                                                                                                                               GENEX
                                                                                                                                                              AAQ06009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                    SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp.
                                                                                                                                                                                                                                                                                 CORP.
                                                                                                                                                                                                                                                                                                                          88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0209236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AATPIALDVKKTKDT-----KPVVKKEERQNVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lancefield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116pp;
                        9-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.9%;
25.2%;
                                                                                        ariants - obtd. using a cloned Streptococcus sp., used for b
                     48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 139; DB 10;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group
                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                        for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
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                   RESULT 21
AARIO011
ID AARIO
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XX AARIO
XX AARIO
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XX Inmau
XX Inmau
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PR 11-D
YX 11-D
YX 11-D
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence may be incorporated into a non-pathogenic host eg. E.coli, where they may be expressed at high levels. The proteins have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                     Sequence
                                                              Protein G variant product carries active regions B1 and B2, be imobilised and exhibits different binding profiles. The protein is useful in purification and detection of Igs and
                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                               Q-PSDB; Q10007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-1989;
14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type 4 GX7809 protein G variant.
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                                                                                                                                                                                                       Immobilised protein G variants – used for detection, isolatiand purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                Fahnestoc SR,
                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAIEAASSD-----ALEALADQTDALQ----SEEAAVVKAD-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EK---
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                        265 AA
                                                                                                                                                              Column
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87WO-US00329.
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86US-0829354
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Pred. No. 0.00
24; Mismatches
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                                                                                                                                                            English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                             23-APR-1986;
19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
21-APR-1992;
                    Protein G isolated from Streptococcus has IgG-binding activity which has been localised to the B repeating structure (see AAR53290). The sequence AAR53294 represents a claimed Streptococcal Protein G
variant comp
IgG-binding
                                                                 Claim
                                                                                                                     N-PSDB;
                                                                                                                      WPI; 1994-159179/19.
N-PSDB; AAQ64648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR53294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR53294 standard;
                                                                                     antibody
                                                                                                                                                                                                                                                     14-FEB-1986;
                                                                                                                                                                                                                                                                          14-FEB-1986;
                                                                                                                                                                                                                                                                                               17-MAY-1994.
                                                                                                                                                                                                                                                                                                                    US5312901-A.
                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                              бeу
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-1995
                                                                                                                                                                          (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB
                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                      lmmunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgG-binding Streptococcus Protein G variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 EPEKPEASIPLVPLTPATPIAKUDAKKUDTKKEDAKKPEAKKUDAKKAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDE------LKKQAIEDKEAT 51
                                                                                   recombinant streptococcal protein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVTEVPRGDAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AASDALEALADQTDALQSEEA-EVVQSDNAASDAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAIEAASSD-----ALEALADQTDALQ----SEEAAVVKAD------N 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIEDTPIIRNGGELTNLLGNSETTLALRNEESATAGYPLPKTDTYKLILNGKTLKGETTT
                                                               3; Column 46; 48pp; English.
comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein G; variant;
n; Lancefield Group
                                                                                                                                                                                                                              86US-0854887.
87US-0063959.
                                                                                                                                                                                                                                                     86US-0829354
                                                                                                                                                                                                                                                                          86US-0829354.
                                                                                                                                                                                                           90US-0540169
                                                                                                                                                                                                                     BBUS-0209236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AATPIALDVKKTKDT-----KPVVKKEERONVNT
                                                                                                                                                                                                                                                                                                                                       /label= Protein_G_variant
/note= "claimed without the
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      label secretion_sequence
           the B domain active site and retaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IgG binding G; bacterial
                                                                                    variants - useful for for therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                         secretion sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     activity;
Fc receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                        protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is one of the repeat regions of GRAB protein from S. pyogenes strain SF370 corresponding to residues 92-119. This fragment is useful in vaccine composition.
                                                                                                                                            related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to
                                                                                                                                                                                                                                 New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRAB protein; protein G related alpha2M binding protein; alpha2-macroglobulin; group A Streptococcus; GAS; antibio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71038 standard; peptide;
                                                                                                                                                                            The patent discloses a new family of proteins termed GRAB (protein
                                                                                                                                                                                                        Claim 3; Page 56; 67pp; English.
                                                                                                                                                                                                                                                                                                             Bjorck LH, Rasmussen
                                                                                                                                                                                                                                                                                                                                                                       02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71038;
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                                                                                                                                                                                                                                                                                                                                          (ACTI-) ACTINOVA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
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                                                                                                                                                                                                                                                                                 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAIEAASSD-----ALEALADQTDALQ----SEEAAVVKAD------N 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPEKPEASIPLYPLTPATPIAKDDAKKDDTKKEDAKKPEAKKDDAKKAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVTEVPRGDAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AASDALEALADQTDALQSEEA-EVVQSDNAASDAW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIEDTPIIRNGGELTNLLGNSETTLALRNEESATAGYPLPKTDTYKLILNGKTLKGETTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response; Streptococcus pyogenes infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyogenes strain
                                                                                                                                                                                                                                                                                                                                                                       98GB-0023975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%;
                                                                                                                                                                                                                                                                                                              X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 139;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SF370 GRAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
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AAG38475
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                    The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a fragment of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-56. This fragment is capable of binding alpha2M and useful in vaccine composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAB protein;
alpha2-macrogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bjorck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71036;
                 AAG38475
                                            AAG38475 standard; Protein; 166
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71036 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune
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                                                                                                                              1 VDSPIEQPRIIPNGGTLTNLLGN 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Page 55; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rotein; protein G
-macroglobulin; gr
                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rasmussen
                                                                                                                                                                                                                                                             23
                                                                                                                                                                                         15.4%; Score 120; DB 21; ilarity 100.0%; Pred. No. 0.0003; Conservative 0; Mismatches 0
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyogenes strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-0023975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       otein G related alpha2M binding protein; vaccine; ulin; group A Streptococcus; GAS; antibiotic; Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SF370 GRAB
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                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                          Length 23;
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                                                                                                                                                                                                                                                                                related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a GRAB peptide EKL 24 useful in vaccine composition. It was used to produce immunoglobulin G (IGG) antibodies specific for native GRAB protein in sheep. The peptide has a cysteine insert at the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRAB; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; peptide EKL
                                                                                                                                                                                                                                                                                                                                                                The patent discloses a new family of proteins termed GRAB (protein related alpha2M binding protein) from Streptococcus pyogenes which
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                                                             plasma
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                                           Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                           alpha2M binding protein for generating a protective immune
group A streptococcus and purifying the binding protein -
                                                                                      dysgalactiae MAG
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                                                                     alpha-2-macroglobulin binding protein;
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A phage lambda EMBL library of S. dysgalactiae 8215 DNA was analyzed for fast-acting alpha-2-macroglobulin (FAM)-, BSA- and IgG-binding activity. Clone lambda-SD1, which expressed all 3 activities, was analyzed to obtain DNA encoding the FAM-binding protein, MAG. The mag gene (given in Q89197) encodes a 44 kDa protein (R71929).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding fast alpha 2-macro:globulin-binding proteins - used to obtain prods. for sepn., detection or quantification or for binding inhibition
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TGEGSNP
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MUELLER H.
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                                                                                                                                                                                                                                                                                                                    DNA encoding a serum albumin binding protein - prods. for sepns., detection, quantification, p stabilisation or vaccine development
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(JONS/) JONSSON H.
(LIND/) LINDBERG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9507300-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pept1de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mag gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1995
                                                                                                                                                                                                              Recombinant, immobilized MAG was used for serum albumin affinity
                                     264
              120
                                                                                   206
                                                           82
                                                                                                        36
                                                                                                                                Local Similarity es 49; Conserv
                                    -- NGKTLKGETTTKAVDAETAEKAFKQYANENGVDGVWTYDDATKTFTVTEMVTEVPGDA
                                                        ADNAASDALEALADQTDALQSEEA-EVVQSDNAASDAWE----
                                                                                ATEILKKYGIGDYYIKLINNGKTAEGVTALKDEILASKPAVIDAPELTPALTTYKLVI--
                                                                                                        AIDELKKQAIED------KEATTAIE---AASSDALEALADQTDALQSEEAAVVK
                                                                                                                                                                                                                                                                                                                                                                     AAQ86080.
                                                                                                                                                                                                                                                                                                                                                                                                      Jonsson H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serum albumin binding protein; protein stabilization,
                                                                                                                                                                             413 AA;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                     detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dysgalactiae strain 8215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rabel= IgG
/note= "IgG binding c
313..387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93SE-0002856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-SE00825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "0
             -----KAATPIALDVKKTKDT------KPVVKKEERQNVNTLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "alpha-2-macroglobulin binding domain" 93.242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Alb
/note- "albumin binding domain"
243..312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Sig_peptide 35..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- A2-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
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                                                                                                                                           14.7%;
26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                      Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "membrane-spanning region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "cell wall binding region"
                                                                                                                                                                                                     and assay.
                                                                                                                               15;
                                                                                                                                          Score 114.5;
Pred. No. 0.(
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                                                                                                                                                     Length
                                                                                                                                                      413;
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              152
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  RESULT 29
AAG38476
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG38476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTEPKKPEASIPLVPLTPATPIAKDDAKKDDTKKDDTKKEDAKKPEAKKEEAKKAATLPT 381
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99US-0134221
99US-0134778
99US-0134941
99US-013553
99US-0135629
99US-0136782
99US-01368392
99US-0136782
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99US-0132484.
99US-0132485.
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99US-0132863.
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99US-0131449
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27-OCT-1999
28-OCT-1999
72
                      17
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                                  40;
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imilarity 26.58;
Conservative
                                                        9908-0148565.
9908-0149368.
9908-0149723.
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9908-0149723.
9908-0149902.
9908-0151066.
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9908-0161466.
-EAAVV----KADNAASDALEALADQTDALQSEEAEVVQSDNAAS 115
                                 ; Score 112; DB 2
; Pred. No. 0.016;
25; Mismatches
                                           21;
                                             Length
                                   28;
                                  Gaps
           60
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16-JUN-1999
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RESULT 31
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ID AAG4:
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AAP70468
ID AAP70
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Matches 44
                     AAG41392 standard; Protein; 191 AA
   AAG41392;
                                                                                                                                                                                                                                          A recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity as protein G from Streptococcus G148 (AAN70757) is claimed. See, for example, AAN70754, AAN70755 and AAN70756.
                                                                                                                                                                                                                                                                                                                                                                      Guss BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP70468 standard; Protein; 480
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                           Example;
                                                                                                                                                                                                                                                                                                           New recombinant DNA molecules - for producing proteins with IgG-binding specificity of protein G or proteins A and G
                                                                                                                                                                                                                                                                                                                                          WPI; 1987-277686/39.
N-PSDB; AAN70757.
                                                                                                                                                                                                                                                                                                                                                                                       (PHAA ) PHARMACIA AB. (GUSS/) GUSS B M.
                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody-binding; IgG; IgA; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of polypeptide possessing IgG-binding protein G from Streptococcus G148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70468;
                                                                    434
                                                                                                         375
                                                                                      138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                             Local Similarity
                                                                   EAKKEDAKKAETLPTTGEGSNP 455
                                                                                     VVKKEERONVNTLPTTGEESNP 159
                                                                                                        DATKTFTVTEM-VTEVPGDAPTEPEKPEASIPLVPLTPATPIAKDDAKKDDTKKEDAKKP
                                                                                                                                             KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYD
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                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                    Lindberg KM,
                                                                                                                                                                                                                                                                                          F1g 2; 39pp; English.
                                                                                                                                                                                                                          480 AA;
                                                                                                                                                                                   Conservative
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                                                                                                                                                                                            14.48;
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                                                                                                                                                                                           Score 112; DB B Pred. No. 0.066;
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                                                                                                                         137
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  28-APR-1999
30-APR-1999
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04-WAY-1999
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11-WAY-1999
                                                                                   14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
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29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000EP-0301439
990S-0135353

990S-0136621

990S-0136392

990S-0137528

990S-0137528

990S-0137522

990S-0137524

990S-0138847

990S-0138847

990S-0139453

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99US-0126785.
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       AAG41391 standard; Protein;
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                                           1 Similarity 27.1
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27.3%;
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; Pred. No. 0.0;
21; Mismatches
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                                                                                                                                                   Length
                                                                                                                                      Indels
                                                                                                                                                     191;
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                                             182
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                                                                                                                                     Gaps
                                                                                         111
                                                                           126
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סיטים סיטים מסיסים מסיס מיטים מיטי

18-JUN-1999
21-JUN-1999
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EP1033405-A2. 6F2P-2000. 25-FEB-1999; 05-MAR-1999; 05-MAR-1999; 05-MAR-1999; 06-APR-1999; 06-APR-1999; 07-APR-1999; 07-APR-1999; 08-APR-1999; 11-APR-1999; 11-A	AAG41391; 18-OCT-2000 Arabidopsis to Protein ident hybridiaation termination so
Challand 2000EP - 0301439 99US - 0123180 99US - 0123768 99US - 0127685 99	(first entry) thaliana protein fragment SEQ ID NO: 51492. tification; signal transduction pathway; metabolic pathway; n assay; genetic mapping; gene expression control; promoter; sequence.
22222226411111110996699449922282777632322222222222222555555555555	2222222111
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990S-0141391 990S-0141391 990S-0142920 990S-0142920 990S-0142920 990S-0143242 990S-0143242 990S-0144325 990S-0144331 990S-0144331 990S-0144333 990S-0144333 990S-0144333 990S-0144334 990S-0144334 990S-0144332 990S-0144334 990S-0144332 990S-0144332 990S-0144332 990S-0144332 990S-0144334 990S-0145086 990S-0145086 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145142 990S-0145143 990S-014716 990S-014716 990S-014716 990S-014716 990S-014716 990S-014716 990S-014716 990S-0148119 990S-0148119 990S-0148119 990S-0148119 990S-0148119 990S-0148119 990S-0148119 990S-0148119 990S-0148115 990S-0149723 990S-0149723 990S-0149723 990S-0149929 990S-0149930 990S-0149930	001000000000000000000000000000000000000

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RESULT 33
AAG41390
ID AAG41
                                                                                                                                                                                 Query Match
Best Local S
Matches 48
                                                                                                                                                                                                                           26-AUG-1999
27-AUG-1999
27-AUG-1999
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24-SEP-1999
24-SEP-1999
26-OCT-1999
31-OCT-1999
32-OCT-1999
 AAG41390 standard; Protein; 316 AA.
                                                       166
                                                                                                                    74
                                                                                                                                        46
                                                                                                                                                             27
                                                                                                                                                  KLALRNEERAIDELKK-------QAIED------KEATTAIEAASSDALEALADQTDALQ 73
                                                                    NAASDAWEKA----ATPIALDVKK------TKDTKPVVKKEERQN 146
                                                                                              KLELQNVEKAHSELKEIEQRERDHQAIEDLKKETKDAKTQLSLLEEELKIAVFEAQEAKD 105
                                                     AATQDALKKAEMAQEATIVVDVELKRRRKAASRILAESKMCAKSTKEVLKSKPRSS
                                                                                                                                                                                    48;
                                                                                                                                                                                 Similarity 27.3
48; Conservative
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99US-0151065
99US-0151080
99US-0151303
99US-0151438
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990S-0161361
                                                                                                                                                                                14.0%; Score 109; DB 2
27.3%; Pred. No. 0.049;
tive 21; Mismatches
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                                                                                                                                                                                   51;
                                                                                                                                                                                                      Length 230;
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                                                                                                                                                                                   56;
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  25-FEB 1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
26-MAR 1999
16-APR 1999
16-APR 1999
16-APR 1999
23-APR 1999
23-APR 1999
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11-MAY 1999
11-JUN 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hybridisation assay; termination sequence.
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
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990S-0123180
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5-0131449.
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망 δ 멍 Qγ В δ

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RESULT 34
AAG20162
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Best Local S
Matches 48
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26-AUG-1999

27-AUG-1999

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27-AUG-1999

30-AUG-1999

31-AUG-1999

31-AUG-1999

31-SEP-1999

10-SEP-1999

16-SEP-1999

20-SEP-1999

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28-CCT-1999

29-CCT-1999
                                     252
                                                                         192
                                                                                                             132
                                                                                                                               27
                                                                                          74
                                                                                                          NAASDAWEKA----
                                    AATQDALKKAEMAQEATIVVDVELKRRKKAASRILAESKMCAKSTKEVLKSKPRSS
                                                                                  SEE-----AGVVKADNA----ASDALEALADQT-DALQSEEAEVVQSD
                                                                       AEEHARERLNVAVLESDFRSLAVVKESAAEELTETEALRACRDETLKTLEMSEREIEDIK
                                                                                                                                                48;
                                                                                                                                                          imi
                                                                                                                                                          larity
                                                                                                                                                Conservative
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990S-0161393
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                                                                                                                                               s; Score 109; DB
s; Pred. No. 0.07
21; Mismatches
                                                                                                                                                       DB 21;
.072;
                                              --TKDTKPVVKKEERQN
                                                                                                                                                                  Length
                                                                                                                                                Indels
                                                                                                                                                                  316;
                                    307
                                                                                                                                               Gaps
                                                                                                           191
                                                                        251
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990S-014780
990S-014772

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Protein identificatine hybridisation assay; termination sequence arabidops is thaliana EP1033405-A2. 06-SEP-2000; 2000EP-25-FEB-1999; 99US-23-AAR-1999; 99US-24-APR-1999; 99US-23-APR-1999; 99U	AAG20162 standard; AAG20162; 17-OCT-2000 (firs Arabidopsis thalia
genetic mapping; gene expres	ndard; Protein; 180 AA. (first entry) thaliana protein fragment SEQ ID NO: 22242.
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23 - JUN 1999 24 - JUN 1999 28 - JUN 1999 28 - JUN 1999 30 - JUN 1999 30 - JUN 1999 30 - JUN 1999 30 - JUN 1999 31 - JUN 1999 32 - JUN 1999 33 - JUN 1999 34 - JUN 1999 35 - JUN 1999 36 - JUN 1999 37 - JUN 1999 38 - JUN 1999 38 - JUN 1999 39 - JUN 1999 30 - AUG 1999 30 - AUG 1999 31	66666666666666666666666666666666666666
99US-0140353 99US-0140554 99US-0140695 99US-0140823 99US-0142154 99US-014230 99US-014230 99US-014230 99US-0142977 99US-014354 99US-014354 99US-014354 99US-0144085 99US-0144335 99US-0144331 99US-0144331 99US-0144331 99US-0144331 99US-0144331 99US-0145086 99US-0145086 99US-0145086 99US-0145086 99US-0145086 99US-0145086 99US-0145086 99US-0145086 99US-0145145 99US-0145218 99US-0145218 99US-0145218 99US-0145218 99US-0145319 99US-0145319 99US-0145319 99US-0145318 99US-0145318 99US-0145319 99US-014704 99US-014704 99US-014704 99US-014703 99US-014704 99US-014704 99US-014704 99US-014704 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148341 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148311 99US-0148312 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313 99US-0148313	905-013946 905-013946 905-013946 905-013975 905-013976 905-013981

07-SEP-

10-SEP-1

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Query Match
Best Local S
Matches 36
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04-OCT 1999
05-OCT 1999
06-OCT 1999
06-OCT 1999
11-OCT 1999
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16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
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25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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                                                                                                                                                                                                               PNGGTLTNLLGNAP-----EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALA 66
                                                                                       AVEAEKKAEAEPVKVEAEPVKAEAEPVKAE 154
                                                                                                                                       ALDVKKTKDTKPVVKKEERQNVNTLPTTGE 155
                                                                                                                                                                                       ETTPAAEPEVAAVEESSSAAAGEAAAVAPEKVEKAATENAE-AKVEAVAVAAPEK--VEV
                                                                                                                                                                                                                                                                                          PKESYMQNEEGSVPNKPVSENVVAKENNTESGEKQNQTVAETSETTSVEAKETSPVEPTK
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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99US-0161405
99US-0161406
99US-0161359
99US-0161361
99US-0161361
99US-0161920
99US-0161992
99US-0161993
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99US-0156596

99US-0156596

99US-0157117

99US-0157753

99US-0158029

99US-0158369

99US-0158369

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99US-0159294

99US-0159329

99US-0159329

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99US-0159637

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99US-0153070.
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99US-0154039.
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151930.
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Pred. No. 0.04;
1; Mismatches
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RESULT 36
ANG20163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from a sequence of the contraction of the printed at the was obtained in electronic format directly from the part of the printed at the was obtained in electronic format directly from the part of the printed at the was obtained in electronic format directly from the part of the printed at the was obtained in electronic format directly from the part of the printed at the was obtained in electronic format directly from the part of the printed at the was obtained in electronic format directly from the printed at the pr
                                     AAG20163;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
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                                                                                                                                                                                                                                                               KAAT-----PIALDVKKTKDTKPVVKKEERONVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                 ALEALADOTDALOSEEAAVVKADNAASDALEALADOTDALOSEEAEVVOS-DNAASDAWE 119
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16-JUN-1999; 17-JUN-1999; 18-JUN-1999;		17-OCT-2000 Arabidopsis ti
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29-SEP-1999;
04-OCT-1999;
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31-AUG-1999;
01-SEP-1999;
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28-OCT-1999;
28-OCT-1999;
                           AAW27286 standard; Protein; 314
   AAW27286;
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13-OCT-1999;
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12-OCT-1999;
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24-SEP-1999;
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16-SEP-1999;
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27-AUG-1999;
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                                                                                                                                                                             MONEEGSVPNKPVSENVVAKENNTESGEKONOTVAETSETTSVEAKETSPVEPTKETTPA 60
                                                                                    KKAEAEPVKVEAEPVKAEAEPVKAE 142
                                                                                                          KTKDTKPVVKKEERONVNTLPTTGE 155
                                                                                                                                 AEPEVAAVEESSSAAAGEAAAVAPEKVEKAATENAE-AKVEAVAVAAPEK--VEVAVEAE
                                                                                                                                             LQSEEAAVVKADNAASDALEALA-DQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVK 130 : | | | | : : : | | | | : : :
                                                                                                                                                                                                      LTNLLGNAP-----EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDA 71
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990S-0161404.
990S-0161405.
990S-0161406.
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990S-0161360.
990S-0161361.
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99US-0158029
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99US-0151080
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-0160768.
-0160770.
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                                                                                                                                                                                                                                                                                                                         This sequence comprises the EspB virulence factor of a rabbit centeropathogenic Escherichia coli (RDEC-1) strain. Its amino acid sequence was deduced from an isolated espB gene (see AAT91293). The predicted EspB polypeptide shows sequence homology more to predicted EspB polypeptide shows sequence homology more to centerohaemorrhagic E. coli (EHEC) than to enteropathogenic E. coli (EHEC). Claimed novel, isolated EspA polypeptides (see also AAW27284-5) are characterised by: (a) being a secreted protein from EPEC or EHEC; and (b) having a mol.wt. of about 25 kD as determined by SDS-PAGE. Recombinant EspA polypeptides can be expressed in host caused by EspA-producing E. coli, and in a method for ameliorating disease caused by EspA-producing coli, and in a method for ameliorating capainst EspA can be used in the diagnosis of infection.
                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                           Matches
Synthetic protein G from gene MD1
                        11-OCT-1995
                                                                       AAR71127 standard; Protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EspA from entero-pathogenic or entero-haemorrhagic E. coli - used immunise against, and treat diseases caused by EspA producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9740063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                               AAR71127;
                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYBR-) UNIV BRITISH COLUMBIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EspB; rabbit enteropathogenic E. coli; RDEC-1; virulence factor;
pathogen; infection; diagnosis; therapy; vaccine; gastroenteriti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1997-535772/49.
                                                                                                                                 SRFMAAVD-KITGSTPFIAVTSLAEGTKTLPTTVSES
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                                                                                                                                                                              TESVADAVEDASSYMQQAMTTATRAASRTSDVADDIADSAQRASQLAENAADAAQKASRA 212
                                                                                                                                                                                                     T----DALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATP 124
                                                                                                                                                                                                                                                                           l Similarity
45; Conserv
                                                                                                                                                                                                                                                                                                                         314 AA;
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                        (first entry)
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Pred. No. 0.15;
3; Mismatches
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DB 18; 68;

314; 21;

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Indels Length

Gaps

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Matches 42
                                                                                                                                                                                                                                                                                                                                                                            culture, diagnosis and therapy. They can be used such as leukaemia and lymphoma, cancer and immune See also AAR71123-8.
                                                                                                                                                                                                                                                                                                                                                                                    function of FC receptors, as well as in antibody production, cell culture, diagnosis and therapy. They can be used to treat disorders such as leukaemia and lymphoma, cancer and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is the prod. of the synthetic protein G gene, MD-1. proteins produced by MD-1 are capable of specifically binding the constant region of the heavy chain of IgG in the same way as neutral FC receptors. They can be used to analyse the structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide(s) which bind the comprising a nontotal portion protein A and/or Protein G
                                                           plasma
                                                                                        S. dysgalactiae
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic;
                                                                                                            22-SEP-1995
                                                                                                                              AAR71929;
                                                                                                                                                 AAR71929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphoma;
            Peptide
                                                                                                                                                                                                  181
                                                                                                                                                                                                                    138
                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                fast alpha-2-macroglobulin binding protein;
na proteinase-inhibitor binding protein.
                                                                                                                                                                                                                                                                                                KKQAIEDKEATTAIEA-----ASSDALEALADQTDALQSEEAAVVKADNAASDALEALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-106854/14.
                                                                                                                                                                                                                                       DATKTFTVTEM-VTEVPGDAPTEPEKPEASIPLVPLTPATPIAKDDAKKDDTKKEDAKKP
                                                                                                                                                                                                                                                          DQTDALQSEEAEVVQSDNAASDAWEK - - - - -
                                                                                                                                                                                                                                                                             KPEVIDASELTPAVTTYKLVIQGKTLKGETTTKAVDAETAEKAFKQYANDQGVDGVWTYD
                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLIED
                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okarma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein G;
                                                                                                                                                                                                                                                                                                                                                          208 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                          (first
                                      dysgalactiae
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                                                                                        MIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4A;
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 Location/Qualifiers
1..30
/label Sig_peptide
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                                                                                                                                                Protein;
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                                                                                                          entry)
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                                      strain SC1
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                                                                                                                                                                                                                                                                                                                   Score 105; DB 1
Pred. No. 0.098;
2; Mismatches
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the amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an immunoglobulin acid sequence of
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                                                                                                                                                                                                                                                                                                                    63;
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                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                Matches
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                                                                                                                                                                                                      A phage lambda GEM-11 library of S. dysgalactiae SC1 DNA was a for fast-acting alpha-2-macroglobulin (FAM)- and IgG-binding activity. One clone, which expressed both activities, was analyzed to obtain DNA encoding the FAM-binding protein, MIG (AAR71929). The mig gene is given in AAQ89196.
                                                                                                                                                                                                                                                                                     DNA encoding fast alpha 2-macro:globulin-binding proteins - to obtain prods. for sepn., detection or quantification or ibinding inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                  Disclosure; Page 31;
                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                        Guss
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                      (MUEL/)
                                                                                                                                                                                                                                                                                                                                                                                               (LIND/)
                                                                                                                                                                                                                                                                                                                                                                                                                  (GUSS/)
           130
                              534
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                                                                                                                                                          Local
                                                                                                                            1 VDSPIEQP-----RIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIED------
KKTKDTKPV--
                                                                                    KEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA-E
                                                                                                                                                                                                                                                                                                                            1995-123382/16.
DB; AAQ89196.
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                              OYANENGVDGVWTYDDATKTFTVTEMVTEVPGDAPTEPEKPEASIPLVPLTPATPIAKDD
                                                                     DDATKTFTVTEKPAVIDAPELTPALTTYKLVI----NGKTLKGETTTKAVDAETAEKAFK
                                                                                                          IDAPELTPALTTYKLIVKGNTFS---GETTTKAV--DAETAEKAFKQYANENGVYGEWSY
                                                                                                                                                                                                                                                                                                                                                                          HINDBERG M.

MUELLER H.

RANTAMAKI L F
                                                                                                                                               Similarity
54; Conserv
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                                                                                                                                                                                       664 AA;
                                                                                                                                                Conservative
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/note= "IgG l
349..418
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/note= "IgG |
279..348
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639..66
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/note= "IgG binding domain
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/note= "IgG binding
489..558
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419..488
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23.9%;
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                                                                                                                                                21;
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Pred. No. 0.41;
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           VKKEERQNVNTLPTTGEESNP
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promoter;
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                                                     ETTPAVQPEVAAVEESSSADAGEAAVVAPEKVENAATENAEAKVEAVAVAAPEKVEV---
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39; Conserv
                                                                                           13.4%; Score 104.5; DB 21; ilarity 26.0%; Pred. No. 0.073; Conservative 25; Mismatches 57;
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99US-0149722

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99US-0161361

99US-0161361
                                                                                         57; Indels 29; Gaps
                                                                                                             Length 151;
                  124
                                                                                           6,
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Db 125 --- AVEAEKKAEAEPVKAEAEPVKAEAEPV 151

Search completed: October 13, 2002, 04:45:33 Job time: 67.6203 secs

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                                    Result
No.
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Listing first 45 summaries
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                                                                                                                                1 (bases 1 to 7.88)
Turkewitz7A-P., Karre
,J. and Klobutcher,L.
         Email: apturkew@midway.uchicago.edu
Seq primer: T3.
                                 Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 606 Tel: 773 702 4374 Fax: 773 702 3172
                                                                                                 Contact: Turkewitz AP
                                                                                                           Unpublished (2002)
                                                                                                                       EST from Tetrahymena thermophila,
                                                                                                                                                                     Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
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Tel: 773 702 4374
Fax: 773 702 3172
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University of Chicago
920 E. 58th Street, Chicago, IL 606
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Turkewitz, A.P., Karrer, K.M.,
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Seq primer: T3.
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
a 222 c 151 g 207 t 3 others
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/db_xref="taxon.5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
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                                                                                                     GCTTTAACCGAGGAGGAGGCGGCT
                                                                                                                                           ValValLysAlaAspAsnAlaAla
                                                                                                                                                                                     Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T.
Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoptere Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA153F11
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Euteleostei; Neoteleostei;
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RESULT 5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                              mRNA sequence
BJ013747
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Medaka EST Project in Takeda's lab
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                                                                       Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. Medaka EST Project in Takeda's lab Unpublished (2001)
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                         Center For Genetic Resource Information National Institute of Genetics
                                                             Contact: Tadasu Shin-i
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/clone_1ib="MF01SSA cDNA"
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/tissue_type="whole embryo"
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/strain="Hd-rR"
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                                                                                                                   BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - :
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                             Email: http://www.frultfly.org/EST, Plate: 258 row: G column: 1
High quality sequence stop: 226.
Location/Qualiflers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 438)
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AA941632
LD25873.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD25873 5prime, mRNA sequence.

AA941632
AA941632
AA941632.1 GI:3101545
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Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvey,D., Brokstein,P., Hong,L., Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly.
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/note="end : T7"
1 329 c 226 g
                                                                                                                                                                 /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Si
XhOI; Sized fractionated cDNAs were directly ligated
pOT2."
                                                                                                                                                                                                   /clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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A0951191 611 bp
Sheared DNA-50A17.TR Sheared DNA
Sheared DNA-50A17, DNA sequence.
A0951191 GI:6774456
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Euphorbia esula
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231 AACGATCGGCGGAATCATATAGAAGACCACACAGACGCAGAGGAGGAGCAGGAACAAGCG 172
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553 bp mRNA linear EST 08-JUN-2000 00257 leafy spurge Lambda HybrizAP 2.1 two-hybrid vector cDNA Library Euphorbia esula cDNA clone 25D 5' similar to Arabidopsis Unknown Protein (accession# AAF24521), mRNA sequence.

BE056346
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1605 Albrecht Blvd., PO Box 5674, Fargo,
Tel: 701 239 1263
Fax: 701 239 1252
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Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)
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vector cDNA Library"
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/dev_stage="3-day induced (decapitated)"
117 c 116 g 159 t
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq_primer: M13-Reverse
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Trypanosoma brucei
                                        CNS06NI7 1163 bp DNA linear GSS 17-JI
T3 end of clone AU0AA012D04 of library AU0AA from strain CBS
of Saccharomyces kluyveri, genomic survey sequence.
AL406805
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The Institute for Genomic Research
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Other_GSSs: Sheared DNA-50A17.TF
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10.1 sheared DNA library
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301 838 0208
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a 175 c
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/rote="Vector: pUCl8; Site_l: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A practical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Approach, eds
Press, 1999).
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/strain="TREU927/4 GUTat 10.1"
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. M. Vaudin and B. Barell, Oxford University
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682 bp mRNA linear EST 01-FEB-201 EBed07_S0001_D10_R IGF Barley EBed07 library Hordeum vulgare cDNA clone EBed07_SQ001_D10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces kluyveri
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 1163)
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Genomic exploration of the hemiascomycetous yeasts: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalls and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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FEBS Lett. 487 (1), 56
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/strain="CBS 3082"
/db_xref="taxon:4934"
/clone="AU0AA012D04"
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EST.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Prerygota; Neoptera; Endopterygota; Diptera; Brachycera;
Musacamaroha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                  BF496493 243 bp mRNA linear EST 19-APR-20 AT10425.5prime AT Drosophila melanogaster adult testes pOTB7. Drosophila melanogaster cDNA clone AT10425.5 similar to CG7289: FBan0007289 located on: 2L 22B8-22B8;: 04/08/2001, mRNA sequence.
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All sequence has a Phred quality
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/clone_lib="IGF Barley EBed07 library"
/tissue_type="Endosperm"
/dev_stage="28 days post anthesis"
/lab_host="DH10B"
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/db_xref="taxon:4513"
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Best Local Similarity:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyce Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 333) (bases 1 to 333) (Copterynski,C., Serano,T., Rubin,G. and Goodman,C. BDGP/HHMI CK Drosophila EST Project Unpublished (1996) Other_ESTs: CK00525.3prime
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333 bp mRNA linear EST 29-
CK00525.5prime CK Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone CK00525 5prime, mRNA seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G. M.
                                                                                                                                                                                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, Plate: AT.104 row: C column: 1 High quality sequence stop: 235. Location/Qualifiers
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On Dec 6, 2000 this sequence version replaced Contact: Stapleton, M.
                                                                                                                                                                          Drosophila
                                                                                                                                                                                                                                      AA140863
AA140863.1 GI:1704336
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//dev_stage="0-3 day old Ore-R males"
/lab_host="plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
//note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
Site_2: Xho1; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
a 65 c 56 g 68 t 1 others
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/db_xref="taxon:7227"
/clone="AT10425"
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/sex="male"
                                                                                                                                                                          melanogaster
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                             ve38f01.yl Soares_mammary_gland_NbmMG Mus musculus IMAGE:820441 5', mRNA sequence.
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               This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in \dot{}
                                                                                                                                                                                                                                                                                                           Mus musculus
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Insert Length: 333 Std Error: 0.00
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One Cyclotron Rd, Berkeley, CA 94720,
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                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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correct orientation)
                                                            MGI:488721
                                                                                                                                                                                    Tumor Gene Index
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                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKt. Cloned into HinDIII, but the site was destroyed to add an adapter sequence. So ClaI is now the restriction enzyme at site I of vector. Primers - 5' universal, 3' m13-20 (reverse), 3' T3, 5' T7."

a 89 c 72 g 91 t 6 others
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/sex="male and female"
/dev_stage="0 to 24 hours old embryo"
/lab_host="xi,1 Blue MRF"
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/clone="CK00525"
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/db_xref="BDGP_EST:BDcln000406"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                  MGI:488721
This clone was previously sequenced data is from the 3' end High quality sequence stop: 348.
                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
TMAGE Consortium (info@image.llnl.gov) for further:
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High quality sequence stop:
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptors
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with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mammary gland"
/dev_stage="4 weeks"
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/clone="IMAGE:820441"
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/organism•"Mus musculus"
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                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMH Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE: 820441
AA423358
                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                         MGI:488721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse
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                                                                            IMAGE Consortium (info@image.llnl.gov)
                                      primer: -28m13 rev2 ET from Amersham
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              Location/Qualifiers
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/dev_stage="4 weeks"
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/db_xref="taxon:10090"
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; Murinae; Mus
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**KEYWORDS** 

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GH25307.5prime GH Drosop
melanogaster cDNA clone
AI405338
AI405338.1 GI:4248425
EST.
                                                                                                                                                      Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                                                                                                   Email: http://www.fruitfly.org/EST, hit genomic sequence AC005749 Plate: 253 row: A column: 7
                                                                                                                                                                                                                                           Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                         Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                              Harvey,D., Brokstein,P.,
                                                                                                                                                                                                                                                                                                            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 491)
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            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                    1. .491
/clone="GH25307"
                                                                 Location/Qualifiers
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/dev_stage="4 weeks"
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/sex="male"
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/clone="IMAGE:820441"
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/strain="C57BL/6J"
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Unpublished (2000)
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Oryza sativa
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AU101404 Rice panicle shorter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki, T. and Yamamoto, K.
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                                                                                                                                                                                                                                                                                     E30571_7A.
                                                                                                                                                                                                                                                                                                           Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                    PROJECT -'RGP'.
                                                                                                                                                                                                                                                                                                                                                           305-8602, Japan
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//dev_stage="adult"
//lab_host="DH5 - alpha"
//lab_host="DH5 - alpha"
//note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
//note="Organ: head; Vector: pOT2; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
pOT2. Plasmid round library."
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                                                                                                                                /sex="male and
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/clone="E30571"
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/sex="male and female"
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                                                                                                                                                                                                                                       organism="Oryza sativa"
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AA540164
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 535)
Harris P. Brokktoin B. Woog I Frans-Halle M. Su G. Teang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA540164 535 bp mRNA linear EST 19-APR-2001
LD19555.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD19555 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu plate: 195 row: E column: 7
High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Project Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harvey,D., Brokstein,P., Hong,L.,
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                                                                                                                                                                                                                                                                                                           117
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                                                                                                                                                                                                                                                                                                         /clone_lib-"LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism "Drosophila melanogaster"
/db xref="BDG-EST:BDC10018642"
/db xref="taxon 7227"
/clone="LD19555"
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51.00
53.85%
42.31%
39.53%
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RESULT 20

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ACCESSION
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                                                                                                                                                                                              4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
                                                                                                                        GAGGATGAC 470
                                                                                                                                                AlaAspAsn 26
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sequence.
BM431282
BM431282.1
                                            BM431282
1Duo12E08
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Plate: 83 row: M column: 13
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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96120 MARC 1BOV Bos taurus
AW659168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                     note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
143 c 151 g 122 t
                                              Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
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Pecora; Bovoidea;
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US-09-847-539A-6_COPY_59_86 (1-28)
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Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of All
110 Agri/For, Dept of AFNS, University of AFNS, Uni
                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
Genome Biology Lab.
National Institute of Genetics
Yata IIII, Mishima, Shizuoka 411, Japan
                                                                                                                                                                        A complementary view of the Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU206045 unpublished oligo-capped cDNA library, Stage Ll Caenorhabditis elegans cDNA clone yk858ell 5', mRNA sequence. AU206045
                                                                                                                                 Contact: Yuji Kohara
                                                                                                                                                                                                                                                                  and Sugano, S.
                                                                                                                                                                                                                                                                                                Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
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Hansen, C., Fu, A., Meng, Y., Li, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea Bovidae; Bovinae; Bos.
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Insert Length: 553 Std Error:
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Site_1: EcoRI; Site_2: Xho I"
124 c 139 g 132 t
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/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMKF'strain"
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/db_xref="taxon:9913"
/clone_lib="Bos taurus Duodenum #1 library"
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                                                       Email: http://www.fruitfly.org/EST, est@fruitf
hit genomic AE003584: arm:2L [1824960,2149443]
estimated-cyto:2284-22D2: 04/09/2001
Plate: AT.202 row: F column: 7
High quality sequence stop: 562.
Location/Qualifiers
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On Dec 6, 2000 this sequence version
Contact: Stapleton, M.
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1 (bases 1 to 563)
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EST.
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One Cyclotron Rd, Berkeley, CA 94720, USA
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Location/Qualifiers
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146 c 14
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/tissue_type="whole animal"
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/clone="yk858e11"
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 567)

1 (bases 1 to 567)

Neoptera; Marcheata; Drosophilidae; Drosophila.

1 (bases 1 to 567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
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                                                                                                                                                                                                                                                              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS06378
Plate: 30 row: C column: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
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159 c 141 g 137 t
              /note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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AT.121-AT.319: DH5-alpha TonA"
                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH03030"
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/clone_lib="AT Drosophila melanogaster adult testes
                                                                    /clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5" - alpha"
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Berkeley, CA 94720, USA
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AspAla Leu Glu Ala Leu Ala AspGln Thr AspAla Leu Gln Ser Glu Glu Ala Ala Valleu Glu Ala Control Cont
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GH19913.5prime GH Drosophila melanogaster head pOT2 Dr
melanogaster cDNA clone GH19913 5prime, mRNA sequence.
AI388871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.fruitfly.org/EST, hlt genomic sequence AC005749 plate: 199 row: B column: 1 High quality sequence stop: 566. Location/Qualifiers
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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1 (bases 1 to 567)
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One Cyclotron Rd, Berkeley, CA 94720,
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                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head: Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head: Vector: pOT2; Site_1 igated into
pOT2. Plasmid cDNA library."
161 c 141 g 138 t
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/db_xref="taxon:7227"
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RESULT 27
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BI637415/c
          DEFINITION
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     AI109571
GH08804.5prime
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003584: arm:2L [1824960,2149443]
estimated-cyto:2284-22D2: 05/19/2001
plate: SD.194 row: C column: 6
High quality sequence stop: 429.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 567)
Barkotais P. Hong I. Transchila M. G. G. Torong
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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B1637415
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/note="Vector: pOT2; Site_1: EcoRI; Site_2: Xi
fractionated cDNAs were directly ligated into
plasmid cDNA library."
a 161 c 141 g 138 t
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culture pOT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD19430"
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Best Local Similarity:
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                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 569)

1 (bases 1 to 56)
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High quality sequence stop: 511
Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
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AA392809.2 GI:13766578
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(bases 1 to 568)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,
Lewis,S. and Rubin,G.M.
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Harvey, D., Brokstein, P., Lewis, S. and Rubin, G.M.
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Lawrence Berkeley National Lab
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2.__plasmid_cDNA library."
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/db_xref="taxon:7227"
/clone="GH08804"
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                Evans-Holm, M., Su, C.,
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               Tsang, G.,
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                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                         Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                           AI388559 581 bp mRNA linear EST 19-APR GH19508.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH19508 5prime, mRNA sequence.
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hit genomic AE003584: arm:2L [1824960,2149443]
estimated-cyto:2284-22D2: 04/10/2001
Plate: LD.121 row: B column: 3
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On Jan 19, 1998 this sequence version replaced gi:2792678.
Other_ESTs: LD12115.3prime
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               Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
                                                                       Contact: Stapleton,
                                                                                                                                               Harvey, D., Brokstein, P., Hong, L.,
                                                                                                                                                                 Muscomorpha; Ephydroidea;
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Fax: 510 486 6798
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcln011306"
/db_xref="taxon:7227"
/clone="LD12115"
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RESULT 30
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1 (bases 1 to 583)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang Lewis,S. and Rubin,G.M.
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AI108834
                                                                                                                                                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS06378
Plate: 81 row: C column: 4
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hit genomic sequence AC005749
Plate: 195 row: A column: 8
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                                                                                                                                                                                                                                            510 486 6798
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164 c
               /clone="GH08128"
/clone_lib="GH Drosophila
/sex="male and female"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="0H5 - alpha"
/lab_host="0H5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhOI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
164 c 144 g 144 t
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/db_xref="taxon:7227"
/db_xref="GH19508"
/clone="GH19508"
/clone_lib="GH Drosophila melanogas
/sex="male and female"
/lab_host="DH5
                                                                                                                                                 Location/Qualifiers
                                                                                           /organism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
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RESULT 31
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Fax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                          Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 224 row: F column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) Other_GSSs: RPCI-23-224F10.TJ
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RPCI-23-224F10.TV RPCI-23
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The Institute for Genomic Researc
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-224F10"
/clone_lib="RPCI-23"
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/sex="remate/sex="DH10B"
//lab_host="DH10B"
//lab_host="DH10B"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Vector: BECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed int
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pOT2. Plasmid cDNA library."
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                                                                                                                                                                                                       Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and hayashizaki,Y.
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BB201301
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
On Jun 30, 2000 this sequence version replaced gi:8866254.
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                      sequencing pipeline with 384 multicapillary sequencer. Gen 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic
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GH02173.5prime GH
                   Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyce Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 633)
                                                                                                       Drosophila melanogaster
Harvey,D.,
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                                                                                                                             fruit fly.
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCACTCTTTTTTTTTTTTTTTYN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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thymus"
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633 bp mRNA linear EST 19-APR-2001 Drosophila melanogaster head pOT2 Drosophila clone GH02173 5prime, mRNA sequence.
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Evans-Holm, M., Su, C.,

Tsang, G

Brachycera;

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                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 643)
Parkets D Brockton Drosophila
                                                                                                                                                             Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                   AA391497 643
LD10172.5prime LD Drosophila
Drosophila melanogaster CDNA
AA391497
            Email: http://www.fruitfly.org/EST, Plate: 101 row: F column: 12 High quality sequence stop: 463.

Location/Qualifiers
                                                                                      BDGP
Lawrence Berkeley National Lab
Perkeley, CA 94720, USA
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BDGP/HIMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
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                                                                                                                                                                                                                                                                                                                    fruit fly.
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Location/Qualifiers
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182 с
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. plasmid cDNA library."
a 182 c 153 g 158 t
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/db_xref="taxon:7227"
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Conservative:
Mismatches:
Indels:
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clone LD10172 5prime, mRNA seq
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                                                            est@fruitfly.berkeley.edu
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RESULT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                             Duke University
Durham, NC 27708-1000,
Tel: 919 613 8164
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                Vascular Plants; project phase Unpublished (2000)
Contact: Elizabeth H. Harris DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE337641 650 bp m
894047D11.yl C. reinhardtii CC-1690,
Chlamydomonas reinhardtii CDNA, mRNA
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                                                                                                                                                                                                                                                                                              chlamy@duke.edu
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               XhoI; This library, constructed by John Davies and Jeffr McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2.
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185 c 154 g 164 t
PolyA mRNA was purified from each sample, pooled
                                                                                                                                                                /organism-"Chlamydomonas reinhardtii"
/strain-"CC-1690 wild type mt+ 21gr"
/db_xref-"taxon:3055"
/clone_lib-"C. reinhardtii CC-1690, normalized,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                         /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
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/db_xref="BBP_EST:BDC1n009443"
/db_xref="taxon:7227"
/clone="LD10172"
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and cDNA
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BI633216/c
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 660)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BI633216
                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu htt genomic AE003584: arm::ZL [1824960,2149443] estimated-cyto::22B4-22D2: 05/23/2001 estimated-cyto::22B4-22D2: 05/23/2001 Plate: SD.272 row: D column: 8 High quality sequence stop: 529. Location/Qualifiers
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Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
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                                                                          /lab_host="DH5-alpha"
/note="Vector: pOT2; Site_1: EcoRI; Site_2: Xhol;
/note="Vector: pOT2; Site_1: EcoRI; Site_2: Xhol;
fractionated cDNAs were directly ligated into pOT;
plasmid cDNA library."
189 c 158 g 163 t 2 others
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/db_xref-"taxon:7227"
/clone-"SD27244"
/clone_lib-"SD Drosophila melanogas
culture pOT2"
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22 ValLysAlaAspAsnAla

AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal

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AI062753/c
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Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                           Email: http://www.fruitfly.org/EST, hit genomic sequence DS06378 plate: 20 row: G column: 1 High quality sequence stop: 566.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 666)
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GH02073.5prime GH Drosophila melanogaster head pOT2 Dr
melanogaster cDNA clone GH02073 5prime, mRNA sequence.
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                                                                                                                                                         POT2.
192
                                                                                                                                                           /clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI: Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
a 192 c 157 g 164 t
                                                                                                                                                                                                                                                                                                    /organism="Drosophila
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pleter de Jong (pde)ong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tab/bac_ends/mouse/bac_end_intro.html Plate: 224 row: J column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) Other_GSSs: RPCI-23-224J19.TJ
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Class: BAC ends.
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
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a 163 c 150 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-224J19"
/clone_11b="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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/strain="C57BL/6J"
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AT03044.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AT03046 5 similar to CG7289:
FBan0007289 located on: 2L 22B8-22B8;: 04/07/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003584: arm:2L [1824960,2149443] estimated-cyto:2284-22D2: 05/19/2001 plate: SD.191 row: E column: 3 High quality sequence stop: 578.
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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203 c 170 g 171 t 1 others
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/lab_host="DH5-alpha"
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/db_xref="taxon:7227"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases i to 797)

1 (bases i to 797)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003584; arm:2L [1824960,2149443] estimated-cyto:22B4-22D2: 04/07/2001 Plate: AT 30 row: D column: 10 High quality sequence stop: 699.

Location/Qualifiers
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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On Dec 6, 2000 this sequence version replaced gi:11577746.
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AT.121-AT.319: DH5-alpha TonA"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI; Site_2: Xho1; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."

a 234 c 195 g 190 t
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Rasmussen M., Muller H.P., Bjorck L.;
"Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin.";
J. Biol. Chem. 274:15336-15344(1999).
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InterPro; IPRO01899; Gram_pos_anchor.
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MEDLINE-21192684; PubMed-11296296;

Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G

Permeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL: AF124399; AAD26338.1; -.

EMBL: AE006573; AAK34185.1; -.
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"Protein GRAB of Streptococcus pyogenes regulates bacterial surface by binding alpha2-macroglobulin. Submitted (JAN-1999) to the EMBL/GenBank/DDBJ data
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Lai H.S., Li
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Q9X5C5;
Q1-NOV-1999
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01-NOV-1999
01-NOV-1999
01-DEC-2001
PROSITE;
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SEQUENCE
                         MEDLINE-99269061; PubMed-10336419; Rasmussen M., Muller H.P., Bjorck L.; Rasmussen M., Muller H.P., Bjorck L.; Rasmussen M., Muller H.P., Bjorck L.; Protein GRAB of streptococcus pyogenes regulates bacterial surface by binding alpha2-macroglobulin. J. Biol. Chem. 274:15336-15344(1999).

EMBL; API24403: AAD26342.1; -. InterPro: IPR001899; Gram_pos_anchor. PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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"Protein GRAB of streptococcus pyogenes regulates proteolysis bacterial surface by binding alpha2-macroglobulin.";

J. Biol. Chem. 274:15336-15344(1999).

EMBL; AF124402; AAD26341.1;

InterPro: IPR001899; Gram_pos_anchor.
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Bacteria; Firmicutes; I
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                                                                                                                                      NCBI_TaxID=1314;
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Similarity 100.
28; Conservative
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Pred. No. 1e-09;
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A SEQUENCE FROM N.A.

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RCC STRAIN-26695 / ATCC 700392:

RX MEDLINE-97394467; PubMed-9252185;

RA Tomb J.-F., White O., Kerlawage A.R., Clayton R.A., Sutton Tomb J.-F., White O., Kerlawage A.R., Klenk H.-P., Gill S., Dougherty B.A., RA Loftus B., Richardson D., Dodson R., Klakness E.F., Peterson S., RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin Porton M.D., Weldman J.M., Karp P.D., Smith H.O., Fraser C.M.,
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01-JAN-1998 (TrEMBLrel. 05, Cre
01-JAN-1998 (TrEMBLrel. 05, Las
01-DEC-2001 (TrEMBLrel. 19, Las
47-1 KDA PROTEIN.
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076220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Proteolytic processing and Ca2+ binding vesicle polypeptides in Tetrahymena."; Mol. Biol. Cell 0:0-0(1997).
EMBL; AF031321; AAC27989.1; -CHAIN 58 377 GRANULE LATT
                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
Helicobacter.
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Tetrahymena thermophila.
Ciliophora;
pylori.";
Nature 388:539-547(1997).
EMBL; AE000634; AAD08377.1;
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NCBI_TaxID=5911;
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Pred. No.
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Pred. No. 1.2e-09;
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Wallin E.,
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01-MAY-1999
01-JUN-2001
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Q935B1;
01-DEC-2001
STRAIN-CT18;
STRAIN-21534947; PubMed-11677608;
MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZJQ7
Q9ZJQ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastric pathogen Helicobacter pylori.
Nature 39:176-180(1999).
EMBL; AE001548; AAD106820.1; -.
InterPro; IPR003423; OEP.
Pfam; PF02321; OEP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; HP1327;
                                                                                                                                                                Plasmid pHCM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99120557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori J99 (Bacteria; Proteobacteria;
                                                                     SEQUENCE FROM
                                                                                                                                 Salmonella
                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trust T.J.;
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                                                                                                          NCBI_TaxID=90370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence comparison of two unrelated mastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                49
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412 AA; 4
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47115 MW; 1724D84A9BFA15DD CRC64;
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Pred. No. 9.
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01-DEC-2001 (TrembLrel
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PUTATIYE EXONUCLEASE.
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Q92FR3;
01-DEC-2001
                                          Q92FR3
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Cordeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413.848-852(2001).
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            the 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97000351; PubMed-8843436;
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e 8 mb Streptomyces coelicolor A3(2) chromosome.";
1. microbiol. 21:77-96(1996).
BL; AL592292; CAC42847.1; -.
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                                                                                                                                                                                                                                                                                                                       AA;
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Matches 10
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28 Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
29 Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
20 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
20 Entian K.-D., Fsihi H., Garcia del Portillo F., Garrido P.,
21 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
21 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
21 Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
22 Madueno E., Movella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
23 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
24 Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
25 Cience 294:849-852(2001).
26 Engli AL596163; CAC95273.1; -.
27 Fistitict TimonoA.
          Redenbach M., Kieser H.M., Denapaite D., Eichner A
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                      SC1F2.16C.
Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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                                                                             SEQUENCE FROM N.A.
STRAIN-A3(2);
STRAINE-97000351; PubMed-8843436;
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Seeger K.J.,
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LIN0040 PROTEIN.
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NCBI_TaxID=1902;
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STRAIN-CLIP 11262
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203 AA;
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076506;
076506;
01-NOV-1998
01-NOV-1998
01-DEC-2001
CILIARY OUTE
DYH4.
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01-MAR-2001
01-MAR-2001
01-OCT-2001
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Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weif D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Danlels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TremBLrel. 16, Created)
01-MAR-2001 (TremBLrel. 16, Last sequence update)
01-CCT-2001 (TremBLrel. 18, Last annotation updat
L-2,4-DIAMINOBUTYRATE DECARBOXYLASE.
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SEQUENCE 276 AA;
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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SEQUENCE
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                                                                                                                                            Conservative
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                                                        PRELIMINARY;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Mcmurray A., Mortimore B., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                   InterPro;
InterPro;
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Lincoln L.M., Gibson T.M.,
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Lee S., Wisniewski J.C., Dentler W.L.,
"Gene knockouts reveal separate function
in Tetrahymena thermophila.";
Mol. Biol. Cell 10:771-784(1999).
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EMBL; Z68117; CAA92197.1;
EMBL; Z68117; CAA92183.1;
EMBL; Z68119; CAA92183.1;
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
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                                                     HSSP; P10587; 1BR2.
InterPro; IPR001609;
                                                                                                                                                       Nature 368:32-38(1994).
                                                                                                                                                                         elegans
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IPR002928;
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Myosin_N.
Myosin_tail.
Peptidase_S8.
                                                      myosin_head
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087677;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                           Puk O., Huber P., Bischoff D., Recktenwald J., Jung G., Suessmith R.D., Van Pee K.H., Wohlleben W., Peizer S.; "Glycopeptide biosynthesis in Amycolatopsis mediterranei function of a halogenase and a haloperoxidase."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     Pfeifer V., Nicholson G.J., Ries J., Recktenwald J., Schefer A.B., Shawky R.M., Schroeder J., Wohlleben W., Pelzer S.;
"A Polyketide Synthase in Glycopeptide Biosynthesis: the Biosynthesis of the non-proteinogenic Amino Acid (S)-5-bihydroxyphenylglycine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recktenwald J., Shawky R.M., Puk O., Pfennig F., Keller U., Wohlloben W., Pelzer S.; Wohlloben B., Pelzer S.; "The nonribosomal biosynthesis of vancomycin-type antibiotics: heptapeptide backbone and eight peptide synthetase modules."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and analysis of the balhimycin biosynthetic cluster and its use for manipulating glycopeptide biosynthes Amycolatopsis mediterranei DSM5908.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01576; Myosin_tail; 2.
PRINTS; PR00193; MYOSINHEAVY.
ProDom: PD000355; myosin_head; 1
SMART; SM00242; MYSC; 1.
PROSITE; PS00136; SUBTILASE_ASP;
SEQUENCE 1968 AA; 225431 MW;
                                                                                                                                        Submitted (AUG-2001) to t
EMBL; Y16952; CAA76551.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amycolatopsis mediterranei (Nocardia mediterranei),
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
NCBI_TaxID=33910;
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                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2001)
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PF02736;
PF01576;
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REMBL; AF047034; AAF37157.1;

InterPro; IPR001525; C5_DNA_meth.
InterPro; IPR000524; HTH_GntR.

InterPro; IPR000524; HTH_GntR.

InterPro; IPR000524; HTH_GntR.

Pfam; PF00392; gntR; 1.

SMART; SM00345; HTH_GNTR; 1.

PROSITE; PS00095; C5_MTASE_2; UNKNOWN_1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription regulation.
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Blochim micabon
Gallbert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F. Barloy-Hubler F., Barnett M.J., Becker A., Bolstard P., Bothe G., Boutry M., Bowser L., Buhrmester J., Cadleu E., Capela D., Chain Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kah Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
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Youn H., Kang.S.-O.;
Submitted (APR-1999) to
-!- SIMILARITY: BELONGS
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Rhizobiaceae;
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Bacteria; Firmicutes; Ac
                                                                                                                                                                   MEDLINE-21368234; PubMed-11474104;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q95VK1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 50.1 KDA PROTEIN.
F19H22.10 OR AT4G38910.
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SEQUENCE FROM N.A.

Bevan M., Murphy G., Ridle

Mayer K.F.X., Schueller C.

"-"++ad (MAR-1999) to th
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Pux Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C. "The composite genome of the legume symbiont Sinorhizobium Science 293:668-672(2001).

EMBL; AL591788; CAC46313.1; -.
                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL035679; CAB38B11.1; -
EMBL; AL161594; CAB80554.1; -.
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 Halobacterium
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Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Isenbarger T.A., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.",

"Genome sequence of Halobacterium species NRC-1.",

"Broc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
O9FHF8:
01-mAR-2001 (TrEMBLrel. 16, Created)
01-mAR-2001 (TrEMBLrel. 16, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
DISEASE RESISTANCE PROTEIN-LIKE.
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InterPro; IPR003029;
InterPro; IPR004365;
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MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fr
Mitchell W.P., Olinger L., Tatusov R.L.,
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Pfam; PF00951; NB-ARC; 1.
Pfam; PF01582; TIR; 1.
PRINTS; PR00364; DISEASERSIST
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                             Hypothetical
SEQUENCE 2
                                                                               Science 282:754-759(1998).
EMBL; AE001313; AAC67995.1; -.
InterPro; IPR003743; DUF164.
Pfam; PF02591; DUF164; 1.
                                                                                                                                                                                                                             Chlamydia trachomatis. Bacteria; Chlamydiales;
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01-DEC-2001
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SMART; SM00255; TIR;
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InterPro; IPR002182; NB-A
InterPro; IPR000157; TIR.
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features of
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PRO) IPRO)3593; AAP
PRO; IPRO)1687; ATP_CTP_A.
Pro; IPRO)0767; Disease_resist.
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Conservative
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Y., Kaneko T., Katoh
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1. 19, Last annotation
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edons; core eudicots; Rosidae;
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OPDZ7-2000 (TrEMBLrel. 15, Cre/
P 01-OCT-2000 (TrEMBLrel. 15, Las
P 01-DEC-2001 (TrEMBLrel. 19, Las
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Q9KYW4;
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., B. Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodso. Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzb. Elsen J., Fraser C.M.;
                                      Cerdeno A.
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE002356; AAF39497.1;
TIGR; TC0677;
                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
         SEQUENCE FROM STRAIN-A3(2);
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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InterPro; IPR003743; DUF164.
Pfam; PF02591; DUF164; 1.
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Bacteria; Chlamydiales;
MEDLINE-97000351;
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NCBI_TaxID=1902;
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PubMed=8843436;
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POSSIBLE LIVER STAGE I
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Q9HPA2;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC59787.1; -. SEQUENCE 1617 AA; 174798 MW; D7A5E04C9287
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"A set of ordered cosmids and a detailed genetic and the 8 mb Streptomyces coelicolor A3(2) chromosome.";
mol. microbiol. 21:77-96(1996).
EMBL; AL355774; CAB90928.1; -
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-20504483;
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Pred. No. 9.6e
4; Mismatches
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01-OCT-2001
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O9KZO5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLUTAMATE-ANMONIA-LIGASE ADENYLYLTRANSFERASE (FRA
                                                                                                                                                                                                                                                                                                                                                             Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima Ohya Y., Watanabe K., Yamazaki M., Kanehori K., K. Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M., "Archaeal adaptation to higher temperatures revealed by gen sequence of Thermoplasma volcanium."; Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
EMBL; APO00995; BAB60191.1; -.
EMBL; APO01697; Pyruvate_kinase.
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SMART; SM00304; HAMP;
SMART; SM00283; MA; 1
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STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031;
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PF02887; PK_C; 1.
S; PR01050; PYRUVTKNASE.
pn001009; Pyruvate_kinase;
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Pred. No. 3.
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Actinobacteria; Actinobacteridae;

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01-MAY-1999 )
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MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite
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Cerdeno A.M., Parkhill J.,
Submitted (MAY-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                            "Nitrogen metabolism in Streptomyces coelicolor A3(2): modification glutamine synthetase I by an adenylyltransferase."; Microbiology 145:2313-2322(1999).
EMBL; Y17736; CAA76840.2;
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'A set of ordered cosmids and a detailed the 8 Mb Streptomyces coelicolor A3(2) che Mol. Microbiol. 21:77-96(1996).
EMBL; AL355752; CAB90882.1;
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Fink D., Falke D., Wohlleben W., Engels A.;
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                                 DALEALA-----DOTDALQSEEA
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    ADENYLYLTRANSFERASE (EC 2.7.7.42)

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Structural analysis of putative hypovirulent in a spontaneous avirulent mutant of Rastonia Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AB015669; BAA32222.1;

InterPro; IPR000637; AT_hook.
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL, AL359214; CAB94589.1; -.
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(JUN-2000) to
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(TrembLrel. 15, Last sequence
(TrembLrel. 15, Last annotation)
L 22.9 KDA PROTEIN (FRAGMENT).
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                                                                                                                                                                                           Harris
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o the
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e EMBL/GenBank/DDBJ databases.
Barrell
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B.G.,
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Streptomyces
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1.5e+02;
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Rajandream M.A.;
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RESULT 36
Q9FGP2
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Best Local S
Matches 13
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Matches
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                                                                                                                                                                                                                          Q9FGP2 PRELIMINARY; PRT; 299 AA.
Q9FGP2;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-1001 (TrEMBLREL. 19, Last annotation update)
Q1-DEC-2001 (TREMBLREL. 19, Last annotation update)
                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isiegas C., Parro V., Mel. Submitted (JAN-1999) to ti EMBL; Y13601; CAA73927.1;
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
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Streptomyces lividans.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Redenbach M., Kleser H.M., Denapatte D.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TK21;
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                        Kaneko T.,
Tabata S.;
                                                               STRAIN-COLUMBIA;
                                                                                     SEQUENCE FROM
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NON_TER 250 25
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13; Conserv
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Similarity 58.8%;
10; Conservative
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of
                                          Asamizu
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to the EMBL/GenBank/DDBJ
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Pred. No. 1.6e
2; Mismatches
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Pred. No. 1.7e
4; Mismatches
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1.6e+02;
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P SEQUENCE FROM N.A.

C STRAIN-ATCC 19089 / CB15;

X MEDLINE-21173698; PubMed-11259647;

X Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K. Paulsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., A. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ella DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., A. Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry M. Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

REMBL; AF062345; AAF03166.1; ...
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                                                                                                                                                                                                                                                  Nelson K.E.,
                                                                                                                                                                                              N.D., Ely B.,
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                                                                                                                                                     Berry K.,
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Q9E338
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Search completed: October 13, 2002, 04:48:07 Job time: 13.1283 secs
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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Q9E338;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POLYPROTEIN.
Alphavirus M1.
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InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 345 AA; 39105 MW; 5E3B5E45D4280449 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and primary analysis of 3' end of two alphaviruses from Hainan Island.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF268025; AAG21223.1;
InterPro; IPR002548; Alpha_El_glycop.
Pfam; PF01589; Alpha_El_glycop; 1.
SEQUENCE 351 AA; 37679 MW; C1691D777E1E6FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Liang G., Zhao W., Zhou G., He H., Fu S., Li L., Jin Q., Fang
Hou Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.
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                                                                                                                                                                                                               5 EALADOTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                      ch 35.7%; Score 46; DB 12; 1 Similarity 41.7%; Pred. No. 2.5e+02; 10; Conservative 4; Mismatches 10
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P46040 frankia aln
O06079 mycobacteri
P02549 homo sapien
P32044 thermoplasm
Q99r40 staphylococ
O02161 caenorhabdi
O9hp81 halobacteri
P71410 halobacteri
P75489 mycoplasma
Q9fci4 streptomyce
P52161 brachydanio
P11927 saccharomyce
P52163 brachydanio
P119234 rattus norv
P35483 pseudomonas
P12759 chlamydomon
O9hr92 halobacteri
O48319 halobacteri
O48319 halobacteri
O48319 halobacteri
O48768 listeria mo
O92dw2 listeria mo
O92dw2 listeria mo
O92567 caenorhabdi
P30141 streptococc
O52871 rhizobium l
P00634 escherichia
P40634 escherichia
P40635 halobacteri
O6845 halobacteri
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P12845 caenorhabdi
Q02728 rhizobium m
Q06281 mycobacteri
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P75417 mycoplasma
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frankia aln
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1 SDALEAL-ADQTDALQSEEAAVVKADNA 27 SDEAEALKSDEAEALKSDEAEARKSDEA 124

Query Match Best Local S Matches 14

h 44.6%; Similarity 50.0%; 14; Conservative

Score 57.5; DB Pred. No. 0.72; 6; Mismatches

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AAA29758.1; AZON7. t; Signal. t; Signal. 309 44 369 44 56 88 86 86 86 77 286 77 286 77 271 286 77 271 286 33694	Cr. Cr. La. La. La. La. La. La. La. La. La. La	587 621 627 759 794 1966 1966 2230 2415 6669
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FANT FO	PRT; 309 AA Jence update) Station updat NF7 / Ghana) EXA; Haemospo EXA; Haemospo  LR.L., Brown I R.L., Brown I R.L	UL25_HSVEB YQO1_CAEEL DNAK_RICPR MFP1_LYCES METE_MYCTU YB52_MYCTU MML5_MYCTU MYSB_CAEEL GOG4_HUMAN SPCA_MOUSE NEBU_HUMAN NIFE_RHISN ALIGNMENTS
TEIN. (BASIC). (CACIDIC). (ROXIMATE TANDEM REPEATS OF E-A-E. E-A-E. DEM REPEATS OF S-E-A-G-T-EP-G.	AA.  a)  porida; Plasmodium.  porida; Plasmodium.  n repeats in two S-antigen  n repeats in two S-antigen  LS:  VACUOLE  VACUOLE  IS MAINLY DUE TO POLYMORPHISM  IS MAINLY DUE TO POLYMORPHISM  IS MAINLY DUE TO POLYMORPHISM  produced through a collaboration atles and the EMBL outstation alles and the EMBL outstation alles and the EMBL outstation as its content is in no way  d. Usage by and for commercial  phttp://www.isb-sib.ch/announce/	p28928 equine herp Q09293 caenorhabdi Q92dy9 rickettsia p93203 lycopersico Q06584 mycobacteri P75034 mycobacteri P75034 mycobacteri P02566 caenorhabdi Q13439 homo sapien P08032 mus musculu p20929 homo sapien P55673 rhizobium s

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STRAIN-K12;
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01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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Blattner F.R., Plunkett Riley M., Collado-Vides
                                                           STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                               "Molecular analysis of asmA, a lo
OmpF assembly mutants of Escheric
Mol. Microbiol. 16:779-788(1995).
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli,
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein asmA precursor.
ASMA OR B2064.
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16-OCT-2001 (Rel. 40, Last annotation upd
Hypothetical protein MPN364 (H91_orf677).
MPN364 OR MP472.
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16-OCT-2001
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NCBI_TaxID=2104;
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BELONGS TO THE MG185 / MG260 FAMILY.
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   G. III, Bloo
J., Glasner
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Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Enterobacteriaceae;
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Pred. No.
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P12845;
01-OCT-1989
01-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science [3]
Eukaryota; Metazoa;
Rhabditidae; Pelode
                        Caenorhabditis elegans
                                     Myosin heavy MYO-2.
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Periplasmic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dut (dUTPase) mutations.";
J. Bacteriol. 174:5647-5653(1992).
-!- FUNCTION: INVOLVED IN THE INHI
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                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                             Local
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BL; D90844; BAA15917.1; -.
BL; D90845; BAA15922.1; -.
BL; M90069; AAA23670.1; -.
R; B42940; B42940.

GGene; EG11361; asmA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
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nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                l Similarity
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vy chain C (MHC C).
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1 22 PC
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Peloderinae;
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             Nematoda;
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oda; Chromadorea;
Caenorhabditis.
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             Rhabditida;
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IN THE ASSEMBLY OF
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-1- FUNCTION: MUSCLE MYOSIN IS A HEAVER CHAIN SUBUNITS (MLC)
-1- SUBUNIT: MUSCLE MYOSIN IS A HEAVER CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARYNGEAL MUSCLE.
-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL CONFOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALXYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SUBFRAGMENT (S2).
-1- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN CRELEGANS.
-1- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN CRELEGANS.
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STRAIN-BRISTOL N2;
MEDLINE-89178677; PubMed-2926820;
MATHYAMB I.N., Krause M.,
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                                                                                                                                                                                                                                      InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N: 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                          SMART; SM00242; MYSC; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
Myosin; Muscle protein; Alkylation; Multigene family.
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M37235; AAA28122.1;
M37236; AAA28123.1;
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MEDLINE-93177026: PubMed-8439670;
Mueller P., Keller M., Weng W.M., Quandt J., Arnold W., Puehler A.;
"Genetic analysis of the Rhizobium meliloti exoYFQ operon: ExoY is
homologous to sugar transferases and ExoQ represents a transmembran
protein.";
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Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti)
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision.
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01-JUL-1993 (Rel.
01-MAR-2002 (Rel.
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                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                       "The complete sequence of the 1,683-kb pSymB mega fixing endosymbiont Sinorhizobium meliloti."
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
-i- FUNCTION: INVOLVED IN SUCCINGGLYCAN (EPS I) STHE ADDITION OF THE FIRST SUGAR (GALACTOSE) T
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Finan T.M., Weidner S., Wong K., Buhrmester J., Chain
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exopolysaccharide production protein EXOF OR RB1068 OR SMB20945.
                                                                                SEQUENCE
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 4 LEALADQTDALQSE-EAAVVKADNAA
                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Periplasmic (Probable).
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                                                                                                                                                                AL603645; CAC49468.1;
                          . Similarity 53.1
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                                                                                45871 MW;
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53.8%;
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RESULT
PAND_M
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Query Match
Best Local Similarity
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Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Dolchar A., Utterback T., Weldman J., Khouri H., Gill J., Mikula Bishai W.;
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LI 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: L-aspartate - beta-al
-!- COFACTOR: Pyruvoyl group (By similarity).
-!- PATHWAY: Pantothenate biosynthesis; secon
-!- SIMILARITY: BELONGS TO THE PAND FAMILY.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamlín N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a c between the SWiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                                              SEQUENCE
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EMBL; AE00717(
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PAND OR RV3601C OR MT3706.1 OR MTCY07H7B
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SIMILARITY).
ASPARTATE 1-DECARBOXYLASE ALPH
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CONVERTED TO A PYRUVOYL GROUP
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01-NOV-1995
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  Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N. Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R. Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., H
                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Putative membrane protein mmpLil.
MMPLil OR ML2617 OR MLCL622.16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                              STRAIN-IN;
                                                                                                                                                                         Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Bioinformatics and the Bioinfor
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P46040;
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                                                                                                                                   SEQUENCE FROM N.A.
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P02549; Q15514;
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Barrell B.G.;
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                                                                                    "The
                                                                                                                                                                                                                                  Homo sapiens (Human
Eukaryota; Metazoa;
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                                                                alpha-spectrin.
                                                                                                    Curtis P.J., Forget B
                                                                                                                                                                                                                      Mammalia; Eutheria;
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Linnenbach A.J., Winkelmann J.C.,
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K., Whitehead
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Doyle J., Manaster J., ruse.

Pour different mutations in codon 28 of alpha associated with structurally and functionally I/74 in hereditary elliptocytosis.";

I/74 in hereditary elliptocytosis.";

Clin. Invest. 88:743-749(1991).
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Linnenbach A.J., Speicher D.W., Marchesi V.T., For
"Cloning of a portion of the chromosomal gene for
alpha-spectrin by using a synthetic gene fragment.
Proc. Natl. Acad. Sci. U.S.A. 83:2397-2401(1986).
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                                                                                                                                                                                                                                                                                                                                                                                Parquet N., Devaux I., Boulanger L., Galand C. Lecomte M.-C., Dhermy D., Garbarz M.; "Identification of three novel spectrin alpha hereditary elliptocytosis: further support for folding unit model of the spectrin heterodimes Blood 84:303-308(1994).
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*Structure of human erythrocyte spectrin. I

domain and its cyanogen bromide peptides.";

J. Biol. Chem. 258:14931-14937(1983).
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J. Biol. Chem.
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  "Heterogeneity of the molecular basis of hereditary pyropoikilocytosis and hereditary elliptocytosis associncreased levels of the spectrin alpha I/74-kilodalton peptide.";
                                                                                                                                                                                                                                                                                             VARIANTS CYS-28; HIS-28; LEU-28 A MEDLINE-91358728; PubMed=1679439; Coetzer T.L., Sahr K., Prchal J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97001215; PubMed-8844207; Maillet P., Alloisio N., Morle L., "Spectrin mutations in hereditary of the control of the c
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                                                                                               .в.,
                                                                                                                                                                                                                                                                           T.L., Sahr K., Prchal
., Manaster J., Palek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
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                                                                                                    Gallagher
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                                                                                               PubMed=1878597;
jher P.G., Valen
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elliptocytosis
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Wilmotte R., Marechal J., Morle L., Baklouti F., Philip Kastally R., Kotula L., Delaunay J., Alloisio N.;

"Low expression allele alpha LELY of red cell spectrin with mutations in exon 40 (alpha V/41 polymorphism) and with partial skipping of exon 46.";

J. Clin. Invest. 91:2091-2096(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devaux I., Bournier O., Galand C., D'Auriol L., Galsahr K.E., Forget B.G., Boivin P., Dhermy D.; "Sp alpha 1/78: a mutation of the alpha I spectrin kindred with HE and HPP phenotypes."; Blood 74:1126-1133(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sahr K.E., Coetter T.L., Moy L.S.,
Jarolim P., Lorenzo F., Miraglia de
Gallamello R.;
 MEDLINE=89323436;
Morle L., Morle F
Garbarz M., Dhermy
                                                                                                                                                                                                                                                  MEDINE-90347052; PubMed-2384601;
MEDINE-90347052; PubMed-2384601;
Morle L., Roux A.-F., Alloisio N., Pothier B., Starck J., Denorce Morle F., Rudigoz R.-C., Forget B.G., Delannay J., Godet J.;
"Two elliptocytogenic alpha I/74 variants of the spectrin alpha domain. Spectrin Culoz (GGT-->GTT; alpha I 40 Gly-->Val) and spectrin Lyon (CTT-->TTT; alpha I 43 Leu-->Phe).";
J.: Clin. Invest. 86:548-554(1990).
                                                                                                                                                                                                                                                                                                                                                                                              J. Biol.
[17]
                                                                                                                                                                                                                                                                                                                                                                                                          spectrin repeat 17 that severely disrupt association of the erythrocyte spectrin J. Biol. Chem. 268:22656-22662(1993).
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dalla Venezia N., Alloisio N., Forissier A., Denoroy L., Aymer Vives-Corrons J.L., Besalduch J., Besson I., Delaunay J.;
"Elliptopoikilocytosis associated with the alpha 469 His-->Pro mutation in spectrin Barcelona (alpha I/50-46b).";
Blood 82:1661-1665(1993).
                                                                                   associated with elliptocytosis at the dimer self-association site Blood 80:809-815(1992).
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J. Clin. Invest.
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MEDLINE=92176375; PubMed=154.
Gallagher P.G., Tse W.T., Cogalkowsky H.S., Baruchel A.,
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Ducluzeau M.-T., Denoroy I
                                                                                                                                                                                                        VARIANT JENDOUBA. MEDLINE-92345619;
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MEDLINE-90347052;
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M.-C., Garbarz M.,
   Dhermy
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PubMed=2568861;
., Roux A.F., Gode
y D., Kastally R.,
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Blood 74:828-832(1989).
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                                                                                                                                                                                                                                                                                                Perrotta S., del Giudice E.M., Allois Delaunay J., Cutillo S., Lolascon A.; "Mild elliptocytosis associated with in spectrin Genova (alpha 1/74).";
                                                                                                                                                                                                                                                                                                                                    VARIANT GENOVA. MEDLINE-94250920;
                                                                                                                                                                                                                                                      Perrotta
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G-->TGG codon change (A)
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STANDARD;
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Siudice E.M., Alloisio
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acidophilum.";
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STRAIN-SSM 1728;
MEDLINE-20479972; PubMed-11029001;
MEDLINE-20479972; PubMed-11029001;
Meepp A., Graml W., Santos-Martinez M.-L., Koretke Ruepp A., Graml W., Stocker S., Lupas A.N., E Mewes H.-W., Frishman D., Stocker S., Lupas A.N., E Mewes H.-W., Frishman D., Stocker S., Lupas A.N., E
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16-OCT-2001 (Rel
Pyruvate kinase
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                                                          MEDLINE-93051217; PubMed-1426985; Potter S., Fothergill-Gilmore L.A "Purification and properties of p
          FEMS Microbiol. Lett. 73:235-239(1992).
-1- CATALYTIC ACTIVITY: ATP + pyruvate =
-1- COFACTOR: REQUIRES MAGNESIUM AND POTA
                                                                                                                   Nature
[2]
                                                                                                                                          acidophilum.
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nase (EC 2.7.1.40) (PK).
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Best Local S
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16-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain N315).
Staphylococcus aureus (strain N315).
Staphylococcus aureus (strain N315).
Staphylococcus group;
                                                                                                                                                                                                                                                                      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Culi L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN+Mu50 / ATCC 700699, and N315; MEDLINE-21311952; PubMed-11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID-158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAND OR SAV2597 OR SA2390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat Aspartate 1-decarboxylase precursor (EC 4.1
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PRODOM; PD001009; PYRUVATE_KINASE;
PROSITE; PS00110; PYRUVATE_KINASE;
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                         This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
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                                                                                                 CATALYTIC ACTIVITY: L-aspartate - beta-al
COFACTOR: Pyruvoyl group (By similarity).
PATHWAY: Pantochenate blosynthesis; secon
SIMILARITY: BELONGS TO THE PAND FAMILY.
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SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
CAUTION: REF.2 HAS PUBLISHED SOME PARTIAL SEQUENCE,
SEQUENCES DO NOT ORIGINATE FROM T. ACIDOPHILUM, RATHI
     European
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Pred. No. 4
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(EC 4.1.1.11)
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                                                WormPep; T09B4.
Mitochondrion;
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Rhabditidae; Pelode:
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                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content
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AP003137; BAB43695.1; ALT_INIT.
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425
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PROBABLE IMPORT INNER MEMBRANE
TRANSLOCASE SUBUNIT TIM44.
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MEDLINE=20504483; PubMed=11016950;

Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Ng W.V., Kennedy S.P., Mahairas G.G., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.
                                                                                                                                                                                                                                                                                     Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the companion of the companion of the control of the companion of 
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-I- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY RHODOPSIN II (SR-II) TO THE FLAGELLAR MOTOR. RESPONDS TO LIGHT
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004089; Chemotaxis_transducer InterPro; IPR003660; HAMP. Pfam; PF00672; HAMP; 1. Pfam; PF00015; MCPsignal; 1.
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16-OCT-2001 (Rel.
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SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
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40, Last sequence update)
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II transducer (HTR-II) (Methyl-accepting phototaxis
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    21
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Pred.
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CF7A8FF04DFF309A CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                             POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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YC88_MYCPM
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Matches 11
YC88_MYCPN
P75489;
16-OCT-2001
16-OCT-2001
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accepting protein.";

Proc. Natl. Acad. Sci. U.S.A. 93:8230-8235(1996).

Proc. Natl. Acad. Sci. U.S.A. 93:8230(1996).

Proc. Natl. Acad. Sci. U.S.A. 93:8230(1996).

Proc. Natl. Acad. Sci. U.S.A. 93:8230(1996).

Proc. Natl. Acad. Sci. U.S. 93:8230(1996).

Proc. Natl. Acad. Sci. U.S. 93:8230(1996).

Proc. Natl. A
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Pfam; PF00015; MCPsignal;
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
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HTR2 OR HTRII.
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InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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Pred. No.
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EXTRACELLULAR (POTENTIAL)
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1182_STRCO
2 Y.182_STRCO
2 OPECIA; 2984B4;
1 01-MAR-2002 (Rel. 41, Created)
1 01-MAR-2002 (Rel. 41, Last sequence update)
1 01-MAR-2002 (Rel. 41, Last annotation update)
1 01-MAR-2002 (Rel. 41, Created)
2 01-MAR-2002 (Rel. 41, Last annotation update)
3 01-MAR-2002 (Rel. 41, Created)
3 02-MAR-2002 (Rel. 41, Last annotation update)
3 02-MAR-2002 (Rel. 41, Created)
3 03-MAR-2002 (Rel. 41, Created)
3 03-MAR-2002 (Rel. 41, Created)
4 10-MAR-2002 (Rel. 41, Created)
5 10-MAR-2002 (Rel. 41, Last sequence update)
5 10-MAR-2002 (Rel. 41, Last annotation update)
5 10-MAR-2002 (Rel. 41, Created)
6 10-MAR-2002 (Rel. 41, Last annotation update)
7 10-MAR-2002 (Rel. 41, Last annotation update)
8 10-MAR-2002 (Rel. 41, Last annotation update)
9 10-MAR-2002 (Rel. 41,
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Best Local
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SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
STRAIN-07105885; PubMed-8948633;
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SIGNAL
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                           This
                                                                                                                                                                                                                               Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MPN288 OR MP547.
                                                                                                                                                                                                                                                                                    Seeger K.J.,
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                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Integral membrane pr
-1- SIMILARITY: BELONGS TO THE UPF0182 FAMILY.
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                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
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HYPOTHETICAL LIPOPROTEIN MPN288.
N-ACYL DIGLYCERIDE (POTENTIAL).
FFA8237DD18D3A05 CRC64;
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1 SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHE BHLH PROTEIN. BINDS DNA AS A HETERODIMER WITH MYC OR MAD.

1 SUBCELLULAR LOCATION: Nuclear.

1 ALTERNATIVE PRODUCTS: 2 ISOFORNS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1 TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE KIDNEY, GILLS AN UTERUS. IT IS ALSO FOUND IN THE BRAIN AND HEART.

1 PTM: PHOSPHORYLATED (PROBABLE).

1 SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                   Schreiber-Agus N., Horner J., Torres R., Chiu F.-C., DePinho R.A "Zebra fish myc family and max genes: differential expression and oncogenic activity throughout vertebrate evolution."; Mol. Cell. Biol. 13:2765-2775(1993).

-i- FUNCTION: TRANSCRIPTION REGULATOR. FORMS A SEQUENCE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Actinopterygii; Neopterygii; Teleostei; Eute
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P52161;
01-0CT-1996
                                                                                            use by non-profit institutions as lon-
modified and this statement is not remov-
entitles requires a license agreement (SC
or send an email to license@isb-sib.ch).
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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                        zFIN; ZDB-GENE-990415-152; max
InterPro; IPR003015; HLH_Myc.
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                                                                                                                                                                                                                                                                                                                                                          DNA-BINDING PROTEIN COMPLEX WITH MYC OR MAD WHICH RECOGNIZES THE CORE SEQUENCE 5'-CAC[GA]TG-3'. THE MYC-MAX COMPLEX IS A TRANSCRIPTIONAL ACTIVATOR, WHEREAS THE MAD-MAX COMPLEX IS A
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AL359214; CAB94589.1;
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12; Conserv
           IPR003015; HLH_Myc
IPR001092; HLH_dim
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Euteleostei; Ostariophysi
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RESULT 18
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1989 (Rel. 12, Cre 01-0CT-1996 (Rel. 34, Las 01-0CT-1996 (Rel. 34, Las Cell division control pro KARI OR YNL188W OR N1611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein; DNA-binding; Transcription regulation; Alternative splicing; Phosphorylation.

DNA_BIND 24 36 BASIC DOMAIN.

DOMAIN 39 80 HELIX-LOOP-HELIX MOTIF (BY DOMAIN B6 107 LEUCINE-ZIPPER (BY SIMILAR VARSPLIC 13 21 MISSING (IN SHORT ISOPORM)

VARSPLIC 13 21 MISSING (IN SHORT ISOPORM)

VARSPLIC 13 21 MISSING (IN SHORT ISOPORM)
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                                                                                                                                                                                                                                                                                                     Vallen E.A., "Genetic inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-87159524;
                       or send an
                                                                      the European
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                                                                                                                                                                                                                                                                                  cerevisiae
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                                                                                                              he Cdc31p-binding protein Karlp is a component of the half bridge the yeast spindle pole body.";
Cell Biol. 128:863-877(1995).
- FUNCTION: KARI 128 REQUIRED FOR FUNCTION OF BOTH INTRANUCLEAR AND EXTRANUCLEAR MICROTUBULES. KARI HELPS LOCALIZE CDC31 TO THE SPINDLE POLE BODY (SPB), CDC31 THEM INITIATES SPB DUPLICATION VIJINTERACTION WITH A DOWNSTREAM EFFECTOR.
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                                                                  SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                  anuclear microtubules in 48:1047-1060(1987).
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м15683;
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                                               and
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9; Conserv
                     and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                        pean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
r B., Piravandi
d (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                              FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00038; HELIX_LOOP_HELIX; 1.
                                                                                                                                                                                                         Courtney
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AAA34716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                    PubMed-7876310;
                                                                                                                                                                                                                                                                                                                               PubMed-8070654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=3030557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                            function in yeast."
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45;
Pred. No.
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HELIX LOOP-HELIX MOTIF (BY SIMILARITY).

LEUCINE-ZIPPER (BY SIMILARITY).

MISSING (IN SHORT ISOFORM).

; 227A31C7C415821A CRC64;
                                                                                                                                                                                                        K., Matzner M.,
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                                http://www.isb-sib
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ment of the
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ter in Saccharomyces
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                                                                                a collaboration
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Matches
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P13234;
P13234;
O1-JAN-1990
O1-APR-1993
                                                                                        high affinity calmodulin-binding protein.";
J. Biol. Chem. 264:2081-2087(1989).
-i- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC ENRICHED IN CEREBELLAR GRANULE CELLS.
-i- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC,
                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain; MEDLINE-89174647; PubMed-2538431; Ohnstede C.-A., Jenson K.F., Sahyoun N.; Ca2+/calmodulin-dependent protein kinase enriched granule cells. Identification of a novel neuronal calmodulin-dependent protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: Z71464; CAA96082.1; -.
PIR; A26455; A26455.
SGD; S0005132; KAR1.
Cell division; Microtubules; Mitosis.
CONFLICT 199 199 A -> V (
                                                                                                                                                         Ono T., Slaughter G.R., Cook R.G., Means A.R. Molecular cloning sequence and distribution
                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY;
MEDLINE-89123272; PubMed-2914893;
Ono T., Slaughter G.R., Cook R.G.
                                                                                                                                                                                                                                                                                                                                                                                       "A novel Ca2+/calmodulin-dependent protein kinase and a male germ cell-specific calmodulin-binding protein are derived from the same
                                                                                                                                                                                                                                                                                                                                                                                                                   Means A.R., Cruzalegui
Slaughter G.R., Ono T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.; "Relationship of genes encoding Ca2+/calmodulin-dependent kinase Gr and calspermin: a gene within a gene."; proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91288548; PubMed-16, Ohmstede C.-A., Bland M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-JAN-1990 (Rel. 13, Created
Ol-APR-1993 (Rel. 25, Last se
16-OCT-2001 (Rel. 40, Last an
Calcium/calmodulin-dependent
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Mammalia; Eutheria; Rodentia;
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                                     CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APR-1993 (Rel. 25, Last sequence update)
OCT-2001 (Rel. 40, Last annotation update)
Clum/calmodulin-dependent protein kinase type IV
2.7.1.123) (CAM kinase-GR) (CAMK IV) [Contains:
                                                                               PROTEIN.
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3; Mismatches
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                                                                                            CALMODULIN-BINDING
                                                                                                                     PROTEIN
                                                                                                                                                                                                                                                                                in
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Murinae; Rat
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TISSUE TESTIS

SPECIFICITY: AND BRAIN.

CALSPERMIN

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PREDOMINANTLY

FOUND

IN MAMMALIAN

SPLICING

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RESULT
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Best Local :
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SEQUENCE FROM N.A.

STRAIN-AVCC 15692 / PAO1:

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene:

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Lag

Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                          PPHH_PSEAE STANDARD;
PPHH_PSEAE STANDARD;
P35483; O9HYU7;
O1-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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BINDIND
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SEQUENCE
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DOMAIN
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InterPro; IPR002290; Ser_thr_pkin
Pfam; PF00069; pkinase; 1.
SMART; SM00220; STKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                           PHOA OR PA3296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
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                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
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en the SWISS Institute of Bioinformatics and the El
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THE SER/THR FAMILY OF PROTEIN
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ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (
POLY-GLU.
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Pred. No.
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RESULT 21
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement.
                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorop
Chlamydomonadaceae; Chlamydomonas
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Interpro; IPR001952; Alk_phosphtse.
Pfam; PF00245; alk_phosphatase; 1.
PRINTS; PR00113; ALKPHPHTASE.
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               WILLINE-89308863; PubMed-2745550; WILLIAMS B.D., Velleca M.A., Curry A.M., Rose "Molecular coloning and sequence analysis of t coding for radial spoke protein 3: flagellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
SIGNAL
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Hvdrolase; Zinc; Magnesium; Periplasmic;
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                                                                                                     STRAIN-21GR;
                                                                                                                      SEQUENCE FROM
                                                                                                                                                                  NCBI_TaxID=3055;
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13; Conserv
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RESULT 22
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MACHINE=25504483; PubMed=11016950;

MEDILINE=25504483; PubMed=11016950;

AN G. W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

AN G. W.V., Kennedy S.P., Maliga N.S., Thorsson V., Sbrogna J.,

AN Shukla H.D., Lasky S.R., Baliga N.S., Thorsson W.J., Hough D.W.,

AN Swartzell S., Weir D., Hall J., Dahl T.A., Weiti R., Goo Y.A.,

AN Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

AN Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

AN Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

AN Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

AN Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

AN Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

AN ALBERT M., Liang P., Riley M., Hood L., DasSarma S.;

T. "Genome sequence of Halobacterium species NRC-1.";

T. "Genome sequence of Halobacterium species NRC-1.";

Dennis P.P., Company C., Co
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat-
Halobacterial transducer protein VI.
HTR4 OR HTPVI OR VNG0006G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J
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STRUCTION: FLAGELLAR RADIAL SPOKES CONTRIBUTE TO THE REGULATION OF DYNEIN ARM ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING. THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBPIBER OF THE OUTER DOUBLET MICROTUBULE, AND A BULBOUS HEAD, WHICH IS ATTACHED TO THE STALK AND APPEARS TO INTERACT WITH THE PROJECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.

SUBCELLULAR LOCATION: RADIAL SPOKE.

PTM: PROTEIN 3 IS ONE OF THE 5 RADIAL SPOKE PROTEINS THAT ARE
                                           European
                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
                                                                                                                                                                                                                                  TRANSDUCTION (BY SIMILARITY).
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A31270; A31270.
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an email to license@isb-sib.ch).
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516 AA; 56784 MW;
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                                                               Pfam; PF00672; HAMP; 1. Pfam; PF00015; MCPsignal; SMART; SM00304; HAMP; 2. SMART; SM00283; MA; 1.
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"A family of halobacterial transducer proteins.";
FEMS Microbiol. Lett. 139:161-168(1996).
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15-DEC-1998 (Rel. 37, Las
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Halobacterial transducer
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Charvota; Rhodophyta;
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the European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-LB 95.79
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport; Chloroplast.
NP_BIND 39 46 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kostrzewa M., Zetsche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93021132; PubMed=1404401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCF16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable ATP-dependent transporter ycf16
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Mendel; 6183; ANTSp;ycf16;1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Large ATP synthase operon of the red alga Antithamnion the corresponding operon in cyanobacteria.";
J. Mol. Biol. 227:961-970(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2767;
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36,
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Pred. No. 1.
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                                                            PRT;
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RESULT 26
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Best Local :
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Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
SEQUENCE FROM N.A.
STRAIN-12067;
MEDLINE-95102110; PubMed-7803815;
                                                                                                                                                         U1-NOV-1997 (Rel. 35,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1642;
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                                                                                                                               Chemotaxis protein cheA CHEA OR LMO0692.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria innocua.
                                                                            Bacillus/Staphylococcus
                                                                                               Listeria monocytogenes Bacteria; Firmicutes;
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01-NOV-1997
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                                                               NCBI_TaxID-1639
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SUBCELLULAR LOCATION: Cytoplasmic (Potential).
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                                                                                                 Bacillus/Clostridium
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Pred. No. 1.16
4; Mismatches
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LEALLHPEQETDLTVEKTYRIAIQIEEAAILKAVRA 154

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RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Comez Lopez N., Hain T., Hauf J., Jackson D.,
RA Charbit A., Koerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294.849-852(2001).
"C. I- FUNCTION: INVOLVED IN THE TRANSMISSION OF SENSORY SIGNALS FROM THE CHEMORECEPTORS TO THE FLAGELLAR MOTORS, CHEA IS
AUTOPHOSPHORYLATED: IT CAN TRANSFER ITS PHOSPHATE GROUP TO EITHER
CHEMORY CONTAINS 1 HISTIDINE KINASE DOMAIN.
"C. SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                              Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                             Pfam; PF01584; CheW; 1.
Pfam; PF02895; H-Kinase_dim; 1.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF01627; Hpt; 1.
Pfam; PF01627; Hpt; 1.
Pfam; PF00512; signal; 1.
Pr0Dom; PD003142; Hpt; 1.
SMART; SM00260; CheW; 1.
SMART; SM00267; HATPase_C; 1.
SMART; SM00273; HPT; 1.
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SEQUENCE
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DNA Seq.
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                                                                                                                                                                                                                                   Chemotaxis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                l Similarity
15; Conser
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); IPRO04105; H-kinase_dim.
); IPRO03594; HATPase_C.
); IPR004359; HIS_KIN_Sig.
); IPR002570; Hpt.
                                                                                                                                                                                                                                                             PS50109; HIS_KIN; 1.
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                                Conservative
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                                            34.18;
41.78;
-ALQSEEAAVVKADNA
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                       Pred. No. 1.16
4; Mismatches
                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

A -> Q (IN REF. 1).

D -> E (IN REF. 1).

K -> E (IN REF. 1).

I -> V (IN REF. 1).
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                                                             Score 44;
                                                                                                                                                                                                                  HISTIDINE KINASE
                                                                                              A -> Q (IN REF. 1).
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63B560C05D8E941C
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les 5;
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                                                               Length 618;
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RA GARDER A., MCMUTTAY A.;

RL SUBMITTED (APR-1996) to the EMBL/GenBank/DDBJ databases.

CC -1- FUNCTION: MUSCLE CONTRACTION.

CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -1- SUBCELLULAR LOCATION: THACK FLIAMENTS (MLC-2).

CC -1- SUBCELLULAR LOCATION: THACK FLIAMENTS (MLC-2).

CC -1- SUBCELLULAR LOCATION: THACK FLIAMENTS OF the myofibrils.

CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARRYNGEAL MUSCLE.

CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARRYNGEAL MUSCLE.

CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC CYCLES OF A 28-RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

CC -1- PIM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SPLIT BURDERLANT (S2)

CC SUBREPACHMENT (S2)

CC SUBREPACHMENT (S2)
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21-JUL-1986 (Rel. 01, 0
01-OCT-1989 (Rel. 12, 1
16-OCT-2001 (Rel. 40, 1
Myosin heavy chain D ()
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                       This
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J. Mol. Biol. 205:603-613(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85201409; PubMed=3888374; Karn J., Dibb N.J., Miller D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 115-365 AND 1492-1763
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                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                     X08065;
M37232;
   M37234;
Z71266;
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                                                                                                                                                                                      requires a license agreement ()
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CAA30854.1; -. AAA28119.1; -. AAA28120.1; -. CAA95848.1; -.
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6:185-237(1985)
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InterPro: IPR004009; Myosin_N.
InterPro: IPR002928; Myosin_tail.
InterPro: IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00736; Myosin_N; 1.
Pfam; PF01576; Myosin_Lail; 1.
PRINTS; PR00133; MYOSINLEAVY.
ProDom; PD000355; Myosin_head; 1.
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01-APR-1993
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                                                             STRAIN-AP4 / SEROTYPE M4;
MEDLINE-92269579; pubMed=1588817;
Stenberg L. O'TOOLe P. Lindahl G.;
"Many group A streptococcal strains express two different immunoglobulin-binding proteins, encoded by closely linked immunoglobulin-catalogy are accorded by four strains
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PIR;
                  characterization of the proteins expressed by four strains different M-type.";
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Myosin; Muscle protein; Coiled coil;
ATP-binding; Methylation; Alkylation
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes
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L; Z71261; CAA95806.1;
L; Z71266; CAA95806.1;
; S02772; MWKW1.
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3 (Rel. 25, Last
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- and Ig-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
  6:1185-1194(1992)
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39.1%;
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ALKYLATION (SH-2).
F -> E (IN REF. 2).
A -> R (IN REF. 2).
V -> D (IN REF. 4).
DV -> GD (IN REF. 4).
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> Q (IN REF. 3).
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9;
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ID YTF3_R
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Q52871;
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-!- FUNCTION: BINDS IGG MOLECULES OF THE IG1, IG2 AND
                                                                                                                             MEDLINE-96312357; PubMed-8763943;
Breil B.T., Triplett E.W.;
"A newly discovered gene, tfuA, involved in the production ribosomally synthesized peptide antibiotic trifolitoxin.";
J. Bacteriol. 178:4150-4156(1996).
-i- SIMILARITY: BELONGS TO THE UPF0142 FAMILY.
                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrictive to the European Bioinformatics institute. There are the content in the European Bioinformatics in the EMBI through the second through the content in the EMBI through through the EMBI through through the EMBI through the EMBI through the EMBI through through the EMBI through through the EMBI through through through the EMBI through through through the EMBI through through through the EMBI through through the EMBI through through the EMBI through through through through through the EMBI through through the EMBI through through through through through through the EMBI through throu
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SEQUENCE FROM
                                                                                                                                                                                                                                                                         STRAIN-T24
                                                                                                                                                                                                                                                                                                                                                                             Rhizobium leguminosarum (biovar trifolii)
Bacteria; Proteobacteria; alpha subdivisi
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 45.4 kDa protein in tfuh 3'region (ORF3).
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Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=386;
                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae;
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SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN THE REGION OF THE MEMBRANE ANCHOR.
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12; Conser
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SEQUENCE FROM N.A.
MEDLINE-87031576; Pubmed-3533724;
Chang C.N., Kuang W.-J., Chen E.Y.;
Chang C.N., Suang W.-J., Chen E.Y.;
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or send a
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                                       Puncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Dav
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew I
Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                Blattner F.R., Plunkett G. III, Bloch C.A., Perna Riley M., Collado-Vides J., Glasner J.D., Rode C. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M
                                                                                                                                                                 STRAIN-K12 / MG1655; MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                       Dubose R.F., Dykhulzen D.E., Hartl D.L.; "Genetic exchange among natural isolates of bacte within the phoA gene of Escherichia coll."; Proc. Natl. Acad. Sci. U.S.A. 85:7036-7040(1988).
                                                                                                                                                                                                                                                                                                                                                                Shuttleworth H., "Sequence of the JM83.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 42
 MEDLINE-82081850;
Kikuchi Y., Yoda
                     SEQUENCE OF 1-77 FROM
                                                                                  SEQUENCE FROM N.A.
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Bacteria; Proteobacteria;
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                                                                                                    complete genome sequence 
nce 277:1453-1474(1997).
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Pro; IPR003776; DU
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14; Conservative
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                                                                                                                         Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 protein
420 AA;
                                                                                                                                                                                                                                                                                                                                                                       ; PubMed=3537962;
Taylor J., Minton N.;
gene for alkaline phosphatase
  ×.
          PubMed-6273802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         license agreement (
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7; Mismatches
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                                                                                                               Escherichia
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                                                                                                                                           K., Mayhew G.F.,
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                                                                                                               K-12.";
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                                                                                                                                   Rose D.
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X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-98202577; PubMed-9533886;
Stec B., Hehlr M.J., Brennan C., Nolte M.,
Kinetic and X-ray structural studies of ti
alkaline phosphatases: insights into the ci
                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE-91186406; PubMed-2010919; Kim E.E., Wyckoff H.W.; Reaction mechanism of alkaline phosph structures. Two-metal ion catalysis."; J. Mol. Biol. 218:449-464(1991).
                                                                                                                                                               Murphy J.E., Stec B., Ma L., Kantrowitz E
*Trapping and visualization of a covalent
intermediate.";
                                                                                                                                                                                                                                                                  "Kinetic and X-ray structural studies alkaline phosphatase (His-412-->Gln) a
                                                                                                                                                                                                                                                                               x-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
MEDLINE-96194161; PubMed-8652582;
MA L., Kantrowitz E.R.;
"Kinetic and X-ray structural studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michaelis S., Hunt J.F., Beckwith J.; "Effects of signal sequence mutations ophosphatase export to the periplasm in J. Bacteriol. 167:160-167(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region coli.";
X-RAY CRYSTALLOGRAPHY MEDLINE-99185045; Publ
                                                    the
                                                                                                                                                                                       MEDLINE=97397347; PubMed=9253408; Murphy J.E., Stec B., Ma L., Kant
                                                                                                                                                                                                                                          Biochemistry 35:2394-2402(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sowadski J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laforet G.A., Kaiser E.T., Kendall D.A.;
"Signal peptide subsegments are not always functionally
interchangeable. M13 procoat hydrophobic core fails to transport
alkaline phosphatase in Escherichia coll.";
J. Biol. Chem. 264:14478-14485(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-82119946; PubMed-7035431; Inouye H., Barnes W., Beckwith J.; "Signal sequence of alkaline phosphatase J. Bacteriol. 149:434-439(1982).
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                                      nucleophile Ser102.";
Mol. Biol. 277:647-662(1998)
                                                                                                                                                Struct. Biol.
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 PubMed=10085061;
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EMBL; V00315; CAA23603.1; ALT_SEQ.
EMBL; X04566; CAA28257.1; -
EMBL; A04566; CAA28257.1; -
EMBL; BERO0145; AAC73486.1; ALT_INIT.
EMBL; U73857; AAB18107.1; -
EMBL; W29665; AAA24365.1; -
EMBL; M29664; AAA24365.1; -
EMBL; M33536; AAA24364.1; -
EMBL; M13763; AAA24361.1; -
EMBL; J01069; AAA24359.1; -
EMBL; J01661; AAA24360.1; -
EMBL; J01661; CAB23260.1; -
EMBL; J01661; CAB23261.1; -
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"A model of
                                                    SMART; SM00098; alkPPc; PROSITE; PS00123; ALKAL
                                                                          PRINTS; PR00113; ALKPHPHTASE. ProDom; PD001868; Alk_phospht
                                                                                             InterPro; IPR001952; Alk_phosphtse
Pfam; PF00245; alk_phosphatase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A model of reaction.";
                                           Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)0 = alcohol + phosphate.

COFACTOR: METALLOENZYME CONTAINING TWO ZINC ATOMS AND A MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE ALKALINE PHOSPHATASE FAMILY.
DATABASE: NAME-ProZyme technical fact sheet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: ISOZYMES 1 & 3 ARE IS A DIMER OF HETEROGENEOUS FROM ISOZYMES 1 AND 3.
                                                                                                                                                                                                                                                                                                                              ; A00776; PAECA.
; A24833; A24833.
; 1AJA; 14-NOV-95
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29 - JAN - 96.
26 - JAN - 96.
26 - JAN - 96.
08 - MAR - 96.
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27-FEB-95
14-NOV-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               license agreement (See http://www.isb-sib.ch/announce/
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         ALKALINE PHOSPHATASE
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"Cohesins: chromosomal proteins that
sister chromatids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          EMBL; Y14278; CAA74655.1; -. EMBL; Z49349; CAA89366.1; -. EMBL; X88851; CAA61313.1; -.
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                                                                                              DOMAIN
                                                                                                                                                                                                Pfam; PF02483; SMC_C; 1. Pfam; PF02463; SMC_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PART OF A CHROMOSOME CONDENSATION MOTOR.

-!- SUBCELLULAR LOCATION: Nuclear (Potential).

-!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-

-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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i; Mismatches
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                                                                                                                                               coil; Nuclear protein. ATP (POTENTIAL).
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Q06845;
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                                                                              Tola protein.
Tola OR HI0383
                                                                                                                                                                                                                                                                                            EMBL;
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"Nucleotide sequence of the genes encoding the L3, L4, equivalent ribosomal proteins from the archaebacterium
                                           NCBI_TaxID=727;
                                                             Bacteria; Proteobacteria;
                                                                     Haemophilus influenzae
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PIR; S43421; S43421.
InterPro; IPR002136; Ribosomal_L4/L1E.
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                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage hy antities requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                               Chissoe S.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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"The DNA sequence of equine herpesvirus-1.
Virology 189:304-316(1992).
-!- FUNCTION: VIRION PROTEIN.
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Rhabditidae; Pelode:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQO1_CAEEL
Q09293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                               InterPro; IPR001097; Mat_tudor
InterPro; IPR000504; RRM.
Pfam; PF00567; TUDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
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     PROSITE;
                                                                                                                          WormPep; EEED8.1;
                                                                                                                                                    EMBL; U23484; AAC46761.1;
                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR
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                               SM00360;
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                                                                                                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/
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protein EEED8.1 in chromosome II.
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Pred. No. 1.4e+02
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RESULT 36
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AC 092DX9
DT 30-MAY
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GN NAK 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 396:133-140(1998).

-!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).

-!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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STRAIN-MADRID E;
MEDLINE-99039499; PubMed-9823893;
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Hypothetical protein; RNA-binding.
DOMAIN 267 346 RNA-BINDII
SEQUENCE 621 AA; 69894 MW; 464DB7EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpi
Rickettsiaceae; Rickettsieae;
NCBI_TaxID=782;
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Chaperone protein dnaK (Heat shock protein 70)
                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Chaperone; ATP-binding; Heat shock;
SEQUENCE 627 AA; 68383 MW; A638A
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30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00012; HSP70;
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                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001023; HSP70.
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| ALDILSINGDVSSDEEAVSVKEESS 39
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                                                EALADQTDALQSEEAAVVK
EALTSLKAALESEDASLIK 579
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P04475; 1DG4.
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9; Conserv
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40, Last annotation updat
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eae; Rickettsia.
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Pred. No.
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464DB7EF91AF63C5 CRC64;
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                                                                                                                           Score 43;
Pred. No. 1
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1.5e+02;
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                                                                                                                                                Length 627;
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RESULT 37
MFP1_LYCES
ID MFP1_LYCES

STANDARD;

PRT;

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RESULT 38
METE_M
AC 006584
AC 006584
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DT 15-JUC
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DE MYCODA
OC MCBLT
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16-OCT-2001
16-OCT-2001
16-OCT-2001
MAR binding
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006584;
MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekala F., Gordon S.V., Eiglmeier K., Cas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
(EC 2.1.1.14) (Methionine synthase, vitamin-Bl2 independent isozyme)
(Cobalamin-independent methionine synthase),
METE OR RV1133C OR MT1165 OR MTC22G8.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. VENT CHERRY; TISSUE-Fruit; MEDLINE-97112038; PubMed-8953774; Meler I., Phelan T., Gruissem W., Spi MFP1, a novel plant filament-like pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Plant Cell 8:2105-2115(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum (Tomato)
Eukaryota; Viridiplantae; Strept
                                                                                                                             SEQUENCE
                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
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                                                                                                               STRAIN-H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BINDS DNA, INTERACTS WITH CHROMATIN VIA MATH ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NU ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR POTENTIALLY WITH THE NUCLEAR ENDELOPE. SUBCELLULAR LOCATION: NUCLEAR MATRIX.
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                                                                                                                          FROM N.A.
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697 ,
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g filament-like p
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43.5%;
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Pred. No.
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1.6e+02;
8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 697;
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IN NUCLEAR
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L outstation -
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Matches 10
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P75034;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation upda)
Hypothetical lipoprotein MPN152 precurse
MPN152 OR MP002.
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      MYCPN
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METAL
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SEQUENCE FROM N.A. STRAIN-ATCC 29342 MEDLINE-97105885;
                                                                                                                    Bacteria; Firmicutes; Mycoplasmataceae; Myco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z95585; CAB09044.1; -. EMBL; AE006995; AAK45422.1; -. TIGR; MT1165; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg ; Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CDC 1551 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rutter S., Seeger K., Skelton S., sulston J.E., Taylor K., Whitchead "Deciphering the biology of Mycobac complete genome sequence.";
Nature 393:537-544(1998).
                                                  SEQUENCE
                                                                                                                                                                       Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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Fleischmann R.D., Alland D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586
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FUNCTION: CATALYZES THE TRANSFER OF A METHLY GROUP FROM 5-
METHYLITETRAHYDROFOLATE TO HOMOCYSTEINE RESULTING IN METHIONINE
FORMATION (BY SIMILARITY).
CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-1-glutamate +
CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-1-glutamate +
CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-1-Glutamate +
CATALYTIC SINC; BINDS ONE ION PER SUBUNIT (BY SIMILARITY).
COPACTOR: ZINC; BINDS ONE ION PER SUBUNIT (BY SIMILARITY).
PATHWAY: TERMINAL STEP IN THE DE NOVO BIOSYNTHESIS OF METHIONIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHASE FAMILY.
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  / M129;
PubMed=8948633;
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649
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onine_synt; 1.
cransferase; Methionine
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43.5%;
                                                                                                                                              Bacillus/Clostridium
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Pred. No. 1.8e
4; Mismatches
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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precursor (E07_orf794).
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1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYCTU
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                                                                                                     Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
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MMPL5 OR RV0676C OR MT0705 OR MTV040.04C.
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-!- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY
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STRAIN-CDC 1551 / Oshkosh;
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laboratory strains."
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 55 4 US-09-813-817-3
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SEQ ID NO 1
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
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APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
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US-09-103-840A-2
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                     SOFTWARE:
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TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 42456-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/762
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 654-2
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jarvik, Jonathan TITLE OF INVENTION: READING TITLE OF INVENTION: TAGGING NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1548 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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California
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202 Coast Blvd., Suite 111
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FRAME INDEPENDENT EPITOPE
US-08-762-106-5 (1-1548)
                                                                                Length:
Matches:
Conservative:
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Matches:
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                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
 1162
                                                              1105
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CI
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                       No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brotman, Harris REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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                                                                             1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla
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AACGCCAAGTGGGAGGCGGACAAGGCG
                                                             GCCGATGCCGTCGAGGCGGCGGCCGCGGAGCTGACGGCG----CAGGCGGAGGAGGCGGCC
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                             ValValLys-----AlaAspAsnAla 27
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202 Coast Blvd., Suite 111
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READING
TAGGING
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 1188
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Matches:
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RESULT 8 US-08-762-106-6 ; Sequence 6, Application US/08762106

Patent No. 5948677
GENERAL INFORMATION:

TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

TAGGING

Jarvík, Jonathan W. VENTION: READING FRAME INDEPENDENT EPITOPE

CORRESPONDENCE ADDRESS:

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RESULT 9
US-09-320-774-6
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Best Local Similarity:
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Patent No. 6265545
GENERAL INFERMATION:
APPLICANT: Jarvík, Jonathan W.
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
HYPOTHETICAL: N
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ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
                                                                                                  NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harris Brotman
                                                                                                                                                                                                                                                                                                                                                        1138 GCCGATGCCGTCGAGGCGGCGGCGGCGGAGCTGACGGCG---CAGGCGGAGGAGGCGGCC 1194
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/762,106
FILING DATE: 09-DEC-1996
                                                                                                                                                  TITLE OF INVENTION:
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CITY: La Jolla
STATE: California
                                    COUNTRY:
                                                         STATE:
                                                                                                                                                                                                                                                                                                                         21 ValValLys-----AlaAspAsnAla 27
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     STREET:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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                                                      La Jolla
California
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202 Coast Blvd., Suite 111
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Matches:
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US-08-961-083-191
; Sequence 191, Appl
; Patent No. 6159469
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et.
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ST
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1195 AACGCCAAGTGGGAGGCGGACAAGGCG 1221
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1138 GCCGATGCCGTCGAGGCGGCGGCGGCGGGAGCTGACGGCG---CAGGCGGAGGAGGCGGCC 1194
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APPLICATION NUMBER: 1
                  FILING DATE
                                                                                        FILING DATE:
                                                                                                                                       COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                               20850
                                                                                                                                                                                                                                                                  Maryland
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9410 Key West Avenue
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Streptococcus pneumoniae Antigens and Vaccines
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                                                                                                                                                                                         3.50 inch, 1.4Mb storage
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Matches:
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Indels:
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REFERENCE/DOCKET NUMBER: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,

36,373

PB340P2

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US-08-960-022-13
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
                                                                               TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1772 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 87 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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87 CambridgePark Drive
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US-08-743-637B-19/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
US-08-743-637B-19
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Patent No. 595...
Patent No. 595...
Parral INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                          TELEPHONE: (414) 277-5000
TELEFAX: (414)277-5591
INFORMATION FOR SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY_AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CITY: MILWAUKEE
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                                                                              TOPOLOGY:
                    ORGANISM:
                                                                                                STRANDEDNESS:
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                  Pseudomonas aeruginosa
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                                                       DNA (genomic)
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                                                                                                                                                                                                                                                        850586.90012
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Matches:
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Alignment Scores: Pred. No.:

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 Query Match: DB:
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                               Percent Similarity:
Best Local Similarity:
                                                                Score:
                                                                                             Alignment Scores:
                                                                                                                              US-08-526-840B-19
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                                                                                                                                                                                                                                                                                      NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 8505
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
                                                                                                                                                                                                                                                    TELEFAX: (414) 277-559
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                           STRANDEDNESS: dou
TOPOLOGY: linear
MOLECULE TYPE: DNA
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
RIOR ADDITION: 435
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                                                                                                                                                                                                       LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Milwaukee
STATE: Wisconsi
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                                                                                                                                             ORGANISM:
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                                                                                                                                             Pseudomonas aeruginosa
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             Matches:
Conservative:
Mismatches:
Indels:
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Indels:
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4 LeuGluAlaLeuAlaAspGlnThrAspAla---LeuGlnSerGluGluAlaAlaValVal

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US-09-847-539A-6_COPY_59_86 (1-28) x US-08-049-282B-1 (1-1149)
                                               Best Local Similarity:
Query Match:
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                                                                                 Percent Similarity:
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                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/049
FILING DATE: 16-APR-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      MOLECULE TYPE:
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TITLE OF INVENTION: PH GENES AND THEIR USES
                                                                                                                                                                                                                       FEATURE
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                         LENGTH: 1149 base pairs
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(415) 543-5043
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NIJJAR, Charanjit
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                                             Conservative: Mismatches: Indels:
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; OTHER INFORMATION:
US-08-537-715-1
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                                                                            US-09-847-539A-6_COPY_59_86 (1-28) x US-08-537-715-1 (1-1149)
                                                                                                                                           Query Match:
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Best Local Similarity:
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Patent No. 5910627
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,282
EILING DATE: 16-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/041
EILING DATE: 15-APR-1994
ATTORNEY/ACENT INFORMATION:
ANAE: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BASTIAN, KEVIN L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 012176-003410US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Keller, Janis
APPLICANT: Nijjar, Charanjit S.
APPLICANT: Ralston, Edward J.
TITLE OF INVENTION: PH Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chuck, George S. APPLICANT: Dooner, Hugo K.
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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727 CTTGAAGCTAGAGCCAATCAGACGGAGGCTACGCTGCAGACAAAGGATACAGGTACTGTG 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/537,715 FILING DATE: 16-FEB-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                     4 LeuGluAlaLeuAlaAspGlnThrAspAla---LeuGlnSerGluGluAlaAlaValVal 22
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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; LOCATION:
PCT-US94-04173-1
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                                                                                                              Sequence 1, Application US/08657392 Patent No. 5843634 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/04:
ETLING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 121:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
   APPLICANT:
APPLICANT:
                                  APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                  APPLICANT:
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                                                                APPLICANT:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
DEDNESS: single
Brate, E.M.
Brennan, C.A.
Bridon, D.P.
Jaffe, K.D.
Krafft, G.A.
Mandecki, W.
March, S.C.
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PCT-Use
Sequence 1, Applica
GENERAL INFORMATION:
APPLICANT: Brate, E.M.
APPLICANT: Brennan, C.A.
APPLICANT: Bridon, D.P.
APPLICANT: Jaffe, K.D.
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US-08-657-392-1
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SOFTWARE: SOFTEPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Genetically Engineered Enzymes And Their
TITLE OF INVENTION: Conjugates for Diagnostic Assays
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
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LENGTH: 1454 nucleotides
TYPE: nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/11
FILING DATE: July 29, 19;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  1088 GCG 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WONG, WEAR KHING
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5324.US.P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              1028 AATGAGAAAGGCTTTTTCCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGATCATGCT 1087
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STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
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                                                                                                                Application PC/TUS9402539
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9, 1993
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Matches:
Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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; Sequence 26, Application; Patent No. 5843634; GENERAL INFORMATION: APPLICANT: Brate, Fapplicant: Brennan, Applicant: Bridon,
                                                                                                          US-08-657-392-26
                                                                                                                             RESULT 19
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PCT-US94-02539-1
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INFORMATION FOR SEQ ID NO:
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ATTORNEY_AGENT INFORMATION:
NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 532.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: March, S.C.
APPLICANT: Russell, J.R.
APPLICANT: Yue, V.T.
TITLE OF INVENTION: Genetically Engineered Enzymes
TITLE OF INVENTION: And Their
TITLE OF INVENTION: Conjugates For Diagnostic Assays
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: SOFTPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02539
                                                                                                                                                                                                                                      1028 AATGAGAAAGGCTTTTTCCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGATCATGCT 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                               1088 GCG 1090
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                                                                                                                                                                                                                                                                                                           968 AACGACTCGGTTCCAACCCTGGCGCAGATGACCGACAAAGCCATTGAACTCTTAAGTAAA 1027
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ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ABBOTT LABORATORIES
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                       Application US/08657392
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Brate, E.M.
Brennan, C.A.
Bridon, D.P.
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Matches:
Conservative:
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Indels:
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RESULT 20
PCT-US94-02539-26
; Sequence 26, Application PC/TUS9402539
; GENERAL INFORMATION:
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1455 nucleotides
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,708
FILING DATE: July 29, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Genetically Engineered Enzymes And Their
TITLE OF INVENTION: Conjugates For Diagnostic Assays
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                         1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 938-5517
TELEPEAX: (708) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: SOFTPC
CURRENT APPLICATION DATA:
                                                                                                                                                      1029 AATGAGAAAGGCTTTTTCCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGATCATGCT 1088
                                                                                                                                                                                                                     969 AACGACTCGGTTCCAACCCTGGCGCAGATGACCGACAAAGCCATTGAACTCTTAAGTAAA 1028
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Mandecki, W.
March, S.C.
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Yue, V.T.
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Matches:
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RESULT 21
US-08-537-715-3
; Sequence 3, Application US/08537715
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 938-3517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33,561
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SOFTWARE: SOFTPC
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1455 nucleotides
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Bridon, D.P.
Jaffe, K.D.
Krafft, G.A.
Krafft, G.A.
Mandecki, W.
March, S.C.
Russell, J.R.
Yue, V.T.
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Matches:
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Indels:
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                     PCT-US94-04173-3
                                        RESULT 22
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1857 base pairs
TYPE: nucleic acid
Sequence 3, Application PC/TUS9404173
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GENERAL INFORMATION:
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FILING DATE: 16-FEB-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 15-APR-1994
                                                                                                                                               1210 CTTGAAGCTAGAGCCAATCAGACGGAGGCTACGCTGCAGACAAAGGATACAGGTACTGTG 1269
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                                                                          1270 AAG 1272
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICANT: Nijjar, Charanjit S.
APPLICANT: Ralston, Edward J.
TITLE OF INVENTION: PH Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chuck, George S. APPLICANT: Dooner, Hugo K.
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                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 481..163
OTHER INFORMATION:
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                                                                                                                                                                4 LeuGluAlaLeuAlaAspGlnThrAspAla---LeuGlnSerGluGluAlaAlaValVal
                                                                                                            Lys 23
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Indels:
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Best Local Similarity:
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                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PH
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 543-9600
                                                                           NUMBER OF SEQUENCES: 1
                                                                                                           TITLE OF INVENTION: Recombinant Antibodies Specific for TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                               1210 CTTGAAGCTAGAGCCAATCAGACGGAGGCTACGCTGCAGACAAAGGATACAGGTACTGTG 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1857 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                              23 Lys 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 15-AP
COUNTRY:
                              CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LeuGluAlaLeuAlaAspGlnThrAspAla---LeuGlnSerGluGluAlaAlaValVal 22
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             New York
                                          7 Skyline Drive
                                                                                                                                                                                         Wels, Winfried S.
Hynes, Nancy E.
Harwerth, Ina-Maria
                                                                                                                                                                              Groner, Bernd
                                                                                                                                             Zwickl, Markus
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481..1632
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                                                          CIBA-GEIGY Corporation
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Matches:
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Query Match:
                                                               Percent Similarity:
Best Local Similarity:
                                                                                                  Score:
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US-09-847-539A-6_COPY_59_86 (1-28) x US-08-235-838-6 (1-2233)
                                                                                                                               Alignment Scores:
                                                                                                                  Pred. No.:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                 FEATURE:
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CLONE: pww616
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HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 23..2155
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             OTHER INFORMATION: /function- "phoA 3' non-coding OTHER INFORMATION: region"
                                                                                                                                                                                                                                                              NAME/KEY: 3'UTR
LOCATION: 2156..2233
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OTHER INFORMATION:
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                                              181
43.50
46.34%
31.71%
33.72%
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Matches:
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                                                                                                                                                                                                                                                                                TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS: ADDRESSEE: NOVARTIS Corporation
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2233 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
                                                   FEATURE:
                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                               MOLECULE TYPE:
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ZIP: 07901-6940
NAME/KEY: CDS
LOCATION: 23..2155
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                 CLONE:
                                                                                                INDIVIDUAL ISOLATE:
                                                                                                                   ORGANISM:
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Hynes, Nancy E
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Zwickl, Markus
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 /note= "89-445 FRP5 heavy chain
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RESULT 25
US-08-928-213B-7
Sequence 7, Application US/08928213B
Patent NO. 6238905
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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LOCATION: 1.22
OTHER INFORMATION:
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                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,213B
FILING DATE: 12-Sep-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                   Cull, Millard G.
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McHenry, Charles S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCG 1807
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                                                                                                                                                                                                                                     STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                       STATE: CA
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MacKnight,
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43.50
46.34%
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region"
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Applic Patent No. 5891699
                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: FR 95-078
FILING DATE: 29-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION UMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MODIFIED BACTERIAL ALKALINE PHOSPHATASES TITLE OF INVENTION: AND THEIR APPLICATION NUMBER OF SEQUENCES: 10
TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: P.C.
STREET: 1755 S.
                                                                                                                                                                                  APPLICATION NUMBER: US/08/673,312 FILING DATE: 28-JUN-1996
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 ValLysAlaAspAsnAla
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-397-8338
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                                                                                                                                                                                                                                       Release #1.0, Version #1.30
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Matches:
Conservative:
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Indels:
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INFORMATION FOR SEQ ID NO:

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SEQUENCE CHARACTERISTICS:

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Best Local Similarity:
Query Match:
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US-08-934-846-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08934846 Patent No. 5882898 GENERAL INFORMATION:
                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1372 GCG 1374
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                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                               SEQUENCE CHARACTERISTICS:
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APPLICANT: Greenwood,
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STRANDEDNESS: doub
TOPOLOGY: linear
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OPERATING SYSTEM:
             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
                                                                                                                TELEFAX: 215-994-2222
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: PA
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                               TYPE: nucleic acid
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linear
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Matches:
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Indels:
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US-09-238-557-3
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Best Local Similarity:
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US-09-847-539A-6_COPY_59_86 (1-28) x US-09-238-557-3 (1-1221)
                                               Query Match:
                                                          Percent Similarity:
Best Local Similarity:
                                                                                             Score:
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                                                                                                                                                           US-09-238-557-3
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Patent No. 6165472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent NO. OLIVIANI ON:
GENERAL INFORMATION:
APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C
APPLICANT: MYENTION: NOVEL FOLC
                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
TO APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/238,557 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4000 Bell / CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                        TOPOLOGY:
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Indels:
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Percent Similarity:
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Query Match:
RESULT 30
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US-08-934-846-1
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US-08-934-846-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pearson, Stewart C. APPLICANT: Greenwood, Rebecca (TITLE OF INVENTION: NOVEL folc
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                                              559 TTCAAGGCTGGTAAGAAGGCA 579
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Matches:
Conservative:
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Indels:
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                                                                                                                                    Sequence 1, Application US/08612521 Patent No. 5786463 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                 APPLICANT: Peery, Robert B
APPLICANT: Skatrud, Paul L
APPLICANT: Thornewell, Susan J
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE
TITLE OF INVENTION: CRYPTOCOCCUS NEOFORMANS
                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252
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CORRESPONDENCE ADDRESS:
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APPLICANT: Greenwood,
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APPLICATION NUMBER:
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ZIP: 19103
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REGISTRATION NUMBER:
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   ADDRESSEE:
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Patent Division/AEH
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Matches:
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Best Local Similarity:
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Patent No. 5834309 5710045
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                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
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MEDIUM TYPE: Floppy disk
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NAME: Hamilton, Amy E
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CITY: Houston
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STRANDEDNESS: double
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CLASSIFICATION:
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                   FILING DATE:
                                  APPLICATION NUMBER: US/08/470,670A
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; LOCATION:
US-08-470-670A-1
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US-08-461-511A-1/c
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID
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APPLICATION NUMBER: US 0:
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
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         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander; Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:179
TELEPHONE: (512) 474-7577
TELEPHONE: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1274 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 aValValLysAlaAspAsnAlaAla 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:090--1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AspAlaLeuGluAlaLeuAla-AspGlnThrAspAla---LeuGlnSerGluGluAlaAl
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                              STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 4433
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Matches:
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Indels:
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RESULT 34
PCT-US94-07089-1/c
PCT-US94-07089-1/c
PCT-US94-07089-1/c
PCT-US94-07089
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Best Local Similarity:
Query Match:
; NAME/KEY:
; LOCATION:
PCT-US94-07089-1
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STREET: HOUSTON
STATE: TX
COUNTRY: Unite
COUNTRY: 77210
"TP: 77210
                                                                                                                                                                   TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/08: FILING DATE: 22 JUNE 1993 ATTORNEY/AGENT INFORMATION: NAME: PARKER, David L.
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1274 base pairs
                                                                                                                                                                                                                  NAME: PARKER, David L.
REGISTATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    FILING DATE: CONCURRICLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1230 GATTCACTCCACGCGATGGCAGCGGCAGACATCGTCCCATCTCCAGAATGAAGAAGTAGC
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                                                    FEATURE:
                                                                  MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
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                                                                                     TOPOLOGY:
                                                                                                STRANDEDNESS:
                                                                                                                                                                                    TELEPHONE: 512-320-7200
TELEFAX: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 avalvalLysAlaAspAsnAlaAla 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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LENGTH: 1274 base pairs
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                                                                                              nucleic acid
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LOCATION:
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STRANDEDNESS: single
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                                                                                    linear
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                                                                DNA (genomic)
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179..751
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Compositions and Methods
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Matches:
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Mismatches:
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RESULT 35
US-08-081-448-1/c
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Best Local Similarity:
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Best Local Similarity:
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                                  Percent Similarity:
                                                           Score:
                                                                          Pred. No.:
                                                                                           Alignment Scores:
                                                                                                                                 US-08-081-448-1
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646008thrup, Thomas E.
NEGISTRATION NUMBER: 33,268
REGISTRATION NUMBER: 3,268
REFERENCE/DOCKET NUMBER: ARCD090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEPAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Vertebrate Apoptosis Gene: TITLE OF INVENTION: Compositions and Methods NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, Craig B. APPLICANT: Boise, Lawrence H.
                                                                                                                                                                                      FEATURE:
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                                                                                                                                                  NAME/KEY:
LOCATION:
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STREET: 321 No. 56
                                                                                                                                                                                                                                      STRANDEDNESS: single
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179..751
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5646008th Clark Street,
                                    Length:
Matches:
Conservative:
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US-09-847-539A-6_COPY_59_86 (1-28) x US-08-081-448-1

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 Query Match:
DB:
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                          Percent Similarity:
Best Local Similarity:
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                                                                   Pred. No.:
                                                                                                            US-08-804-227C-
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Patent No. 587699
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/804
FILING DATE: February 21, 199
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-62
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
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APPLICANT: ROSteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                 LOCATION: FEATURE:
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                                                                                                                     NAME/KEY:
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OPERATING SYSTEM:
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                         Length:
Matches:
Conservative:
Mismatches:
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RESULT 38
US-09-254-733-4/c
US-09-254-733-4/c
; Sequence 4, Application US/05
; Patent No. 6277596
; GENERAL INFORMATION:
; APPLICANT: WATANABE, MANABU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 805,447.1090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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No.:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 805.447.4112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Martin, Frank
APPLICANT: Danilenko, Dimitry
TITLE OF INVENTION: A FIBROBLAST GROWTH FACTOR
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                    297 CAGGCTGATAAACTCCAGGATTCCGAAGCGGCTGTGGTCGTGGCG 253
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                                                                                                                                                 10 GlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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1840 DeHavilland Drive
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbh1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPFIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(wMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08090013 Patent No. 5443750
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MORIYA, TATSUKI
APPLICANT: AOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: (7)..(914)
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LOCATION: (279)..(334)
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      APPLICANT: CONVENTS, ANDRE C
APPLICANT: BUSCH, ALFRED
APPLICANT: BAECK, ANDRE C
                                                                                                                                                                                                                              TITLE OF INVENTION: CELLULASE AND SOFTENING CLAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 927
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                                                                                                                    STREET: 5299 SPR
CITY: CINCINNATI
STATE: OHIO
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ValLysAlaAspAsnAlaAla 28
                                                                                                                                                                            ADDRESSEE:
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                                                                                                                  OHIO
                                                                                              USA
                                                                                                                                                      3: THE PROCTER & GAMBLE COMPANY 5299 SPRING GROVE AVENUE
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59.26%
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COMPATIBLE
PC-DOS/MS-DOS
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Matches:
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Query Match:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAECK, ANDRE C.
APPLICANT: CEULEMANS, RAPHAEL ANGELINE A.
APPLICANT: BUSCH, ALFRED (NNN)
TITLE OF INVENTION: COMPACT DETERGENT COMPOSITIONS WITH
TITLE OF INVENTION: HIGH ACTIVITY CELLULASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 513-627-4854
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDENNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91:
FILING DATE: 06-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATEL, KEN K.
REGISTRATION NUMBER: 33,99
                     APPLICATION NUMBER: US/0 FILING DATE: 11/19/93 CLASSIFICATION: 252 ATTORNEY/AGENT INFORMATION:
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ANDLICATION NUMBER. UF ORGANIA 228
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-6437
TELEFAX: 513-627-4854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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LOCATION:
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                                                                                                                                                                                                                               TRY: USA
45253-8707
ZERBY, KIM WILLIAM
                                                                                                                                                                                                                                                                    ОПО
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Search completed: October 13, 2002, 06:32:14 Job time: 1240.98 secs
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; LOCATION: 10..924
US-08-081-328-1
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,323
REFERENCE/DOCKET NUMBER: CM356M
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-2885
TELEFAX: 513-627-2885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
FEATURE:
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|468 GAAGATGCCGACGCCGCCC 448
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Matches:
Conservative:
Mismatches:
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Title: Perfect score: Total number of hits satisfying chosen parameters: Scoring table: OM protein -9 protein search, using sw model BLOSUM62 283138 seqs, US-09-847-539A-6_COPY_59_86 129 Gapop 10.0 , October 13, SDALEALADQTDALQSEEAAVVKADNAA 28 Copyright 2002, 04:38:53; Search time 7.63636 Seconds (without alignments) 352.328 Million cell updates/sec GenCore version (c) 1993 - 2002 96089334 Gapext 0 residues 5.1.3 Compugen Ltd

Post-processing: Minimum Match 0% Maximum DB Bd seq length: 0
seq length: 2000000000

Minimum

Maximum Match 100% Listing first 45 summaries

Database

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1: pir1:*
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3: pir3:*
4: pir4:* pir2:* pir3:* pir4:*

score and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

## SUMMARIES

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84	2186	572	557	480	787	765	764	732	618	539	526	425	353	345	123
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hypothetical prote	hypothetical prote	transcription init	transport ATP-bind	pyruvate kinase (E	probable lipoprote	transducer protein	Htr2 transducer [i	helicase [imported	probable outer mem	nickel transport s	probable semialdeh	hypothetical prote	chorismate mutase/	hypothetical prote	aspartate 1-decarb

Cell 40, 775-783, 1985 A;Title: Conserved sequences flank variable tandem repeats in two S-antigen gnes A;Reference number: A90863; MUID:85176931 A;Accession: B22011 C;Date: 30-Sep-1987 #sequence_revision
C;Accession: B22011 S-antigen precursor - malaria parasite (Plasmodium falciparum) (strain NF7/Ghana) C; Species: Plasmodium falciparum A; Molecule type: DNA A; Residues: 1-309 < COW> R;Cowman, A.F.; Saint, R.B.; Coppel, R.L.; Brown, G.V.; Anders, R.F.; Kemp, D.J. Cell 40, 775-783, 1985 30-Sep-1987 #text_change 09-Jun-2000 of. טי

A; Experimental source: clone NF7.S
A; Note: the intact NF7 S-antigen contains about 35 more C; Comment: The S-antigen is secreted by the parasite. A;Cross-references: GB:M10130; NID:g160670; PIDN:AAA29758.1; PID:g160671

of the 8-residue repeats

F;24-309/Product: S-antigen #status predicted <MAT>
F;97-256/Region: 8-residue repeats (S-D-E-A-E-A-L/R-K)
F;257-271,272-286/Region: 15-residue repeats C; Keywords: malaria; surface antigen; tandem repeat F; 1-23/Domain: signal sequence *status predicted <S C; Superfamily: plasmodium S-antigen <SIG>

Q Query Match Best Local S Local Similarity 1 SDALEAL-ADQTDALQSEEAAVVKADNA 27 Conservative 44.6%; Score 57.5; DB Pred. No. 2.1; 6; Mismatches 6, DB 1; 7; Length 309; Indels 1;

Gaps

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97

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hypothetical protein Hp1327 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: G64685
R;Tomb, J.F; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. R;Tomb, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Fitle: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467

A;Accession: G64685 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 1-412 <TOM>

A;Cross-references: GB:AE000634; GB:AE000511; NID:g2314489; PIDN:AAD08377.1; PID:g231

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hypothetical protein lmo0047 [imported] - Listeria C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 C;Accession: AH1080 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend,
                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999 (;Accession: B71831  
C;Accession: B71831  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Rature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557  
A;Accession: B71831
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B71831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein jhp1247 - C:Species: Helicobacter pylori A:Variety: strain J99
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A; Residues: 1-213 <WAB>
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A;TILLe: Sequence analysis of an insertion A;Reference number: JC1150; MUID:92290280
A;Accession: JC1152
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A; Residues: 1-412 <ARN>
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5; Mismatches
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A;Cross-references:
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A;Accession: AI1437
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1080
C; Genetics:
A; Note: SC1
                                                           A; Molecule type: DNA
A; Residues: 1-276 < PAR>
                                                                                                                                         submitted to the EMBL Data A; Reference number: 217215
                                                                                                                                                                                                ketoacyl reductase homolog - Streptomyc
C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision
C;Accession: T29125
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A; Residues: 1-203 <GLA>
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A;Experimental source: strain EGD-
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A; Residues: 1-203 <GLA>
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                                                                                                                    A; Reference number: A; Accession: T29125
                                                                                                                                                                               R; Parkhill, J.; Barrell, B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: lin0040
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7; Mismatches
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Voss, H.; W
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K.D.; F
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Fsihi,
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Wehla
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**X** 

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A;Molecule type: DNA
A;Residues: 1-677 <HIM>
A;Cross-references: EMBL:AE000047; GB:U00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the A;Reference number: S73327; MUID:97105885
A;Accession: S73798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MG260 homolog H91_orf677 - Mycoplasma pneumoniae (s
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                      C; Accession:
R; Lincoln, L.
                                                                                                                                                                                                                                                                                                                                                                                  dynein beta heavy chain - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
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                                                                                                                         A;Genetic code: SGC5
A;Introns: 286/3; 666/3; 4360/2; 4535/3 C;Superfamily: dynein heavy chain, ciliary C;Keywords: P-loop
                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: T14914
                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, June 1999
A;Description: A gene knockout reveals that dynein beta heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                       T14914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily:
                                                                                                                                                                                            A;Gene:
                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                                                           A;Molecule type: D
A;Residues: 1-4589
                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
                                                                Matches
                                                                               Query Match
Best Local
3205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                              Conservative
                                                                                                                                                                                                                                               <LIN>
                                                                                                                                                                                                                       EMBL:AF072878; NID:g5209335; PID:g3309593; PIDN:AAC26117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.5%;
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                                                                                                                                                                                                                                                                                                                                     .m.; Asai, D.J.; Forney,
Library, June 1999
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                                                            Score 51; DB Pred. No. 2.8e 3; Mismatches
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2.8e+02,
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November 1996
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A; Residues: 1-617 <BLAT>
             A; Gene:
                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Function
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A; Residues: 1-32 <WAN>
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RESULT 10

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A; Molecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-353, 'NEFYRCCHANDQQVGFAGNYSTAGQT'
A; Cross-references: EMBL:U11035; NID:g684919;
A; Cross-references: Strain K-12
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c;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: G64972; B42940; S77641
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                            A;Status: Proceeding type: DNA A;Molecule type: DNA A;Residues: 1-617 <HAY> A;Residues: 1-617 <HAY> A;Cross-references: GB:BA000007; PIDN:BAB36294.1; PID:g13362340; GSPDB:GN00154 A;Cross-imental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                 gasawara, N.; Yasunaga, T.; Kuhara, S. DNA Res. 8, 11-22, 2001
A;Tille: Complete genome sequence of A;Reference number: A99629; MUID:2111
A;Accession: G99987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: sequence extracted from NCBI backbone R; Misra, R.; Miso, Y. Mol. Microbiol. 16, 779-788, 1995
Mol. Microbiol. 16, 779-788, 1995
A; Title: Molecular analysis of asmA, a locus in A; Reference number: S77641; MUID: 96065706
A; Accession: S77641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Wang, L.; Weiss, B.
J. Bacteriol. 174, 5647-5653, 1992
J. Bacteriol. 174, 5647-5653, 1992
A; Title: dcd (dCTP deaminase) gene of Escherichia coli:
A; Reference number: A42940; MUID:92380941
A; Accession: B42940
                                                                                                                                                                                                                                                                                                                                                                                                                                               suppressor of ompF assembly mutants [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: G90987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000296; GB:U00096; NID:g1788373; PIDN:AAC75125.1; PID:g17883 A;Experimental source: strain K-12, substrain MG1655 R;Wang, L.; Weiss, B.
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                                                                                                                                                                                                                                                                                                                                                                                        R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-22/Domain: signal sequence *status predicted F;23-380/Product: yegA protein *status predicted
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  Best Local
Matches
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  l Similarity
11; Conserv
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45.8%;
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                        38.8%;
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  Score 50; DB Pred. No. 46; 5; Mismatches
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56231; PMID:11258796
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A:Molecule type: DNA
A:Residues: 1-131, 'E',133-285,'S',287-419,'K',421-1247,'C',1249-1270,'QTS',1274-1807,
A:Residues: 1-131, 'E',133-285,'S',287-419,'K',421-1247,'C',1249-1270,'QTS',1274-1807,
A:Cross-references: EMBL:X08066; NID:g6787; PIDN:CAA30855.1; PID:g295767
R:D1bb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. B1ol. 205, 603-613, 1989
J. Mol. B1ol. 205, 603-613, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myosin heavy chain C [similarity] - Caenorhabditis elegans N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Caenorhabditis elegans C;Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_change 19-Jan-2001 C;Accession: T22232; T24967; S05697; S02773
A;Molecule type: DNA
A;Residues: 1-64,'V',65-131,'E',133-285,'S',287-419,'K',421-1247,'C',1249-1270,'QTS',127
A;Cross-references: EMBL:X08066
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C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
                                                                                                                A; Title: Sequence analysis of the complete Caenorhabditis A; Reference number: S02771; MUID: 89178677 A; Accession: S02773
                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: S05282 A; Accession: S05697
                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross·references: EMBL:268119; PIDN:CAA92197.1; A;Experimental source: clone T18D3
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A;Residues: 1-1968 <WILL>
A;Cross-references: EMBL:Z68117; PIDN:CAA92183.1; GSPDB:GN00028; CESP:T18D3.4
A;Experimental source: clone F45E6
A;Accession: T24967
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                                                                                       A; Status: nucleic acid sequence not shown
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A; Residues: 1-617 <STO>
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Best Local S
Matches 11
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80; MUID:21074935; PMID:11206551
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Pred. No. 46;
5; Mismatches
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46;
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lanta, E.;
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th, T.; Connerton, P.; C., S.; Moule, S.; O'Gaora, P., S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simm A;Authors: Parry, C.; Quail, M.; Rutherford and State of a multiple drug ann 502; PMID:11677608
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                                                          A; Molecule type: DNA
A; Residues: 1-445 <BEV>
                                                                                                 A; Reference number: Z15184
A; Accession: T06051
                                                                                                                                       R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, I
                                                                                                                                                                             hypothetical protein F19H22.10 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 24-Nov-1999 C;Accession: T06051
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A; Residues: 1-142 <PAR>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable regulatory protein STY3684 [imported] - Salmonella ente
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
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Best Local Similarity
Whiches 9; Conserve
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F;125/Modified site: N6,N6-trimethyllysine (Lys)
F;180/Binding site: ATP (Lys) #status predicted
F;708,718/Active site: Cys #status predicted
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A; Gene: myo-2;
                                         A; Cross-references:
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th, T.; Connexton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
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                      EMBL:AL035679; GSPDB:
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39.1%;
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Pred. No.
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Pred. No.
                  GSPDB:GN00062; ATSP:F19H22.10 lumbia; BAC clone F19H22
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1.6e+02;
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13;
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drug resistant
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Salmonella enterica
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R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Tille: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95975
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt,
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
A; Accession: A84305
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                                                                                                     L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                           A;Cross-references: GB:AL591985; PIDN:CAC49468.1; PID:g15140954; GSPDB:GN00167 A;Experimental source: strain 1021, megaplasmid pSymB R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlpela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical outer membrane protein, similar to Wza, OMA family C;Species: Sinorhizoblum meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change C;Accession: D95975
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A; Residues: 1-684 <STO>
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A;Introns: 37/3; 270/1; 312/2
C;Superfamily: Arabidopsis thaliana hypothetical protein F19H22.10
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                                                                                         A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-421 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leithauser, B.; Keller, K.; Cruz, R.;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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13; Conserv
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Similarity 43.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE004437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB Pred. No. 70; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID: g10581003; PIDN: AAG19805.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uist, B.; Pan, M.; Shukla, H.D.;
M.J.; Hough, D.W.; Maddocks, D.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     from the N2-fixing
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                                                                                                                                                                                                                                                  F.; Barloy-Hubler
N.A.; Fisher, R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.; Lowe,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۳.
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36.8%;

Score 47.5;

B

2;

Length 421;

74

LEAAEDAEDATQAEPAATPTAAAAA

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C;Genetics:
A;Gene: nif2
C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A; Reference number: A70500; MUID:98295987
A; Accession: B70955
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
T09236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: panD
G;Superfamily: aspartate 1-decarboxylase
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase;
F;9,11,58/Active site: Lys, His, Tyr *status predicted
F;24-25/Cleavage site: Gly-Ser (autolytic) *status predicted
F;25/Modified site: pyruvic acid (Ser) (in mature form) *status predicted
                                                                                                                                                                                                                                                                                                                                                                    C:Species: Frankia alni
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T09236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; MoLecule type: DNA
A; Residues: 1-139 <COL>
A; Cross-references: GB: Z95557; GB: ALL23456;
A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aspartate 1-decarboxylase (EC 4.1.1.11) - N;Alternate names: panD protein C;Species: Mycobacterium tuberculosis
                                                                                                                                                                                 A; Experimental source: strain
                                                                                                                                                                                                    A; Cross-references: EMBL:L29299; NID:g3953454; PID:g497435
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-192 <BEN>
                                                                                                                                                                                                                                                                  A; Status: translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T09236
                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A; Reference number: Z16624
                                                                                                                                                                                                                                                                                                                                                   R; Benson,
                                                                                                                                                                                                                                                                                                                                                                                                                                nifZ protein - Frankia alni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;54/Binding site: substrate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: B70955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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Matches 14; Conserv
                                        Matches
                                                       Query Match
Best Local
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4 LEALADQTDALQSEEAAVVKADNAA 28
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                                                                                                                     nitrogen fixation
                                                         Similarity
                                        Conservative
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40.9%;
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                                                       36.4%;
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                                                         Score
Pred.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47;
                                                                                                                                                                                                                                                                                                                                November 1998
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                                        Mismatches
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                                                         . 47;
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                                                     DB
35;
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25;
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RESULT 22
AB1677
conserved hypothetical protein TC0677 [imported] - Chlamydia muridarum (strain tc.Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Species: Chlamydia muridarum, Tc0677 [imported] - Chlamydia muridarum (strain tc.Species: Chlamydia muridarum, Tc0677 [imported] - Char-2000 #text_change ll-May-2000 C;Accession: A81677
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000
a.Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitrogenase Nifz chain - Frankia sı
N;Alternate names: Nifz protein
C;Specles: Frankia sp.
C;Date: 10-Sep-1995 #sequence_revi.
C;Date: 10-Sep-1995 #sequence_revi.
C;Accession: JC4207
R;Harriott, O.T.; Hosted, T.J.; Ber
Gene_161, 63-67, 1995
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A71519
hypothetical protein CT398 - Chlamydia trachomatis (serotype D, strain uwa/c;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: A71519
C:Accession: A71519
C:Accession: A71519
                                                                A; Reference number: A81500; A; Accession: A81677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, F
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen
A;Reference number: A71570; MUID:99000809
A;Accession: A71519
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A; Residues: 1-192 <HAR>
A; Cross references: GB:L29299;
C; Comment: This protein has an
                         A; Molecule type: DNA
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A:TITLE: Sequences of nifx, nifw, nifz, nifB
A:Reference number: JC4203; MUID:95369734
A:Accession: JC4207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE001313; GB:AE001273; NID:g3328823; PIDN:AAC67995.1; PID:g332882
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-254 <A
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C;Keywords: nitrogen fixation
                                           Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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8; Conserva
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52.0%;
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A; Residues: 1-333 < KUR>
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Best Local
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                                                                                                                                     position:
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2 DALEALADQTDALQSEEAAVVKA
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Similarity

36.4%;

Score 47; Pred. No.

2

Length 333

PID:g15156994;

GSPDB:GN00169

Conservative

3

Mismatches

9;

indels

0;

Gaps

0

24

circular chromosome

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R:Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                 C;Date: 30-Sep-2001 #sequence_revision C;Accession: A97586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; l.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M..
A; Title: Genome Sequence of the Plant Pathogen A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                       A; Gene: Atu1876
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE002336; GB:AE002160; NID:g7190707; PIDN:AAF39497.1; A;Experimental source: strain Nigg (MoPn) C;Genetics: A;Gene: TC0677
                                                                                                               hypothetical protein AGR_C_3443 {imported} - Agrobacterium tumefaciens (strain C; Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-307 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE008688; PIDN: AAL42872.1; A; Experimental source: strain C58 (Dupont)
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C; Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number:
A;Accession: AB2807
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3; Mismatches
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Pred. No. 46;
9; Mismatches
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                                                                                               30-Sep-2001
                                          Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                      DB
57;
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Kutyavin, T
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              Biotechnology
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              Agent Agrobacterium
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spectrin alpha chain - human (Spectrin alpha chain - human (C.Species: Homo sapiens (man) (C.Species: A0296; S13138; A05282; C.Accession: A35716; A45755; A23533; A91528; A42872; A02965; S13138; A05282; C.Accession: A35716; A45755; A23533; A91528; A42872; A02965; S13138; A05282; A15282; A15
                                                                                                                                         A: Molecule type: DNA
A: Residues: 320-450 < CLIN>
A: Residues: 320-450 < CLIN>
A: Cross references: GB: M13233; NID: g182242; PIDN: AAA53103.1;
R: Curtis, P.J.; Palumbo, A.; Ming, J.; Fraser, P.; Cloe, L.;
Gene 36, 357-362, 1985
Gene 36, 357-362, 1985
A: Title: Sequence comparison of human and murine erythrocyte
A: Reference number: A91528; MUID: 86083178
A: Accession: A91528
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SJHUA
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A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Recession: G87236
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A; Residues: 1-394,'G','396-533 <SA2>
A; Residues: 1-394,'G','396-533 <SA2>
A; Residues: 1-394,'G','396-533 <SA2>
A; Cross-references: GB:M29983
A; Note: the authors translated the codon GGT for residue 395 as Ala
R; Linnenbach, A.J.; Speicher, D.W.; Marchesi, V.T.; Forget, B.G.
Proc. Natl. Acad. Sci. U.S.A. 83, 2397-2401, 1986.
A; Title: Cloning of a portion of the chromosomal gene for human erythrocyte alpha-spectr
A; Reference number: A23533; MUID: 86205962
A; Accession: A23533
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A;Cross-references: GB:J05244
A;Cross-references: GB:J05244
R;Sahr, K.E; Tobe, T.; Scarpa, A.; Laughinghouse, K.; Marchesi, S.L.; Agre, P.; Linn J. Clin. Invest. 84, 1243-1252, 1989
J. Clin. Invest. 84, 1243-1252, 1989
A;Title: Sequence and exon-intron organization of the DNA encoding the alphal domain A;Reference number: A45755; MUID:90009318
A;Accession: A45755
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A;Title: The complete cDNA and polypeptide sequences
A;Reference number: A35716; MUID:90170949
A;Accession: A35716
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A; Residues: 1-1013 <STO>
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A;Cross-references: GB:M11049; R;Speicher, D.W.; Weglarz, L.;
                                                                      A; Molecule type: mRNA
A; Residues: 1451-1687 <CUR>
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NID:g338310;
DeSilva, T.M
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Pred. No.
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                                                                                                                                                                                                                                    murine erythrocyte alpha-spectrin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             James, K.D.; Thomson, N.N., Feltwell, T.; Fraser, A.; Hamlin, N.;
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2e+02;
                                     PIDN: AAA60569.1;
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                                                                                                                                                                                                                                                                                                               PID:g182243
Meo, P.; Sh
                                 PID: 9553648
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                                                                                                                                                                                                                                                                                                               Shane,
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Linnenbach,
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Holroyd,
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B4325
C:Date: 02-Feb-2001 #sequence_revision 02-Fe
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                             C; Accession:
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F;1081-1181/Domain: spectrin/dystrophin repeat hom F;1182-1287/Domain: spectrin/dystrophin repeat hom F;1288-1393/Domain: spectrin/dystrophin repeat hom F;1394-1498/Domain: spectrin/dystrophin repeat hom F;1499-1604/Domain: spectrin/dystrophin repeat hom F;1605-1710/Domain: spectrin/dystrophin repeat hom F;1711-11816/Domain: spectrin/dystrophin repeat hom F;1817-1925/Domain: spectrin/dystrophin repeat hom F;1817-1925/Domain: spectrin/dystrophin repeat hom F;1816-2032/Domain: spectrin/dystrophin repeat hom F;2041-2146/Domain: spectrin/dystrophin repeat hom F;2070-2302/Domain: spectrin/dystrophin repeat hom F;207
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A;Residues: 7-92, X',94-96,110-151;317-342;345-366,'Z',368-370,'X',372-373;387-434;45
R;Lusitani, D.M.; Qtaishat, N.; LaBrake, C.C.; Yu, R.N.; Davis, J.; Kelley, M.R.; Fun
J. Biol. Chem. 269, 25955-25958, 1994
A;Title: The first human alpha-spectrin structural domain begins with serine.
A;Reference number: A38928; MUID-95014412
A;Contents: annotation; determination of structural domain
C;Comment: Spectrin associates with band 4.1 and actin to form the cytoskeletal super
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Speicher, D.W.; Davis, G.; Yurchenco, P.D.; Marchesi, V.T. J. Biol. Chem. 258, 14931-14937, 1983
A;Title: Structure of human erythrocyte spectrin. I. Isolation A;Reference number: S13138; MUID:84087887
A;Accession: S13138
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J. Biol. Chem. 258, 14938-14947, 1983
A;Title: Structure of human erythrocy;
A;Reference number: A92408; MUID:8408
A;Accession: A02965
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A;Title: Properties of human red cell spec
A;Reference number: A42872; MUID:92340516
A;Accession: A42872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;792-897/Domain: spectrin/dystrophin F;898-983/Domain: spectrin/dystrophin F;984-1031/Domain: SH3 homology <SH3>
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                                                                                                                                                                                 Matches
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Best Local
953 DSMKALRNQANACQQQQAAPVE
                                                                               2 DALEALADQTDALQSEEAAVVK 23
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9; Conserv
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974
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t homology <SP13>
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S.P.; Mahairas,

G.G.;

Berquist,

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Pan,

Shukla, H.D.;

02-Feb-2001 #text_change 16-Feb-2001

sp.

D.W.;

Maddocks,

D.G.;

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A; Reference number: A81000; MUID:20
A; Accession: A81203
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-106 <TET>
A; Cross references: GB: AE002396; GE
A; Experimental source: serogroup B, C; Genetics: NMB0404
                                                                                                                                                                          Conserved hypothetical protein NMB0404 [imported] - Neisserla meningitidis (strain MC58 C;Species: Neisserla meningitidis
C;Species: Neisserla meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: A81203
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J., Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Sclence 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Title: Complete genome sequence of Neisserla meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
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A01203
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halbbacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
A; Accession: D84325
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C;Keywords: nucleotidyltransferase
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A;Title: Nitrogen metabolism in Streptomyces coelicolor A;Reference number: Z25448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [glutamate--ammonia-ligase] adenylyltransferase (EC 2.7.7.42) [imported] - Streptomyces C;Species: Streptomyces coelicolor C;Species: 18-Aug-2000 **sequence_revision 18-Aug-2000 **text_change 18-Aug-2000 **C;Datc: 18-Aug-2000 **sequence_revision 18-Aug-2000 **text_change 18-Aug-2000
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A; Residues: 1-784 <FIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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; Pred. No. 1.
2; Mismatche
                                              GB:AE002098; NID:g7225622; PIDN:AAF40843.1; PID:g72256:
B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:CAA76840
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Pred. No. 1
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.8e+02;
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32

mutase/prephenate dehydratase -

Thermotoga maritima (strain MSB8)

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Jabld
                                                                                                                                                  C;Geneti
A;Gene:
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene:
C;Superi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.; Shiba, T.; Hattori, M.; Ógasawara, N.; Hayashi, H.; Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Accession: E90066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-345 <S
                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: A87375
                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein CC1013 [imported] - Caulobacter crescentus C; Species: Caulobacter crescentus
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A;Residues: 1-123 <KUR>
A;Cross-references: GB:BA00001B; PID:913702554; PIDN:BAB43695.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E90066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aspartate 1-decarboxylase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
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Best Local S
Matches 10
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Best Local S
Matches 11
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Gene: CC1013
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Best Local :
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303
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                                 6 ALADQTDALQSEEAAVVKADNAA 28
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ALAEQFDRLHADKAATAKMGTAS
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11; Conserv
                                                                                          Similarity
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ilarity 42.9%;
Conservative
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                                                                                                                                                                                    GB:AE005673; NID:g13422303; PIDN:AAK22997.1; GSPDB:GN00148
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42.3%;
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Pred. No.
                                                                                        Score
Pred.
325
                                                                      Mismatches
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25;
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R:Langston, Z.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, April A:Description: The sequence of C. elegans
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A; Molecule type: DNA
A; Residues: 1-353 <ARN>
A; Cross-references: GB: AE001701; GB: AE000512;
A; Cross-references: Strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria

A:Paference number: A72200; MUID:99287316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_C;Accession: A72410 R;Nelson, K.E.; Clayton, R.A.; Garrett, M.M.; Stewart, A.M.;
                                                                      adman, S.; Yuan, Y.; Brody
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                    R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, i. Lory, S.; Olson, M.V.
                                                                                                                                                 probable semialdehyde dehydrogenase PA1253 [imported] - Pseudomonas aerugino
C;Speckes: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: The sequence
A; Reference number: Z20103
A; Accession: T25873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A; Introns: 28/1; 83/3; 110/3; 160/3; 182/1; 203/2; 232/1; 263/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U97405; PIDN:AAB53011.1; GSPDB:GN00019; A;Experimental source: strain Bristol N2; clone T09B4
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A; Residues: 1-425 <LAN>
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 A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337 A;Accession: C83488 A;Status: preliminary
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Best Local S
Matches 10
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10; Conservative
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Similarity 50.0%;
10; Conservative
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41.7%;
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                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; LC
Pred. No. 1.1e+02;
""matches 8;
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Pred. No.
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; Pratt, M.S.;
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                                                       aeruginosa PA01,
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 425
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; Phillips, C.A.; Richardson,
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K.; Lim,
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A; Gene:
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A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-526 <STO> A;Cross-references: GB:AE004555; GB:AE004091; NID:g9947183; PIDN:AAG04642.1; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 01-Dec-2000 #sequence_revision
C;Accession: G83720
                                                                                                                                                                                                                                                                                                                                            R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species:
                                                                                                                                                                                      A;Cross-references: GB:AP001509; GB:BA000004; A;Experimental source: strain C-125
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-539 <STO>
                                                                                                                                                                                                                                                                                    A; Accession: G83720
                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                A;Status: preliminary
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380 LELIYDKTDPLQKAMAETMQAEWAA 404
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                                4 LEALADQTDALQSEEAAVVKADNAA 28
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6; Mismatches
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                                                                        Score 46; DB 2; Louis Pred. No. 1.4e+02; 5; Mismatches 9;
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1.4e+02;
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s A;Reference number: AB0502; PMID:11677608
A;Accession: AE0770
                                                                                                                                                                                                                                                                                                                                                                                   C;ACCession: AE0770
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable outer membrane assembly protein STY2333 [imported] - Sa C;Species: Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
                                                                                                                                A;Cross-references:
C;Genetics:
A;Gene: STY2333
                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-618 <P/
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                                                                 Query Match
Best Local
LADQTDALQSEEAAVVKADN
                                            Similarity
9; Conser
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                                       Score 46; DB 2; Le
pred. No. 1.6e+02;
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Proc. Nat
A; Title:
                                                                                 transducer protein htrII [validated] - Halobacterium salinarum N;Alternate names: methyl-accepting taxis protein htrII; transc C;Species: Halobacterium salinarum C;Species: Halobacterium salinarum C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change
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T44946
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: AB4160; MUID:20504483
A; Accession: F84394
                     R; Zhang, W.; Brooun, A.; Mueller, M.M.; Alam, M. Proc. Natl. Acad. Sci. U.S.A. 93, 8230-8235, 1996
                                                              C; Accession:
                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Halobacterium salinarum transducer protein htrII
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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A; Residues: 1-764 <STO>
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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A; Residues: 1-732 <STO>
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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan,
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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C;Species: Halobacterium sp. NRC-1
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2e+02;
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  Halobacterium salinarium
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                                                                                   #text_change 18-Aug-2000
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R;Himmelreich, R.; Hilbert, H.; 1996
R;Himmelreich, R.; Hilbert, H.; 1996
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the language of the sequence number: S73327; MUID:97105885
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A;Accession: T44946
A;Status: preliminary; translated
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A;Experimental source: strain flx15
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A; Residues: 1-787 <HIM>
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A; Residues: 1-765 <ZHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
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                                                                                                                                                                                 DB 2;
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-MODEL-frame+_p2n.model -DEV-x1h
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-LOOPEXT-0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-buman40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-40
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09847539_GGGN_1_1_148_@runat_10102002_093105_4982 -NCPU-6 -ICPU-3
-NO_MIDTY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LOWLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Copyright (c) 1993 - 2002 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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                       Streptococcus
                                                       GRAB protein; protein G related alpha2M binding protein; vaccalpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                                                        Streptococcus
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                                                                                                                 29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New alpha 2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein -
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             GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
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                                                 Streptococcus
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P-PSDB; AAY71046.
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immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13;
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ain G of group G Streptococcus. GRAB protein and peptides derived
it are used in vaccine compositions for generating a protective
ne response against group A Streptococcus. Antibodies against GRAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1mmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAB protein; protein G related alpha2M binding protein; vaccine; lpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; mmune response; Streptococcus pyogenes infection; ds.
SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla
                                                                                                                                                                                                                                                                                                                                                                                         2000-365572/31.
DB; AAY71043.
                                                                                                                                                                                                                                                                                                                                                                                                                              Rasmussen
                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98GB-0023975
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/product= "GRAB protein"
/note= "Does not include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..777
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                                                                                                                                                  151 C;
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                       AAD00561 (1-777)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           include
                                                            Matches:
Conservative:
Mismatches:
Indels:
                                                 Gaps:
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RESULT 6
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          Query Match:
                       Percent Similarity:
Best Local Similari
                                               Score:
                                                          Pred.
                                                                    Alignment
                                                                                                                           related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain AP49. The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                            Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                            Sequence 853 BP;
                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD00563 standard;
                                                         No.:
                                                                                                                                                                                                                                     The patent discloses a new family of proteins termed GRAB (protein
                                                                                                                                                                                                                                                                                 New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                        Bjorck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200026240-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                              (ACTI-) ACTINOVA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response; Streptococcus pyogenes infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
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pha2-macroglobulin; group A Streptococcus; GAS; antibi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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DB; AAY71045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValValLysAlaAspAsnAlaAla
                       Similarity:
                                                                                                                                                                                                                                                           Page 64; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                      Rasmussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pyogenes strain AP49
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37..852
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         Conservative: Mismatches: Indels:
Gaps:
                                              Matches:
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                                                                                           G; 190 T; 0
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0000853
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US-09-847-539A-6_COPY_59_86 (1-28)

AAD00563 (1-853)

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RESULT 7
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ID AAT67618
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              This sequence encodes a H. pylori secreted or periplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be sequenced.
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT67618;
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                                                                                                                                                                                                                                                                                                                            Claim 23; Page
                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1996
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  from H.
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                                                                                                                                                                                                                                                                                                                       268; 1481pp;
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95US-0487032
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pylori by PCR amplification
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ing compound; bacterium;
duodenal ulcer disease;
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                                                                                                                                                                                                                                                   pylori secreted or periplasmic a vaccine to prevent or treat H
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547..549,
given"
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life cycle; activator;
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Best Local Similarity:
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                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                   diagnosis;
                                                                                                                                                                                                                                                                                                 Cytoplasmic; vaidentification;
                                                                                                                                                                                                                                                                                                                       H. pylori secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production,
                                                                        Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat infection, and to detect Helicobacter
                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                      AAT67B91;
                                                           Claim
                                                                                                                             Berglindh OT,
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                                                                                                                                                                                                                                                                                           bacteria; inhibitor;
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                                                           23;
                                                                                                       AAW20638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576
                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                          Page 770-771;
                                                                                                                                                                                                                                                                                   ds.
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                                                                                                                                                                                                                                                                                                         vaccine;
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                                                                                                                              Smith
                                                                                                                                                           96US-0630405
95US-0487032
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                                                                                                                                                                                                                                                                                          ccine; prevention; treatment;
binding compound; bacterium;
itor; duodenal ulcer disease;
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69.57%
52.17%
44.19%
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                                                                                                                                                                                                                                                                                                                                                                     DNA;
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                                                                                                                                                                                                                                                                                                                       periplasmic
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                                                                                                                                                                                                                              "no stop codon given"
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                                                          1481pp;
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                                                                                                                                                                                                                                                                                                                                                                     ВP
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                                                           English.
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                       protein
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                                                                                                                                                                                                                                                                                           chronic
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                                                                                                                                                                                                                                                                                                 infection; envelope;
life cycle; activate
                                                                                                                                                                                                                                                                                                                        02ce10216orf1
                                                                                related or preven
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12
                                                                                 prevent H.
                                                                                                                                                                                                                                                                                          gastritis;
                                                                                                                                                                                                                                                                                                  activator;
                                                                                pylori
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The present sequence encodes a H. pylori secreted or periplasmic profile to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides.

protein.

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RESULT 9
AAX30461
ID AAX3
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                          14-JUL-1997;
28-OCT-1996;
06-DEC-1996;
          73 ORPs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                         are
                                                                                                                                                                                               Alm
                                                                     Recombinant
                                                                                          Claims 3, 4;
                                                                                                                          Helicobacter pylori nucleic acids products for the detection, prever
                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                              07-MAY-1998
                                                                                                                                                                                                                                                                                                                                    W09818323-A1
                                                                                                                                                                                                                                                                                                                                                                                secreted
                                                                                                                                                                                                                                                                                                                                                                                            Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                H. pylori secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                    (ASTR ) ASTRA
                                                                                                                                                                                                                                                                                       28-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori
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                                                         disclosed,
                                                                                                                                                                                               RΑ,
 treating or reducing the
                                                                                                                                                                       1998-271811/24.
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                                                                                                                                                              AAY10994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                               Smith D;
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                                                                                                                                                                                                                                                                                                                                                                                          probe;
                                                                                         Page 126-127; 279pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                   AB.
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96US-0739150.
96US-0759739.
                                                     substantially together with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
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                                                                                                                                                                                                                                                                                                                                                                                          diagnostic;
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                                                                                                                           prevention
                                                      pure preparations of H. pylori polypeptides the nucleic acids encoding them. In all,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
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                                                                                                                                                                                                                                                                                                                                                                                          cell envelope protein;
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                                                                                                                                     and proteins - used
 of H.
                                                                                          English.
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pylori
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infections,
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                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins sequences (ABL018737-ABB72072).
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ABL13527
       The sequence data for this specification, but was obta
                                                                                                                             Claim 1;
                                                                                                                                                   genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes can be used diagnostically for detecting the presence Helicobacter in a sample. The products are also of use in scr for compounds having the ability to interfere with the H. pyl cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide
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                                                                                                                                                                                              P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical;
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                                                                                                                                                                        New isolated nucleic
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DB; ABB69424.
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          but was obtained
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                                                                                                                                                                                                                                                                                                                                                                                           gene;
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                                                                                                                             21pp + Sequence Listing; English.
                                                                                                                                                             detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                    biology;
                    patent did not form
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          in electronic
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Indels:
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                    part of the
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           directly
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Score:
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Query Match:
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ABL13526/c
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 Alignment Scores:
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                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01876-ABL30511), expressed DNA sequences (ABL0187737-ABB72072).
                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1062
                  Sequence 6398
                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                       Claim 1; SEQ ID NO 35060; 21pp + Sequence Listing; English.
                                                                                                                                                          genes from Drosophila
interactions ·
                                                                                                                                                                           New isolated nucleic
                                                                                                                                                                                                                      Venter JC, Adams
                                                                                                                                                                                                                                        (PEKE ) PE
                                                                                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell.signalling; insecticide;
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)B; ABB69423.
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                  1688 A; 1632 C; 1352 G; 1726 T; 0 other;
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Matches:
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Best Local Similarity:
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30-APR-1999;
04-MAY-1999;
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
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28-APR-1999;
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14-MAY-1999;
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                  21-MAY-1999;
24-MAY-1999;
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19-MAY-1999
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                Hybridisation assay; genetic mapping; gene expressio protein identification; signal transduction pathway;
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                                                                                                                                                                                                                                                                                                                       GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla
                                                                DNA fragment
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Matches:
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Mismatches:
Indels:
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                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016-ABL30511), expressed DNA sequences (ABL01640-ABL16175) and the encoded proteins
                                                            The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                           Claim
                                      Sequence 16135
                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and
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11-JUL-2000; 2000US-0614150
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RESULT 16
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US-09-847-539A-6_COPY_59_86 (1-28) x ABL01876 (1-25461)
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at ftp.wipo int/
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P-PSDB; ABB57773.
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RESULT 17
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 RESULT 19
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                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                           Sequence 2618
                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 33553; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes from Drosophila interactions -
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11-JUL-2000;
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168 GTACGAGGAGATCGTGCC
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            ABA03041;
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interactions -
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11-JUL-2000;
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                                 ABA03041 standard;
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                                                                                                22 ValLysAlaAspAsnAla
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                                                                                                                                                                                                                                                                                                             sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from
                                                                             GTACGAGGAGATCGTGCC
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DB; ABB68579.
                                                                                                                                            AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal
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51291 GGAGTTGAAAAAGAAAAC

21 ValValLysAlaAspAsn

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51231

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US-09-847-539A-6_COPY_59_86 (1-28)
                                                 Query Match:
                                                                 Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                    The present sequence is the genome sequence of Listeria monocytogenes BGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate genes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser K Kunst F, Cossart I Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; gene therapy; vaccine; biosyntt vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                  specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                         organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related polypeptides
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                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                            polynucleotifes are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (C iI). (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical c lmaging of sites expressing (II). (I) and (II) are useful for treating (C disorders involving aberrant protein expression or biological activity. (The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations (C responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and C and no acid sequences. AAS64197-AAS94564 represent novel human (C alagnostic coding sequences of the invention.)

CC Note: The sequence data for this patent did not appear in the printed (S territor) in the printed (S territor) is the sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chroma and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                   Sequence
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23-AUG-2000;
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2000US-0649167
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                  x AAS94455 (1-3711)
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                                                                                       Alignment
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                                                                                                                                                                                                                                                                                  genes from Drosophila and interactions -
                                                                                                                                             specification,
                                                                                                                                                                            cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG011), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins
                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling
                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 29020; 21pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology;
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                                                                                                            Sequence 1616
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11-JUL-2000;
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                                                                                                                                                                    (ABB57737-ABB72072).
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                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                        sequence data for this patent did not form
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
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 ABL25849 (1-1616)
                                                                                                            439 G; 273
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                                                                 Length:
Matches:
                                            Mismatches:
                                                     Conservative:
                                 Indels:
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                                                                                                                                                                                                                          The invention signalling and
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ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
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                          sequence 20, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET UNMBER: 45185
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                              Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                  US-08-757-669A-20/c
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
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                                                                                              APPLICANT:
APPLICANT:
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                                                                      TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 LeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu 49
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18
35
63
0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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                                                                                                                       STATE: New York
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
                Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
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Bohenzky, Roy A.
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ZIP: 10036
COMPUTER READABLE FORM:
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U.S.A.
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Best Local Similarity:
Query Match:
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APPLICANT: RUSSO, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Edelman, Isidore S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-847-539A-6 (1-159) x US-08-757-669A-20 (1-32207)
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Mismatches:
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Matches:
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957 GCGACGGATCTCTATGAAGCCAGCATCAAAAAGACGGATACCGCCAAGAGTGTTTATGAC 1016
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Patent No. 5948676

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Russo, James J.

APPLICANT: Russo, James J.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: Immediate Early Protein From Kaposi's

TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA

TITLE OF INVENTION: Encoding Same And Uses Thereof

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5393
23
12
51
51
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Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                        15661-20017.00
APPLICATION NUMBER: US/08/591,079 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661
TELEPHONE: (202) 887-0764
TELERAX: (202) 887-0764
TELERAX: 90-4030 MRSHFORRSWSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Salmonella typhi
STRAIN: TY2
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40.70%
26.74%
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                                              CLASSIFICATION: 435
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Best Local Similarity:
Query Match:
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2386 GAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAG 2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 SerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspVal 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AspAlaLeuGlnSerGluGluAlaAlaValVysAlaAspAsnAlaAlaAserAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 LeuargasnGluGluargalaIleaspGluLeuLysLysGlnalaIleGluaspLysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2626 CAGGAGGAGCAGGAGTTAGAGGAGGTGGAAGAGCAGGAGGAGGAGGAG 2673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LysLysThrLysAspThrLysProValValLysLysGluGluArgGln 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3489
118
35
63
0
                                                                                                                        MEDIUM TIFE: LIMPY ALS.

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0406

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TELEFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-847-539A-6 (1-159) x US-08-728-323A-1 (1-3489)
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1185 Avenue of the Americas
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%Sequence 20, Application US/08770379
%Patent No. 5849564
%GENERAL INFORMATION:
APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5
65.00
45.69%
15.52%
8.37%
                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-728-323A-1
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Pred. No.:
                CITY: Nev
STATE: Ne
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 GluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThr 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,079
                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-847-539A-6 (1-159) x US-09-115-746-9 (1-1419)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/08591079
; Patent No. 5972899
; GENERAL INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
TELEPHONE: (202)672-5300
TELERX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1419 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                              1.57
67.00
42.22%
20.00%
8.62%
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LOCATION: 1..1416
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Best Local Similarity:
Query Match:
DB:
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ZIP: 20006-1812
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STATE:
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1109 CCCGGCTATGCACAAGCTGAAGCGCGGGTAGAACAGGCCGGAAAAGAAGAAGCGACAGAGGC 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 AlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThr 97
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APPLICANT: Chen, Yaling
TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3622
23
12
51
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TOWN PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFX: (202) 887-0764
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3622 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOCLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Salmonella typhimurium
STRAIN: SibB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6 (1-159) x US-08-591-079-7 (1-3622)
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                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: /product= "SipB"
COTHER INFORMATION: /gene= "SipB"
US-08-591-079-7
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STREET: 2000 Pennsylvania Avenue,
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08591079 Patent No. 5972899 GENERAL INFORMATION:
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40.70%
26.74%
8.49%
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575..2356
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ZIP: 20006-1812
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Best Local Similarity:
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                             46 GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-216-894-9
Sequence 9, Application US/08216894
Sequence 9, Application US/08216894
Setent No. 5876734
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTONKEY/AGERT INFORMATION:
                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                US-09-847-539A-6 (1-159) x US-08-973-462-1 (1-6152)
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REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Foley & Lardner
: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                     Length:
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                 8.01
68.00
42.06%
15.89%
8.75%
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; SEQ ID NO 1
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1
                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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STREET: 30
                                                                                                                Alignment Scores:
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TELEX: 9'
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                                                                                                                                     Pred. No.:
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943 GCAGCTGAAGCCACGAAGGTTGCCGAAGCGGAGGAAGCAGAAGGCAGCTGAAGCCACGAAG 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 GluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThr 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763 GAGAAGCAGAGGAGCTGAAGCCACGAAGGTTGCCGAAGCGGAGAAGCAGAAGGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 AlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823 GAAGCCACGAAGGTTGCCGAAGCGGACAAGCAGAGGCAGCTGAAGCTGAAGGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kirchhoff, Louis V.
APPLICANT: Cosu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           1419
18
20
52
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELB PC compatible
COMPUTER: TEM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PROR APPLICATION NUMBER: 08/216,894
FILING DATE:
                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
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Matches:
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1003 GTTGCCGAAGCGGAGAAGCAGAAGGCAGCT 1032
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; Sequence 9, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1419 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomlc)
FEATURE:
                                                                                                                                                                                                                                                                              1.57
67.00
42.22%
20.00%
8.62%
                                                                                                                                                                                        1..1416
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Best Local Similarity:
                                                                                                                                                                 NAME/KEY: CDS
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LOCATION:
US-08-216-894-9
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Percent Similarity:
Best Local Similarity:
Query Match:
         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 AAAGAAAAAGCGTNTCAAGATATCTTAANTGCACAANCAACTAATGATGTTACGCAAATT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [11:::11]
588 CTGCAGGCATGCAAGCTTGAGTCTTCTNTAATTCAAAGCACACAACCAGCANCAGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AATACAACTGGCGCTACAACTGAAGAGAAAATGCAGCAAAAGATTTAGTTTTANAAGCT
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605
20
119
55
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 AATGATCAAGCAGTTGCTGATATTCAAGGTATTACTGGAGAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                      COUNTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
OPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1997
FILING DATE: 24-SEP-1996
ATTORNEY,AGENT INFORMATION:
NAME: Glumi, Edward R
REGISTRATION NUMBER: 38,891
REFERRICE/POCKET NUMBER: 38,891
REFERRICE/POCKET NUMBER: 38,891
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-847-539A-6 (1-159) x US-08-936-165A-93 (1-605)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08973462B Patent No. 6191270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 93:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.127
71.00
41.49%
21.28%
9.14%
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LENGTH: 605 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity:
Query Match:
                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-973-462-2
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
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APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1996-02-06
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE PALENT ON OF: 2.0
SEQ ID NO 2
LENGTH: 5361
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APPLICANT: DAUBERSES, PIERRE
APPLICANT: DAUBERSES, PIERRE
APPLICANT: DAUBERSES, PIERRE
APPLICANTON: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1996-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PALCALIN VEI. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 GAAGAAAGTGTAGAAGAAAATGACGAAGAAAGTGTAGAAGAAAATGTAGAAGAAAATGTA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 GAAGAAAGTGTAGCTGAAAATGTTGAAGAAAGTGTAGCTGAAAATGTTGAAGAAAGTGTA 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742 GAAGAAAATGACGACGGAAGTGTAGCCTCAAGTGTTGAAGAAAGTATAGCTTCAAGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 GATGAAAGTATAGATTCAAGTATTGAAGAAAATGTAGCTCCAACTGTTGAAGAAATCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 GCTCCAAGTGTTGTAGAAAGTGTGGCTCCAAGTGTTGAAGAAAAGTGTAGAAAAAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
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17
28
62
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AlaLeuAspValLysLysThr 132
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68.00
42.06%
15.89%
8.75%
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: P. falciparum
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US-08-973-462-2
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us-09-847-539a-6.rni

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YSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 93, Application US/08936165A; Patent No. 6348582; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Black, Michael
Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
Lonetto, Michael
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.18
75.00
49.00%
21.00%
9.65%
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LOCATION: 544..7990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2256 AATGGCCTCATTCAAGAAGTAGAAGATGGCAAGCAAGAACTGGAGAAGAAGGATGAAGAA 2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLy9AlaAlaThrProIle 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AlaLeuAspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGln 145
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APPLICANT: Lee, Wan-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESSONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11310
FILING DATE: 19-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6 (1-159) x PCT-US93-11310-12 (1-4868)
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Matches:
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                                                                                                                                                                                       FP-CJ 9790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-328-254-5
Sequence 5, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REPERENCE/POCKET NUMBER: FP-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-8949
TELEFAX: 619-535-8949
                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 4868 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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COMPUTER: IBM PC compatible
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49.00%
21.00%
9.65%
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MEDIUM TYPE: Floppy
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STATE: California
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PCT-US93-11310-12
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Best Local Similarity:
Query Match:
                                                                                                                        CLASSIFICATION
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5917 GAAAAAGAGCAAGAGAAAGTACAGATGAAAGAAAAATCAAGCACTGCCATGGAGATGCTT 5976
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21
28
51
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Version #1.25
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Mismatches:
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            SOFTWARE: PAGENTIN ROLEGUSE #1.0, VETS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-0CT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/14,239
FILING DATE: 22-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERRACE/POCKET NUMBER: P-CJ 1191
TELEFAN: (619) 535-9001
TELEFAN: (619) 535-901
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COMPUTER READABLE FORM:
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Patent No. 5821070
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: SHAN, BEI
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: German P 42 36 708.5
ATORNEY,AGENT INFORMATION:
NAME: Kurf G. Briscoe
RECISTRATION NUMBER: 33.141
RECISTRATION NUMBER: Bayer 8885-KGB
TELECOMUNICATION INPORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
STATE: CALTFORM
                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2233 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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75.00
47.568
30.498
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Best Local Similarity:
Query Match:
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75 GACAAC 70
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2016 GAAAAAGAGCAAGAGAAGTACAGATGAAAGAAAATCAAGCACTGCCATGGAGATGCTT 2075
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-535-8949 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4868 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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STATE: CALIFORNIA
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Best Local Similarity:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Later Sequence Protein, and Methods of Use
NUMBER OF SEQUENCES:
ACORRESPONDENCE ADDRESS:
RORRESPONDENCE ADDRESS:
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STREET: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7848 TGTAAGGCCAAAGAGGGGAGAATCTTAGTAGTCAAGTAGAGGTGTCTTGAAGTTGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-847-539A-6 (1-159) x US-08-353-700-2 (1-10136)
                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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Gaps:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10136 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103-2307
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                           ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
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7728 GAAAAAGAGCAAGAGAAAGTACAGATGAAAGAAAAATCAAGCACTGCCATGGAGATGCTT 7787
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Sequence 1, Application US/08145705A

Patent No. 5489513

GENERAL INFORMATION:
APPLICANT: Springer, Wolfgang; Plempel, Manfred;
TITLE OF INVENTION: SPECIFIC GENE PROBES AND
TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC;
TITLE OF INVENTION: INVESTIGATION OF CANDIDA
TITLE OF INVENTION: ALBICANS
NUMBER OF SOUDENCES: 44

CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STAME: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 inch, 1.4 MB storage
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: U.S.A.
21P: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: NEC POWERMATE 1 Plus
OPERATING SYSTEM: DOS
SOFTWARE: WORDPEFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                           LENGTH: 10136 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: 1inear
MOLECULE TYPE: DNA (genomic)
                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4004
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   1.01
76.00
49.00%
21.00%
9.78%
NAME: Reed, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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06-SEP-1993

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Fatent No. 610055
GENERAL INFORMATION:
APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: LINDBERG, Martin
APPLICANT: RANTAMAKI, Lisa K.
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
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                                           61743/102
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 61743
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEX: 904136
INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-JUL-1996
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62.50%
59.38%
11.71%
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288..1526
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288..1526
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Best Local Similarity:
Query Match:
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COUNTRY: USA
ZIP: 20007-5109
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LOCATION:
                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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US-08-669-408B-9
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128 AspvallysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
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APPLICANT: RATTUER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRALENCE TO SET OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: A
ADDRESSEE: DANN, DORFWAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                2526
18
2
12
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 61743/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08353700 Patent No. 5599919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                TELERAX: (202,
TELERAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TWOTH: 2526 base pairs
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  85.00
62.50%
56.25%
10.94%
                                                                                                                                                                                                                                                                                                              mat_peptide
506..2497
                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                          506..2497
                                                                                                                                                                                                                           linear
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Best Local Similarity:
Query Match:
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LOCATION:
                                                                                                                                                                                                                           TOPOLOGY:
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LOCATION:
US-08-669-408B-1
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Sequence Sequence Sequence

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FOR PRODUCING INHIBITOR-BINDING PROTEINS
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY GOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT RC-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,408B
FILING DATE: 03-JUL-1996
           09-080-855-30
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US-08-466-390-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-680-897-1
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STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: MISLLER, Hans-Peter
APPLICANT: RANTAMAKI, Liisa K,
TITLE OF INVENTION: METHOD AND MEANS FOR
TITLE OF INVENTION: PLASMAPROFEINASE IN)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9302855-3

FILING DATE: 06-SEP-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08669408B Patent No. 6100055 GENERAL INFORMATION:
              3622
5393
32207
32207
1695
11932
11932
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11932
11932
11932
11932
867
867
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                                                              444444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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-MODEL-frame+_p2n.model.bbv=xlh
-Q-Cgn2_1/USPTO_spool/US09847539/runat_10102002_092549_3456/app_query.fasta_1.526
-Q-Cgn2_1/USPTO_spool/US09847539/runat_10102002_092549_3456/app_query.fasta_1.526
-Q-Cgn2_1/USPTO_spool/US09847539-runat_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_nentra_n
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Sequence 2, M
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                                                                                                      October 13, 2002, 02:17:36; Search time 51.8663 Seconds
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PcTu3_COMB.seq:*
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Compugen Ltd
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US-08-69-408B-1
US-08-633-700-2
US-08-145-705A-1
US-08-139-937-12
US-08-133-1310-12
US-08-93-11310-12
US-08-93-115-12
US-08-93-1462-2
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                                                                                                                                                                                                                                                                                                                        383533 seqs, 122816752 residues
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              GenCore version
Copyright (c) 1993 - 2002
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Listing first 45 summaries
                                                                                                                                                                                                                                           Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
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length: 2000000000
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¹²³ ThrProllealaLeuAspVal 129 :::111 | 11 | 428 GCCTCTGTGGCCTCTCTGTG 408

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PT New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess boddversity.

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217 AGCGCAGAATCCTCAAAAACGGCTGCCGCATCGTCAGCCAGTTCGGCGGCGTCATCGGCA 276
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                 50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
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AAS74086 standard; cDNA; 782
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Best Local Similarity:
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83 AspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer 102

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerse chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of date and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence date for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 ASDAlaProGluLysLeuAlaLeuArgAsDGluGluArgAlalleAspGluLeuLysLys 42
                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             728 TCAGCCAGTGCCACCGCCGCCGGAAATCGGCAGAAAGCGCCCGCATCGTCTGCTTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 GlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla
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Mismatches:
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23-AUG-2000; 2000US-0649167
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Best Local Similarity:
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                                                   WO200175067-A2.
               Homo sapiens.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, ollymers chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
infections, abscesses and spontaneous abortion. This sequence represents DNA encoding the S. dysgalactiae Mig protein of the invention.
                                                                                                                                                                                                                                                                       128 AspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                               Sequence 2010 BP; 735 A; 393 C; 381 G; 501 T; 0 other;
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Matches:
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG13175.
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                                                                                  Alignment Scores:
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                              diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
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337 GCCACGACGACAGAGAGAGAGAGAGAGAGGCAGCGAGGGCAGCTCAG 396
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medical imaging; diagnostic; genetic disorder; ss.
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polypeptide and polynucleotide sequences have applications in
                                                                                                                                                              Sequence 3069 BP; 818 A; 832 C; 784 G; 635 T; 0 other;
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Cand to produce other types of the invention of mutations diagnostic coding sequences of the invention.

Canno acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #18239.
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126 AlaLeuAspValLys 130
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Length:
Matches:
Conservative:
Mismatches:
Indels:

83.00 43.01% 27.96% 10.68% 23

Percent Similarity: Best Local Similarity: Query Match:

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Alignment Scores:

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stroptococcal infection, mastitis, septicaemia; meningitis; bacteracmia; impetigo; arthritis; urinary tract infection; abscess; antiinflammatory; spontaneous abortion; antibiotic; antiarthritic; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a vaccine composition comprising a vehicle and an Fc receptor protein. The exceptor protein. The sequence and composition are useful for treating or preventing a bacterial infection e.g. a streptococcal infection which causes mastitis in a vertebrate subject. The vaccine compositions can also be used to treat other streptococcal infections cansed by S. agalacties, such as septicaemia, meningitis, bacteraemia, impetigo, arthritis, urinary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; Fc receptor; bacterial infection; Streptococcus agalactiae;
                                                                                        1226 GCCACGACGCCATCCACGAAGGCGACAGAGGCTGCTGGCAGTGCGACGCGCGCAGCTCAG 1167
                                TCATCGGCGTCTGCTTCAAAAGATGAGGCGACCAGACAAGCGTCAGCAGCGGAAGAGCAGC 1227
                                                                                                                                            90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                     SerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspVal 129
                                                                      AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel vaccine composition comprising Mig protein (Fc receptor) of Streptococcus dysgalactiae useful for treating or preventing streptococcal infection such as mastitis in vertebrates -
AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "S. dysgalactiae Mig protein"
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,		ysgln/     ACCAG	euGlu/ ::    TCGAGG	laAsp/ :: CTTCT/
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1		PGluLe	rSerAs :::• GACATO	avalva       
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       Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of a synthetic protein G gene, MD-1. The proteins produced by MD-1 are capable of specifically binding the constant region of the heavy chain of IgG in the same way as neutral Fc receptors. They can be used to analyse the structure and function of Fc receptors, as well as in antibody production, cell culture, diagnosis and therapy. They can be used to treat disorders such as leukaemia and lymphoma, cancer and immune disorders.
                                                                          Synthetic; protein G; IgG; Fc receptors; heavy chain; leukaemia; lymphoma; cancer; autoimmune disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           region of an immunoglobulin
the amino acid sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 22241.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide(s) which bind the Fc comprising a nontotal portion of
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                                       Synthetic protein G gene, MD1.
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11-OCT-1995 (first entry)
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P-PSDB; AAR71127.
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Best Local Similarity:
Query Match:
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                                                                                                                                    Synthetic.
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108 GAAACTCTGCCGACTACTGGTGAAGGTTCTAAC 140
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P-PSDB; AAR71128.
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3686 AAGGAAGCCGCCAGCAGCGAAGAGGAGCCTAGCAAGGTTGTGGACTCTGCGGAACCCAAG 3745
                                                3746 GAGGCAGAGAGCAATACGGATGAGAGCGCCACGCCCGTTCCTATTGATGTTTCTACCGCC 3805
                           104 GlualaGluValValGlnŞerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThr 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 AspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of an expression vector constructed to produce SG-3 (synthetic protein G). SG-3 is capable of specifically binding the constant region of the heavy chain of IgG in the same way as neutral FC receptors. It can be used to analyse the structure and function of FC receptors, as well as in antibody production, cell culture, diagnosis and therapy. They can be used to treat disorders such as leukaemia and lymphoma, cancer and immune disorders.
                                                                                                                                                                                                                                                                                            Fc receptors; heavy chain; leukaemia;
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the amino acid sequence of
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                                                                                                   3806 CCCGCATCCAATGATGTCAGCAAG 3829
                                                                                   124 ProlleAlaLeuAspValLysLys 131
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                                                                                                                                                                                                                                                             Expression cassette for SG-3.
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Best Local Similarity:
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128 AspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
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                                                                                                                                                                                             Synthetic; protein G; IgG; Fc receptors; heavy chain; leukaemia; lymphoma; cancer; autoimmune disease; ds.
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                                                                                                                                                  Chimearic synthetic protein G gene,
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AA084887 standard; cDNA; 603
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ABL03676 standard; cDNA; 5366
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                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

(ABS7737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln
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                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5513; 21pp + Sequence Listing; English.
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                                                             23-MAR-2001; 2001WO-US09231.
                                                                                     23-MAR-2000; 2000US-191637P,
11-JUL-2000; 2000US-0614150,
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41.67%
23.15%
10.81%
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Best Local Similarity:
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           WO200171042-A2
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RESULT 31 ABL03676

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp
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                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 5510.
                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5366 BP; 1512 A; 1199 C; 1311 G; 1344 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
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11-JUL-2000; 2000US-0614150.
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(first entry)
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                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                            pharmaceutical; gene;
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P-PSDB; ABB59573.
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Best Local Similarity:
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                                                                                                                           Drosophila;
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26-MAR-2002
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Pred. No.:
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imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human hote: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                           GCGTCATCGGCATCATCGGCGTCTGCTTCAAAAGATGAGGCGACCAGACAAGCGTCAGCA 2205
                                                                                                                                                                                                                                                                                                                                                                                                                                       2206 GCGAAGAGCAGCGCCACGACGGCATCCACGAAGGCGACAGAGGCTGCTGGCAGTGCGACG 2265
                                                                                                                                                                                                                                                                                                                                                                    AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125
                                                                                                                                                                                                                                                                          GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu 65
                                                                                                                                                                                                                                                                                                                       66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla 85
                                                                                                                                                                                                                                                                                                                                       126 AlaLeuAspValLysLysThrLysAspThrLysProValValLysLysGlu 142
                                                                                                                                     Sequence 3411 BP; 921 A; 898 C; 918 G; 674 T; 0 other;
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16
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plasma proteinase-inhibitor binding protein; ss.
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/note= "putative promoter region"
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/note=_"putative promoter region"
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/note= "putative promoter region"
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467..472
                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
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86.00
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 dysgalactiae mig gene.

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Best Local Similarity:
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23.27 GACGCTAAAAAACCAGAAGCTAAGAAAGAAGGTAAGAAGAAGAAGAAGAAGAGCTAAGAAAGCT 2386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 AspvallysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
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                                                                                                                                                                                                                                                                                                                                                                                                                          Rantamaki LK;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 31; 50pp; English.
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506..2500
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LINDBERG M.
MUELLER H.
RANTAMAKI L K.
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                                                                                              mat_peptide
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(LIND/) I
(MUEL/) N
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for eatern normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in itssue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                        1780 GAAAAGCAGGCTGCTGCTAAGGCCAAAAAGGCTGCCGAGGAGGCCGCCAAAATCGCTGCC 1721
                                                                                                                                                                                                                                                                                                                                                                                                                1720 GAAGAGGGTCTCCTGGCTGAAGCTGCCGCCCAAAAAGCAGCGGAAGAAGGTAAAGCCCTA 1661
                                                                                                                                                                                                                                                                                            86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                    106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGLuLysAlaAlaThrProIle 125
                    26 GluLysLeuAlaLeuArgAsnGluCluArgAlalleAspGluLeuLysLysClnAlalle 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                     66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
                                                                                                                                                                                                                                                  1660 AAAGCCGCTGAAGATGCTGCCCAGAAAGCTGCCGAAGAAGCGCGTCTAGCGGAGGAGGGCT
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                                                                                                             46 GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #18238.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                         86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                  106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125
                                                                                      1522 GCCGCCCAAAAGGTCGCCGAGGAAGCTGCCCAAAAAGCTGCTGAGGAAGCTCGCCTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genomic polynucleotide SEQ ID NO 12481.
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Conservative:
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
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interactions
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ABL20336;

ABL20336 RESULT a

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US-09-847-539A-6 (1-159) x ABL20336 (1-11145)

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1330 GAAACTCTTCCTACAACTGGTGAAGGCAGCAACCCA 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity as protein G from Streptococcus G148 (AAN/0757) is claimed. See, for example, AAN/0754, AAN/0755 and AAN/0756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA molecules - for producing proteins with 19G-binding specificity of protein {\tt G} or proteins A and {\tt G}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1469 BP; 545 A; 280 C; 297 G; 347 T; 0 other;
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Matches:
Conservative:
Mismatches:
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459.530
/*tag= f
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531.566
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1152..1361
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1362..1469
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Best Local Similarity:
Query Match:
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                                             misc_feature
                                                                                                                                                                                                                                                                                                                                 20-MAR-1987;
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 12484.
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ABL20337 standard; DNA; 2121 BP
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11-JUL-2000; 2000US-0614150.
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genes from Drosophila and
interactions -
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                                                                                                                                                                                                                                          pharmaceutical; gene; ds
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                                                    ABL20337;
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148 AsnThrLeuProThrThrGlyGluGluSerAsnPro 159

AspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147

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06-SEP-1993;
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              A phage lambda EMBL3 library of S. dysgalactiae 8215 DNA was analyzed for alpha-2-macroglobulin-, BSA- and IgG-binding activity. Clone lambda-SD1, which expressed all 3 activities, was analyzed to obtain DNA encoding the SA-binding protein, MAG. The mag gene (given in Q86080) encoded a 44 kba MAG protein (R71670). Recombinant, immobilized MAG was used for serum albumin affinity purification, detection and assay.
                                                                                  Sequence 1555 BP; 582 A; 242 C; 305 G; 426 T; 0 other;
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19
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plasma proteinase-inhibitor binding protein; ss.
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/note= "putative promoter region"
230..235
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Matches:
Conservative:
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/note= "putative promoter
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Disclosure; Page 29-30; 38pp; English
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198..203
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288..389
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Best Local Similarity:
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                                                                                                  Alignment Scores:
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128 AspValLysLysThrLysAspThrLysProValValLysLysCluGluArgGlnAsnVal 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoding polypeptide possessing IgG-binding activity of protein G from Streptococcus G148.
                                                                                                                                                                                                                                         DNA encoding fast alpha 2-macro:globulin-binding proteins - uso to obtain prods. for sepn., detection or quantification or for binding inhibition
                                                                                                                               Rantamaki LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1555 BP; 583 A; 242 C; 304 G; 426 T; 0 other;
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Matches:
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                                                                                                                               Guss B, Jonsson H, Lindberg M, Mueller H,
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91.00
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                                                                                     (RANT/) RANTAMAKI L K.
GUSS B.
JONSSON H.
LINDBERG M.
                                                                                                                                                                   WPI; 1995-123382/16.
P-PSDB; AAR71928.
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                                                                MUELLER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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1222 AATGCTGCAGCGTCACAACAATCAGCCGCCACGTCTGCCTCCACCGCGGCCACGAAAGCG 1281
                                                                                                             90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                               70 AspalaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
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 dysgalactiae mag gene.

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(JONS/)
(LIND/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guss B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, collymerase chain reaction (PER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) and its binding antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in classomatics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and confine sequences of the invention.

Contact the sequence data for this patent did not appear in the printed confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed of the confine in the printed in electronic format directly from WIPO confined in the printed in the confined in the printed in the confined in the printed in the confined in the printed in the confined in the printed in the confined in the confined in the printed in the printed in the confined in the printed in the confined in the p
                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1383 BP; 331 A; 349 C; 439 G; 264 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1383
24
13
31
0
                                                                                                                               DNA encoding novel human diagnostic protein #16029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 16029; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                             AAS80225 standard; cDNA; 1383 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.00126
93.00
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35.298
11.978
23
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73.
P-PSDB; ABG16038.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                WO200175067-A2.
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                 11-OCT-2001.
                                                              AAS80225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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DNA encoding a serum albumin binding protein - used to obtain prods. for sepns., detection, quantification, protein stabilisation or vaccine development
WPI; 1995-123386/16
                                       P-PSDB; AAR71670
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1342 GAAACGAACGCATCATCAAGTGCC 1365 AAQ86080 standard; DNA; 1555 BP (first entry) 21-SEP-1995

gene; serum albumin binding protein; protein stabilization;

Streptococcus dysgalactiae strain 8215.

/*tag= b /note= "putative promoter sequence" /*tag= c /note= "putative promoter sequence" 264..269 a "putative promoter sequence" Location/Qualifiers 198..203 230..235 249..254 /*tag=

/*tag= d /note=_"putative promoter sequence" /*tag= e 288..1527 /*tag= f 288..389 276..281

/*tag= g 390..1524

/*tag=

WO9507300-A 16-MAR-1995

94WO-SE00825. 93SE-0002856 06-SEP-1994;

GUSS B. JONSSON H. LINDBERG M.

Lindberg M; Jonsson H,

US-09-847-539A-6 (1-159) x AAS80225 (1-1383)

50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69

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Page 13

us-09-847-539a-6.rng

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Protein G isolated from Streptococcus has IgG-binding activity which has been localised to the B repeating structure (see AAR$390). The nucleotide sequence AA604648 codes for a claimed Streptococcal Protein G variant comprising the B domain active site and retaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; dlagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "encodes 30 amino acid secretion sequence"
                                                                                                                                                                                                                                                                                                              New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 798 BP; 277 A; 161 C; 177 G; 183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           798
233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #20300.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAla
                               91..798
/*tag= b
/product= Protein_G_variant
                                                                                                                                                                                                                                                                                                                                              Disclosure; Columns 9-12; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                               (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-847-539A-6 (1-159) x AAQ64648 (1-798)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS84496 standard; cDNA; 1380 BP
                                                                                                                                                86US-0829354.
86US-0854887.
87US-0063959.
                                                                                                                                                                                 88US-0209236.
90US-0540169.
92US-0871539.
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105.00
72.73%
69.70%
13.51%
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1..90
/*tag=
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                                                                                                                                                                                                                                                                            WPI; 1994-159179/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                     Pahnestock SR;
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                                                                                                                            14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                              US5312901-A.
                                                                                                                                                                                             19-JUN-1990;
21-APR-1992;
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                                                                                                                                                 14-FEB-1986
                                                                                                                                                            23-APR-1986
sig_peptide
                                 mat_peptide
                                                                                                     17-MAY-1994
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags consideritying expressed generating antibodies against it, detecting or to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in casponsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and adiagnostic coding sequences of the invention.

Consideration, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1279 TCAGAGGCCGCCACTTCAGCACGAGATGCGGTGGCCTCAAAAGAGGCACAAAATCATCA 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AspalaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsanAlaAlaSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1380 BP; 331 A; 348 C; 438 G; 263 T; 0 other;
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24
13
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wlpo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 20300; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-847-539A-6 (1-159) x AAS84496 (1-1380)
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                                                                                                                                                                                              Tang YT;
                                                                    30-MAR-2001; 2001WO-US08631
                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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54.41%
35.29%
11.97%
                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                   P-PSDB; ABG20309
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                              Drmanac RT,
                                   11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
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RESULT

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4 ProlleGluGlnProArglleIleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsn 23
                                                                                                                                                                                                                                                                                                                                                                                                                           Protein G variant product carries active regions B1 and B2, it may be imobilised and exhibits different binding profiles. The bound protein is useful in purification and detection of Igs and framents.
                                                                                                                                                                                                                                                                                                                                                               Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19G-binding Streptococcus Protein G variant coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 798 BP; 277 A; 161 C; 177 G; 183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 11; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Wroble MH;
                        Type 4 GX7809 protein G variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ64648 standard; DNA; 798 BP.
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105.00
72.73%
69.70%
13.51%
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86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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 13-MAR-1991 (first entry)
                                                                            Streptococcus sp GX7809
                                                                                                                                                                                                                                                                                                 Fahnestoc SR, Lee T,
                                                  Immunoglobulins; 19;
                                                                                                                                                                                                                                                                                                                         WPI; 1991-006758/01.
                                                                                                                                                                                                                                                                         (GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR10011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sp
                                                                                                                                                                                             14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
                                                                                                                                                       19-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-1995
                                                                                                    US4977247-A.
                                                                                                                              11-DEC-1990
                                                                                                                                                                                 19-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ64648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence may be incorporated into a non-pathogenic host eg. E.coli, where they may be expressed at high levels. The proteins have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 798 BP; 277 A; 161 C; 177 G; 183 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Streptococcus sp. Lancefield Group G strain.
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                                                                                                                                        Sequence encoding Protein G variant.
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86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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105,00
72,73%
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                                                             AAQ06009 standard; DNA; 798
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                                                                                                                (first entry)
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P-PSDB; AAR07004.
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14-FEB-1986;
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19-JUN-1987;
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LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu

21

ValAspSerProlleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu

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do Oy Ob

40

9

511 ACAGCAGCAGCAGCAGATACTGTGGCAGCAGCGGCAGCTGAAAATGCTGGGCAGCA- 569

ВР.

AAN91099 standard; DNA; 798

570 GCTTGGGAAGCAGCGGCA 587

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RESULT 17

AAN91099 ID AAN

99

AlaLeuGluAlaLeuAla

61

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d

51 CTGGGGGAATTCAGAGACACTGGCTTTGCGTAATGAAGAGAGTGCTACAGCTGATTTG
41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp

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The present invention describes a construct for connecting an antibody or antibody fragment to a liposome. The construct comprises protein G' or antibody fragment to a liposome. The construct comprises protein G' and a linking molety for connecting the protein G' to the liposome.

Also described are: (1) a cliposomal delivery vehicle comprising: (a) a cliposome; and (b) a connecting molety connected to the liposome, which specifically binds the Fc region of an antibody, for connecting the control of the liposome; by providing a construct comprising a linking molety and a connecting molety and a connecting molety and a connecting molety and a connecting molety and connecting molety and a connecting molety and a connecting molety and a connecting molety and the construct and sonicating the liposome, for binding to binding moleties are exposed on a surface of the liposome, for binding to binding molety, and to facilitate the binding between them. The connecting molety, and to facilitate the binding between them. The products can be used for the delivery of diagnostic or therapeutic gent, e.g. antibiotics, antidepressants, antidepressants, antitumourlgenics, antivirals, cytokines, hormones, imaging agents. Connecting molety provides a liposomal delivery complex having improved connecting molety provides a liposomal delivery complex having improved connecting molety provides a liposomal delivery complex beying improved the connecting molety provides a liposomal delivery complex provides a liposomal delivery complex provides a liposomal delivery complex provides a liposomal delivery complex provides a liposomal delivery complex provides a provide the connecting molety provides a liposomal delivery complex provides a liposomal delivery complex provides a liposomal delivery complex provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome provides a liposome p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New liposome constructs comprising a liposome connected to an antibody, used, e.g. for delivery of cytotoxic agents to malignant cells -
liposomal delivery complex; connecting moiety; antibody; Fc region; diagnosis; therapeutic agent; antibiotic; antidepressant; antiviral; antitumourigenic; cytokine; hormone; imaging agent; neurotransmitter; stimulant; cytotoxic agent; malignant cell; ss.
                                                                                                                                                                                                                                                                                                                                             /transl_except= (pos:705..707,aa:Met)
                                                                                                                                                                                                                                                                                              /*tag= b
/product= "protein G'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an unidentified protein and protein G'
                                                                                                                                                                                    Location/Qualifiers
292..603
/*tag= a
705..1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US11177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0086347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-062383/05.
P-PSDB; AAY57610, AAY57611.
                                                                                                                                     Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDGS-) SDG INC
                                                                                                                                                                                                                                                                                                                                                                                                    W09959643-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lau JR;
                                                                                                                                                                                       Key
CDS
                                                                                                                                                                                                                                                                  CDS
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Protein G; immunoglobulin; Fc receptor; ds.

Streptococcus sp.

WO8810306-A. 29-DEC-1988.

(first entry)

04-JUL-1990

AAN91099;

Protein G gene variant.

88WO-US02084 87US-0063959

20-JUN-1988; 19-JUN-1987;

SQ Sequence 1576 BP; 572 A; 270 C; 330 G; 404 T; 0 other;

Alignment Scores:

Pred. No.:

142.00

Matches:

Percent Similarity:

60.61%

Mismatches:

Best Local Similarity:

18.28%

Indels:

1 Gaps:

1 Gaps:

US-09-847-539A-6 (1-159) x AAZ47931 (1-1576)

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24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAla 36
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              g
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US-09-847-539A-6 (1-159) x AAN91099 (1-798)

Gene encodes protein G variant of non-pathogenic streptococcus allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones

277 A; 161 C; 177 G; 183 T; 0 other;

and treatment of disease

Sequence 798 BP;

Alignment Scores:

.. 9

798 23 1 9 0 0

Length: Matches: Conservative: Mismatches: Indels:

1.04e-05 105.00 72.73% 69.70% 13.51%

Best Local Similarity:

Query Match:

Percent Similarity:

Gaps:

of

Cloned protein G variant genes - expressing proteins having immunoglobulin-binding properties protein G and derived from Streptococcus sp.

WPI; 1989-023848/03. P-PSDB; AAP94785.

(GENE-) GENEX CORP

Fahnestock SR;

Claim 4; Page 83; 116pp; English

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796 ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCGGCAGCTGAAAATGCTGGGGGCAGCA 855
                                                                                                                                                                                                                                                                                                                                  A 2.4kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7805 using the 1.9kb Protein G coding sequence from Streptococcus GX7809. The Protein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus strain G 148; protein G'; protein G primer; liposome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 LysLysGlnAlaileGluAspLysGluAlaThrThrAlaileGluAlaAlaSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ValAspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
                                                                                                                                                                                                                                                                          New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy
     /transl_except= pos:2350..2352, aa:Gly
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37
4
25
0
                                                                                                                                                                                                                                                                                                                                                                                                                          other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                     (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB
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                                                                                                                                                                                                                                                                                                              Example 5; Fig 9; 48pp; English.
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                                                                                              86US-0829354.
86US-0854887.
87US-0063959.
88US-0209236.
90US-0540169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.05e-12
155.00
62.12%
56.06%
                                                                         86US-0829354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              856 GCTTGGGAAGCAGCGGCA 873
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                                                                                                                                                                                                                                    WPI; 1994-159179/19.
P-PSDB; AAR62944.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2383 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                              Fahnestock SR;
                                                                                                                       19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                         14-FEB-1986;
                                                                                                 14-FEB-1986;
23-APR-1986;
                                                 17-MAY-1994
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                                                                                                                                                       Protein G gene product may be modified allowing the variant to be imobilised and exhibit different binding profiles. The bound protein is useful in purification and detection of Igs and framents.
                                                                                                                                                                                                                                                                                                                                                        ValAspSerProlleGluGlnProArglleIleProAsnGlyGlyThrLeuThrAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                      21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                            Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus Protein G gene derived from strain GX7805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aa:Gln
aa:Leu
aa:Gly
                                                                                                                                                                                                         Sequence 2383 BP; 867 A; 409 C; 481 G; 626 T; 0 other;
                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_except= pos:1381..1383,
/transl_except= pos:1702..1704,
/transl_except= pos:1972..1974,
                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                               US-09-847-539A-6 (1-159) x AAQ10002 (1-2383)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                   Wroble MH;
                                                                                                                                Disclosure; Fig 9; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ75036 standard; DNA; 2383
                                                                                                                                                                                                                                           2.05e-12
155.00
62.12%
56.06%
19.95%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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/*tag= b
558..564
/*tag= c
577..2358
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                                 Fahnestoc SR, Lee T,
                                                        WPI; 1991-006758/01.
P-PSDB; AAR10005.
           (GENE-) GENEX CORP
                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                Alignment Scores:
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-35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10_signal
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P-PSDB; AAR07014
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                                                                                                                                                                                                              ACAGCAGCAGCAGTAGCCGATACTGTGGCAGCAGCGCAGCTGAAAATGCTGGGCAGCA 856
                                   A 1.9kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7809. The Protein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains
                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                   1 ValAspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu
                                                                                                                                                                                                                                        21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
                                                                                                                                                                                                                                                                           41 LysLysGlnAlalleGluAspLysGluAlaThrThrAlalleGluAlaAlaSerSerAsp
                                                                                          Sequence 1950 BP; 706 A; 323 C; 398 G; 523 T; 0 other;
                                                                                                                     1950
37
4
25
0
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoding Protein G with three active sites.
antibody detection and purification and for therapy
                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                  Streptococcus sp. Lancefield Group G strain
                                                                                                                                                                                   US-09-847-539A-6 (1-159) x AAQ64644 (1-1950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..2355
/*tag= a
                  Example 2; Fig 3; 48pp; English
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155.00
62.128
56.068
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86US-0829354.
86US-0854887.
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87US-0063959
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                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENEX
                                                                        are claimed.
                                                                                                            Alignment Scores:
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19-JUN-1987;
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23-APR-1986,
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                                                                                                                                                        Query Match:
DB:
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796 ACAGCAGCGGTAGCCGATACTGTGGCAGCAGCGGCAAAATGCTGGGGCAGCA 855
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                                                                                                                                                                                                                                                                                                                                                                                                                  21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 LysLysGlnAlaileGluAspLysGluAlaThrThrAlaileGluAlaAlaSerSerAsp
                                                                                  Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed
                                                                                                                         The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                              2383
37
4
25
0
                                                                                                                                                                                   T; 0 other;
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                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                    Sequence 2383 BP; 867 A; 411 C; 479 G; 626
                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6 (1-159) x AAQ06019 (1-2383)
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577..2355
/*tag= a
                                                        Disclosure; Flg 9; 48pp; English.
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155.00
62.12%
56.06%
19.95%
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86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
88US-0209236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AlaLeuGluAlaLeuAla 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulins; Ig; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sp GX7805
                                                                                                                                                                                                                                                                          Best Local Similarity:
                            immunoglobulin.
                                                                                                                at high levels.
                                                                                                                                                                                                                                                           Percent Similarity:
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14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
                                                                                                                                                                                                                Alignment Scores:
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DB:
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Alignment Scores:
Pred. No.:
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                                                                       41 LysLysGlnAlalleGluAspLysGluAlaThrThrAlalleGluAlaAlaSerSerAsp 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immobilised protein G variants - used for detection, isolation and purificn. Immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1950 BP; 706 A; 323 C; 398 G; 523 T; 0 other;
 37
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                                                                                                                                                                                                                                                                                                    Sequecne encoding Streptococcus GX7809 protein G.
Matches:
Conservative:
Mismatches:
Indels:
                                      Gaps:
                                                      US-09-847-539A-6 (1-159) x AAQ06017 (1-1950)
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
578..2248
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 8; 52pp; English
                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                            AAQ10001 standard; DNA; 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-0354264.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                                                                                857 GCTTGGGAAGCAGCGGCA 874
                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-0354264
                                                                                                                                                                                      AlaLeuGluAlaLeuAla 66
                                                                                                                                                                                                                                                                                13-MAR-1991 (first entry)
155.00
62.12%
56.06%
19.95%
                                                                                                                                                                                                                                                                                                                      Immunoglobulins; Ig; ds.
                                                                                                                                                                                                                                                                                                                                        Streptococcus sp GX7809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fahnestoc SR, Lee T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-006758/01.
P-PSDB; AAR10004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE-) GENEX CORP.
       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
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41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp 60
                                                                                                                                                                      21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 40
                                                                                                                 SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant streptococcal protein G variants - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus Protein G gene derived from strain GX7809
1950
37
4
25
0
             Matches:
Conservative:
Mismatches:
Indels:
  Length:
                                                                 Gaps:
                                                                                          US-09-847-539A-6 (1-159) x AAQ10001 (1-1950)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= Protein_G
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465..470
/*tag= a
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87US-0063959.
87US-0209236.
90US-0540169.
92US-0871539.
1.57e-12
155.00
62.12%
56.06%
19.95%
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                                                                                                                                                                                                                                                                                               61 AlaLeuGluAlaLeuAla 66
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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/*tag= b
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578..1924
/*tag= d
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P-PSDB; AAR53290.
                    Percent Similarity:
Best Local Similarity:
Query Match:
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23-APR-1986;
19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
21-APR-1992;
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-35_signal
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677 GITGATICACCAATCGAAGATACCCCAATTATTCGTAATGGTGGTGAATTAACTAATCTT 736
                                                                                                                                                                                                                 797 ACAGCAGCGGTAGCCGATACTGTGGCAGCAGCGGCAGAAATGCTGGGGCAGCA 856
                                                                                                                                                                                               41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed at high levels.
The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                  Recombinant Protein G variants - obtd, using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1950 BP; 706 A; 323 C; 398 G; 523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sp. Lancefield Group G strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                   US-09-847-539A-6 (1-159) x AAN91094 (1-1950)
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578..1921
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3a-c; 48pp; English.
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86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoding Protein G.
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                                                                                                                                                                                                                                                              61 AlaLeuGluAlaLeuAla 66
||| || || || || || 857 GCTTGGGAAGCAGCGGCA 874
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P-PSDB; AAR07012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1988;
14-FEB-1986;
23-APR-1986;
17-FEB-1987;
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Pred. No.:
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                                677 GTTGATTCACCAATCGAAGATACCCCAATTATTCGTAATGGTGGTGAATTAACTAATCTT 736
                                                                                                      41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloned protein G variant genes - expressing proteins having immunoglobulin-binding properties protein G and derived from Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
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37
4
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Mismatches:
Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                              AAN91094 standard; DNA; 1950 BP
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155.00
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578.1918
/*tag= a
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/*tag= c
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/*tag= b
565..571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-023848/03.
P-PSDB; AAP95030.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                      Protein G gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fahnestock SR;
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-35_signal
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RBS CDS

AAN91094 RESULT

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41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                                                                                                                                                              Protein G; immunoglobulin; Fc receptor; ds.
                                                                                                                                  AAN91093 standard; DNA; 1950
                                                                         856 GCTTGGGAAGCAGCGGCA 873
                                                                                                                                                                               (first entry)
                                                           61 AlaLeuGluAlaLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-023848/03.
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                                                                                                                                                                                                       Protein G gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fahnestock SR;
                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-1987;
                                                                                                                                                                               04-JUL-1990
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-35_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed at high levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1949 BP; 705 A; 323 C; 398 G; 523 T; 0 other;
                                                                    Sequence encoding Protein G with two active sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                    Streptococcus sp. Lancefield Group G strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8a-c; 48pp; English,
                                                                                                                                            Location/Qualifiers
577..1920
 BP
AAQ06018 standard; DNA; 1949
                                                                                                                                                                                                                                                                                                                                      88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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155.00
62.12%
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465..470
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487..492
/*tag= c
565..571
/*tag= d
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-297491/39.
                                                                                             Immunoglobulin; ds.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding Proteir
immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                     14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                             17-JAN-1991
                                                                                                                                                                                                                                                                  US4956296-A.
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                                                                                                                                                                                                       -10_signal
                                                                                                                                                                               -35_signal
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DB:
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87US-0063959 88WO-US02084

Location/Qualifiers 465..470 /*tag= c

Sp

/*tag= d 578..1918 /*tag= a

/*tag= b 565..571 487..492

BP.

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Gene encodes protein G of non-pathogenic streptococcus sp. allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones and trearment of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ValaspSerProileGluGlnProArgileileProAsnGlyGlyThrLeuThrAsnLeu 20
                      expressing proteins having immunoglobulin-binding properties of protein G and derived from Streptococcus sp.
                                                                                                                                                                                                                                          Sequence 1950 BP; 705 A; 323 C; 398 G; 524 T; 0 other;
                                                                                                                                                                                                                                                                                                         1950
37
4
25
0
                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Cloned protein G variant genes -
                                                                                                                                                                                                                                                                                                         1.57e-12
155.00
62.12%
56.06%
19.95%
                                                                                       Disclosure; ; 11pp; English.
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Best Local Similarity:
Query Match:
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protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain AP49. The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 LysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLys 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 CAATCAGATAACGCTGCTAGTAGCGCCTTAGAAGCATTAGCGGATCAAGCAGAAGCGTTTA
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/note= "Does not include stop codon"
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain KTL9. The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                      New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
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Mismatches:
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                                         99WO-GB03631
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P-PSDB; AAY71043.
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Query Match:
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                                         02-NOV-1999;
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The patent discloses a new family of proteins termed GRAB (protein Grelated alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to
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                                                                                                                                                                                            Streptococcus pyogenes strain AP49 partial GRAB protein encoding DNA.
                                                                               61 GGCAATGCTCCAGAAAAACTGGCATTACGTAATGAAGAAGAAGAGCATTGATGATTAAAA
                                                                                                                               LeuGlualaLeualaaspGlnThrAspAlaLeuGlnSerGluGlualaalaValValLys
                                                                                                                                                             181 TTAGAAGCATTAGCGGATCAAACAGACGCTTTACAATCAGAAGAAGCTGCGGTTGTTAAA
22 GlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLys
                                                                LysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                             142 GluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGlu 156
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37..852
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                                                                                                                                                                                                             protein; protein G related alpha2M binding protein; vaccine;
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750.00
99.35%
99.35%
96.53%
                                                                              AAD00562 standard; DNA; 469
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/*tag= a
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
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02-NOV-1999; 02-NOV-1998;

Bjorck LH,

New Co.g

11-MAY-2000

composition

Query Match:

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protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding full-length GRAB protein from S. pyogenes strain SF370.
                                                                                                                                                                                                                                                                                                                                                                                              218
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                                                                                                                                                                                                                  ValAspSerProlleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu
                                                                                                                                                                                                                                                              LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes strain KTL3 partial GRAB protein encoding
                                                                                                               764
159
0
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0
                                                                              BP; 279 A; 131 C; 159 G; 195 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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/product= "GRAB protein"
/partial
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1..504
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Best Local Similarity:
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain KTL3.
                                                                                                                                                                                             New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GTGGACTCACCTATCGAACAGCCTCGAATTATTCCAAATGGCGGAACCTTAACTAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGlu 156
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156
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Matches:
Conservative:
Mismatches:
Indels:
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100.00%
97.81%
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Best Local Similarity:
Query Match:
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WO200026240-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 504
                                                  02-NOV-1999;
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P-PSDB; AAY71042.
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                                                                                                              AAD00559;
                                                                              RESULT
                                                                                                              The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus yapogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding full-length GRAB protein from S. pyogenes strain SF370.
                                                                                                                                                                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 100
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                                                                                                                                                                                                                                                                                                                                   Sequence 654 BP; 234 A; 118 C; 143 G; 159 T; 0 other;
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159
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Matches:
Conservative:
Mismatches:
Indels:
                                                   "Mature GRAB protein"
       "GRAB protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                         (1-654)
                                                                                                                                                                                                                            Claim 13; Page 63; 67pp; English.
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777.00
100.008
100.008
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                                                                                                                      98GB-0023975
/*tag= a /product= "
1..99 /*tag= b | 100..651 /*tag= c /product= "
                                                                                                                                                         Bjorck LH, Rasmussen M;
                                                                                                                                       (ACTI-) ACTINOVA LTD.
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Best Local Similarity:
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                                                                                                     02-NOV-1999;
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                                                                                    11-MAY-2000
                sig_peptide
                                 mat_peptide
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The patent discloses a new family of proteins termed GRAB (protein Grelated alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to
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GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.
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                                                                                                                                                                                                                                                                                           Streptococcus pyogenes strain SF370 GRAB protein encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "GRAB protein"
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159..710
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/*tag=
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - nu	OM protein – nucleic search, using frame_plus_p2n model
Run on:	October 13, 2002, 02:10:56 ; Search time 229.572 Seconds (without alignments) 1189.122 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-847-539A-6 777 1 VDSPIEQPRIIPNGGTLTNLKKEERQNVNTLPTTGEESNP 159
Scoring table:	BLOSUM62 Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
Searched:	1736436 seqs, 858457221 residues
Total number of	Total number of hits satisfying chosen parameters: 3472872
Minimum DB seq length: 0	Length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Maximum DB seq length: 2000000000

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N_Geneseq_032802:*

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5: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*

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18: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

20: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

21: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

22: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

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24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

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26: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

27: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:* Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
	77	00	654	~	AAD005	Streptococcus
7	777	100.0	764	21	355	Streptococcus pyog
m ·	9	۲.	0	21	920	treptococcus
4.0	n c	٠,	Oι	7 5	AAD00562	treprococcus
n u	2	, a	2 0	7 7	AAD00363	reproceeds
) r	י כ			1 =	30	cieptococcus
~ oc	'n	. 6	r LC	10	16	ache
9	S	. 6	'n	10	601	rotein G gene
10	S	6	LO.	11	501	e encoding
11	3	9.	ın	12	AAQ10001	ding
12	2	6.	io i	15	AAQ64644	treptoco
13	S	σ,	ന	Ξ:	AAQ06019	Sequence encoding
4.	s t	٠. د	20 0	77	AA010002	Sequence encoding
15	Ω-		a a	15	AAU/5036	0 1
7.0	<i>t</i> <		S 0	17	AM64/931	protein G cene var
18	0	. n	0	11	AA006009	1ng
19	0	m	CO.	12	AAQ10007	pro
20	0	ω.	c C	15	AAQ64648	IgG-binding Strept
21	93	ď	œ	23	AAS84496	DNA encoding novel
22	93	ď	മ	23	AAS80225	nov
23	91	∹.	LO I	16	AAQ86080	S. dysgalactiae ma
24	91	i,	n	10	AAQ89197	S. dysgalactise ma
7.5	3 8	-i -	20	, a	AAN/U/5/ ABI 20337	Sequence encoding
2 6	200	1 -	4	, כ ל	AB1.20336	Drosophila melanog
1 (1	86		341	53	AAS82434	DNA encoding novel
29	82	ö	C	16	AAQ89196	S. dysgalactiae mi
30	84	٥.	C)	23	ABL03677	Drosophila melanog
31	84	٠.	· O	23	ABL03676	
35	83	٥,	-	16	AAQ84884	n casset
m (	83	٠.	0	16	AAQ84887	Chimearic synthet1
ω c	m c		~ ·	16	AAQ8486	protein
. r			ب ب	7 6	AAC38/90	Arabidopsis thaita
3 2 2 2	0 G		o -	2 4 5	AAS18114 /	2000
. ee	81		+ 40	23	AAS77362	DNA encoding novel
39	81	0	LO CO	23	AAS89837	encoding nove
4	77	6	œ	23	AAS74086	encoding
c 41	77	•	_	23	AAS79794	encoding nov
4	16		-	22	AAH52591	spidermidia
43	92	٠	0	22	AAH54801	. epidermidis
44	16	•	·	17	AAT34578	netochore pro
45	75	•	a,	22	ААН90726	FE 3
					ALIGNMENTS	
RESILL	_					
000						
XX AA	AAD00560 s	standard;	i; DNA;	654	BP.	

Streptococcus pyogenes strain SF370 GRAB protein coding region. (first entry) 29-AUG-2000 AAD00560; 

GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.

Streptococcus pyogenes.

Location/Qualifiers 1..654 Key

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```
APPLICANT: Narva, Kenneth E
APPLICANT: Schwab, George E
APPLICANT: Schwab, George E
APPLICANT: Payne, Jewel M
TITLE OF INVENTION: Gene Encoding No. 5439881el Nematode-Active
TITLE OF INVENTION: Toxins Cloned from Bacillus thuringiensis Isolates
TITLE OF INVENTION: Toxins Cloned from Bacillus thuringiensis Isolates
TITLE OF INVENTION: Toxins Cloned from Bacillus thuringiensis Isolates
CORRESPONDENCE: 18
ADDRESSEE: Jeff Lloyd
STREET: 2421 N.W. 41st Street
CITY: Gainesville
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.8%; Score 41; DB 1; Length 395
Best Local Similarity 40.9%; Pred. No. 1.9e+02;
Matches 9; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 3.20UN
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,783
FILING DATE: 19930419
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
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TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 905-81010
                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACLILUS THURINGIENSIS
INDIVIDUAL ISCLATE: PS69D1
IMMEDIATE SOURCE:
CLONE: E. COli NM522(PMYC2317) NRRL B-18816
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INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08049783 Patent No. 5439881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 EELLKKVDDLKKELEAAIKAEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 EALADQTDALQSEEAAVVKADN 26
                              SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
TYPE: AMINO ACID
                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
1..395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-07-876-280-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-049-783-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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Patent No. 5262158
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Payne, Jewel M.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESSONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1,7e+02;
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COMPUTRY: USA
ZIP: 3260
COMPUTRY: SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRATING DATA: 19920430
FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01676A
FILING DATE: 19930226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.8%; Score 41; DB Best Local Similarity 43.5%; Pred. No. 1.7e Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842,644
FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPET, IVEC P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: STAMBROOK I
TELECOMMUNICATION INFORMATION:
TELECHNUME: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 ADSLMQLARQVSRLESGQAALPK 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein
PCT-US93-01676A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                     FILING DATE: 19
CLASSIFICATION:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 39
US-07-876-280-9
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APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: JUNBERG, MARTHAIN
APPLICANT: MUBLICR, Hans-Peter
APPLICANT: RANTAMAKI, Liisa K.
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Standard No.
APPLICANT: Standard No.
APPLICANT: Standard No.
APPLICANT: Standard No.
APPLICANT: Standard No.
AUTAGENICITY TESTING USING REPORTER
TITLE OF INVENTION: GENES WITH MODIFIED METHYLATION FREQUENCIES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/669,408B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 61743/102
TELECOMMUNICATION INFORMATION:
TELEPRAN: (202)672-5309
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE (202)672-5309
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%; Score 41; 47.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/669,408B
03-JUL-1996
                                         Sequence B, Application US/08669408B Patent No. 6100055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SDALEALADQTDA--LQSEEAAV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 173 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 419 Seve
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
21P: 20007-5109
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
PCT-US93-01676A-4
                       US-08-669-408B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                            RESULT 35
US-09-568-486-6
Squence 6, Application US/09568486
Sequence 6, Application US/09568486
Patent No. 6355459
GENERAL INFORMATION:
APPLICANT: Schuph, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENER FOR THE BIOSYNTHESIS OF EPOTHILONES
TITLE OF INVENTION: GENER FOR THE BIOSYNTHESIS OF EPOTHILONES
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SSOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 6
LENGTH: 3798
LENGTH: 3798
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Sequence 6, Application US/09568472

Petent No. 6358719

GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
MUMBER OF SEO ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
SEOTUMBER: PATENTIN VET. 2.0
SEOTUMBER: PATENTIN VET. 2.0
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                         Db 3434 DALRSMAEAGAEVQIVEADVARRDDVA 3460
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2 DALEALADQTDALQSEEAAVVKADNAA 28
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ORGANISM: Sorangium cellulosum
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US-09-568-486-6
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Matches 10; Conserva
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Gaps

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RESULT 34

US-09-568-480-6

Sequence 6, Application US/09568480

Patent No. 6355458

GENERAL INFORMATION:
APPLICANT: Schupp, Thomas

APPLICANT: Light No. James

APPLICANT: Light No.
APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Gorlad, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT FILING DATE: 1999-66-17

PRIOR APPLICATION NUMBER: 09/335,409

PRIOR APPLICATION NUMBER: 09/335,409

PRIOR SEQ ID NOS: 30

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 6
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molhar: Istvan
APPLICANT: APPLICANT: APPLICANT: APPLICANT: Oyr, Devon
APPLICANT: Gyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
               Score 42; DB 4; Length 3798;
Pred. No. 2e+03;
6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 42; DB 4; Length 3798; ilarity 37.0%; Pred. No. 2e+03; Conservative 6; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DAFE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3434 DALRSMAEAGAEVQIVEADVARRDDVA 3460
                                                                                                                             Db 3434 DALRSMAEAGAEVQIVEADVARRDDVA 3460
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                                                                                                    2 DALEALADQTDALQSEEAAVVKADNAA 28
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US-09-567-969-6
; Sequence 6, Application US/09567969
; Patent No. 6355457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Sorangium cellulosum
                 32.6%;
ilarity 37.0%;
Conservative
                 Query Match
Best Local Similarity
Matches 10; Conserva
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Matches 10; Conserva
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APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lirkle, Ross
APPLICANT: GIRLS
FOR THE BLOSYNTHESIS OF EPOTHILONES
TITLE OF INVENTION: GENES FOR THE BLOSYNTHESIS OF EPOTHILONES
TITLE OF INVENTION: GENES
CURRENT APPLICATION UNBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 66
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APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                   Length 2890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 3; Length 3798;
Pred. No. 2e+03;
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Pred. No. 1.5e+03;
6; Mismatches 11.
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
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Sequence 6, Application US/09568102
Patent No. 6346404
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                                                                                                RESULT 31
US-09-335-409-6
; Sequence 6, Application US/09335409
; Patent No. 6121029
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US-09-335-409-6
                                                                                              ; ORGANISM: Sorangium cellulosum
US-09-413-814-67
                                                                                                                                                               Query Match 32.6%;
Best Local Similarity 37.0%;
Matches 10; Conservative 6
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Best Local Similarity 37.0%;
Matches 10; Conservative (
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 3798
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
             SOFTWARE: Paten
SEQ ID NO 67
LENGTH: 2890
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Length 427; Indela

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Query Match 32.6%; Score 42; DB 4; Le Best Local Similarity 47.4%; Pred. No. 1.5e+02; Matches 9; Conservative 5; Mismatches 5;
                                                           LENGTH: 427
TYPE: PRT
ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Brevibacterium lactofermentum
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18-09-521-668B-20
Sequence 20, Application US/09521668B
Patent No. 6303383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/09413814
Patent No. 6225064
  NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                  256 LDMLADQSDAGEDMDAVLV 274
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                                        SEQ ID NO 18
LENGTH: 427
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APPLICANT: NANO, SOBEI
APPLICANT: KANO, SOBEI
APPLICANT: KIMURA, EIICHIRO
APPLICANT: MATANATSU, TSUYOSHI
TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
FILE REFERENCE: 0010-1099-0
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT APPLICATION NUMBER: JP 11-69896
PRIOR PPLING DATE: 1999-03-16
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                                                                                                                                                                                        APPLICANT: Briles, David E.
APPLICANT: Hollingshead, Susan
APPLICANT: Becker, Robert
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCCCCAL SURFACE
TITLE OF INVENTION: PROYEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURLIS, MOTILS & SAFFORD
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLILIG DATE: US/08/710,749
FLILIG DATE: 435
CLASSIFICATION: 435
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27;
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Pred. No. 27;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                      Sequence 18, Application US/09521668B
Patent No. 6303383
GENERAL INFORMATION:
                                                                                                              %3-08-710-749-8

Sequence 8, Application US/08710749

PATENT NO. 5955089

GENERAL INFORMATION:

APPLICANT: Briles, David E.
2 DALEALADQTDALQSEEAAVVKAD 25
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45.5%;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.5'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
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: USA
                                                                                                                                                                                                                                                                                                                                                                              New York
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APPLICANT: NAKAMURA, JUN
APPLICANT: NAKAMURA, JUN
APPLICANT: NAKAMURA, EICCHIRO
APPLICANT: MATSUI, KAUHIKO
APPLICANT: MATSUI, KAUHIKO
APPLICANT: MATSUI, KAUHIKO
APPLICANT: NAKAMATSU, TSUYOSHI
TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
FILE REFERENCE: 0010-1093-0
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Cougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 32.6%; Score 42; DB 4; Le
Best Local Similarity 47.4%; Pred. No. 1.5e+02;
Matches 9; Conservative 5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 43; DB 1; Length 744; 38.5%; Pred. No. 2.1e+02; tive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Denoif, Bradley S.
APPLICANT: Denoif, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATE:
APPLICATION TOWNER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFCATION: 435.
ATTORNEY AGENT INPORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: X 8231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FILING DATE: 17-MAR-1993
APPLICATION WUMBER: 68 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 577370071s, Allen E.
REGISTRATION NUMBER: 34,490
REPERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEFAX: (415) 387-1125
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: LILLY CORPORATE CENTER STATE: INDIANAPOLIS CONTACT IN CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONTACTOR CONT
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Best Local Similarity 38.5
Matches 10; Conservative
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MOLECULE TYPE: protein
US-08-804-227C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-764-100-25
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-804-227C-5
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APPLICANT: Van Grinsven J., Martinus Q.
APPLICANT: De Haan, Petrus T.
APPLICANT: Gielen L., Johannes J.
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic TITLE OF INVENTION: Compounds.
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 33.3%; Score 43; DB 4; Length 418; Best Local Similarity 33.3%; Pred. No. 1e+02; Matches 9; Conservative 5; Mismatches 13; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DIASPECTUE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARR: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,846
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DICKIRSON, TOOM Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 DHQETLGDSLEAIAEQKAGIFKAGKKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/032,235
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ADDRESSEE: Sandoz Agro, Inc
STREET: 975 Callfornia Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                       19103
                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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                                              COUNTRY:
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   Indels
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APPLICANT: Dearson, Stewart C.
TITLE OF INVENTION: NOVEL folC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                167 DHQETLGDSLEAIAEQKAGIFKAGKKA 193
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                                                                                                                                                                         Sequence 2, Application US/08934846 Patent No. 5882898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DICKINSON, Todd Q
REGISTRATION NUMBER: 28,354
REPERENCE/POCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09238557
Patent No. 6165472
GENERAL INFORMATION:
                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca CTITLE OF INVENTION: MOVEL FOLC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
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Best Local Similarity
9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   19103
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                                                                                                                                    RESULT 23
US-08-934-846-2
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                13; Indels
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Sequence 4, Application US/09238557

Belent No. 6165472

GENERAL INFORMATION:

APPLICANT: Pearson, Stewart C.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCES: ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre

CITT: Philadelphia

COUNTY: US

7.10.
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SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                             ATTORNEY AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELECHONE: 215-994-2252
TELEPHONE: 215-994-2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,846
                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-934-846-4
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33.38;
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Best Local Similarity 33.3%;
Matches 9; Conservative
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER:
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Indels 13;
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Pred. No. 1.6e+02;
6; Mismatches 9; Indels 13
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Patent No. 5882898
GENERAL INFORMATION:
PAPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folc
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                               SOFTWAREN PAILLIAN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 3 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
APPLICATION NUMBER: GB 91-810079.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTICATION NOMBER 105-FEB-1991
ATTORNEY_AGENT INFORMATION:
NAME: Pfelifer, Hesna J.
REGISTRATION NUMBER: 22.640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMDUNICATION INFORMATION:
TELEFAX: (908)522 6940
TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARATERISTICS:
LENGTH: 711 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:: || || || 555 NDSVPTLAQMIDKAIELLSKNEKGFFLQVEGASIDKQDHAA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SDALEALADQTDA-----LQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FSSLENC DOS
GURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.7
Best Local Similarity 31.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
NUMBER OF SEQUENCES:
                                                                                                           New Jersey
: USA
                                                                                   CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-465-473B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
US-08-934-846-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                   Sequence 7, Application US/08235838

Patent No. 5571894

GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5571894man
APPLICANT: Arich, Ina-Waria
APPLICANT: Azickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43.5; DB 1; Length 711;
Pred. No. 1.6e+02;
6; Mismatches 9; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Antibodies Specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 91-810079,3
APPLICATION NUMBER: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elner, James Scott
REGISTRATION NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SDALEALADQTDA------LQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                              SSEE: CIBA-GEIGY Corporation
7: 7 Skyline Drive
Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ins-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-465-473B-7; Sequence 7, Application US/08465473B; Patent No. 5939531; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 31.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-235-838-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10532
                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Length 471;

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LENGTH: 471 amino acid residues TYPE: amino acid
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Best Local Similarity 31.7%;
Matches 13; Conservative
      INFORMATION FOR SEQ ID NO:
                              SEQUENCE CHARACTERISTICS
                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                        STRANDEDNESS:
                                                                                                                                                                          ) ORGANISM:
PCT-US94-02539-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brate, E.M.
APPLICANT: Brate, E.M.
APPLICANT: Bridon, D.P.
APPLICANT: Jaffe, K.D.
APPLICANT: Jaffe, K.D.
APPLICANT: Mandecki, W.
APPLICANT: Mandecki, W.
APPLICANT: March, S.C.
APPLICANT: Wee, V.T.
TITLE OF INVENTION: Genetically Engineered Enzymes
TITLE OF INVENTION: Conjugates For Diagnostic Assays
CORRESPONDENCE ADDRESS:
ADDRESSE: ABBOTT LABORATORIES
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60^*C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:: || || || 315 NDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SDALEALADQTDA-----LQSEEAAVVKADNAA 28
CLASSIFICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/100,708
FILLING DATE: July 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WONG, WEAN Khing
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5324.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 938-3517
TELEFAX: (708) 938-3517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/ACENT INFORMATION:
NAME: Wong, Wean Khing
REGISTATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5324.PC.01
TELECOMMUNICATION INFORMATION:
TELEPAX: (708) 938-3517
TELEFAX: (708) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/02539
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acid residues
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: SoftPC
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: prote ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM:
US-08-657-392-31
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                                               Gaps
                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLUM IIFE: FLUCHY UIES.

COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,213B
FILING DATE: 12-Sep-1997
CLASSIFICATION: CUNKOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MACKIGHT, Kamrin T.
REGISTRATION NUMBER: ENZYCO-02550
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-795-8410
TELEPHONE: 415-797-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              RESULT 18
(Sc.08-298-213B-8
; Sequence 8, Application US/08928213B
; Patent No. 6238905
; GENERAL INFORMATION:
; Seville, Mark
; Seville, Mark
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                :(:: || || || 315 NDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAA 355
Score 43.5; DB 5; Pred. No. 1e+02; 6; Mismatches 9;
                                                                                     1 SDALEALADQTDA------LQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.7%; Score 43.5; DB 4; Best Local Similarity 46.2%; Pred. No. 1.2e+02; Matches 12; Conservative 7; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-928-213B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 EAMERLARRSDAL-SLEVALLEAGRA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DALEALADQTDALQSEEAAVVKADNA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 528 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
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APPLICANT: Galle, A.D.
APPLICANT: Mandecki, W.
APPLICANT: Mandecki, W.
APPLICANT: March, S.C.
APPLICANT: Muscell, J.R.
APPLICANT: Russell, J.R.
APPLICANT: Russell, J.R.
APPLICANT: Russell, J.R.
APPLICANT: Musc, V. T.
TITLE OF INVENTION: Genetically Engineered Enzymes And Their TITLE OF INVENTION: Conjugates For Diagnostic Assays
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 43.5; DB 5; Length 449; 31.7%; Pred. No. 95; ive 6; Mismatches 9; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|:: || || || 293 NDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LQSEEAAVVKADNAA 28
                                                                                                                                                                                            SOFTWARE: SOLLEC
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US94/02539
FILING DATE:
CLASSIFICATION:
ATTORNEY, FAGENT INFORMATION:
NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5324.PC.01
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (708) 938-3517
TELEFAX: (708) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: SOFTPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,392
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acid residues
TYPE: amino acid
STRANDEDNESS:
                                                     COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08657392
Patent No. 5843634
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brennan, C.A.
Bridon, D.P.
Jaffe, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 31.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brate, E.M.
APPLICANT: Brennan, C.
APPLICANT: Bridon, D.P
APPLICANT: Jaffe, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SDALEALADQTDA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 60064-3500
                                       Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-02539-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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APPLICANT: March, S.C.
APPLICANT: Russell, J.R.
APPLICANT: Russell, J.R.
TITLE OF INVENTION: Genetically Engineered Enzymes And Their TITLE OF INVENTION: Conjugates For Diagnostic Assays NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ABBOTT LABORATORIES
STREET: Once Abbott Park Road
CITY: Abbott Park Road
CITY: Abbott Park Road
CITY: Abbott Park Road
CITY: BABOTT LABORATORIES
STREET: Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: CCDS/MS-DOS
SOFTWARE: SoftPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,392
FILING DATE:
CLASSIFICATION NUMBER: US/08/657,392
FILING DATE:
APPLICATION NUMBER: 08/100,708
FILING DATE:
APPLICATION NUMBER: 08/100,708
RECIERRATION NUMBER: 33,561
REGIERRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5324.US.PI
TELECOMMUNICATION NUMBER: 5324.US.PI
TELECOMMUNICATION NUMBER: 5324.US.PI
TELECOMMUNICATION NUMBER: 53257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brate, E.M.
APPLICANT: Brate, E.M.
APPLICANT: Bradon, D.P.
APPLICANT: Jaffe, K.D.
APPLICANT: Mandecki, K.D.
APPLICANT: Mandecki, W.
APPLICANT: Mandecki, W.
APPLICANT: March, S.C.
APPLICANT: Wussell, J.R.
APPLICANT: Tue, V.T.
TITLE OF INVENTION: Genetically Engineered Enzymes
TITLE OF INVENTION: Conjugates For Diagnostic Assays
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 NDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.5; DB 2;
Pred. No. 95;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 449 amino acid residues TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9402539 GENERAL INFORMATION:
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One Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.7%;
Best Local Similarity 31.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (708) 938-35
TELEFAX: (708) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SDALEALADQTDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
PCT-US94-02539-2
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                                                                                                                                                                                                                 Length 383;
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                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: PCT/US94/04173
FILING DATE: 15-APR-1994
                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PH GENES AND THEIR USES NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMDALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,282
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 12176-34-1PC
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 543-5600
TELEFANE: (415) 543-5643
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.7%; Score 43.5; D
52.4%; Pred. No. 78;
tive 5; Mismatches
                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                               Score 43.5; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08657392
Patent No. 584364
GENERAL INFORMATION:
APPLICANT: Breanan, C.A.
APPLICANT: Bridon, D.P.
APPLICANT: Bridon, D.P.
APPLICANT: Wafft, G.A.
APPLICANT: Mandecki, W.D.
APPLICANT: Mandecki, W.
                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US94-04173-4; Sequence 4, Application PC/TUS9404173; GENERAL INFORMATION: APPLICANT:
  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            111 |:||:| | 11 | 244 LEARANQTEATLQTKDTGTVK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 LEARANQTEATLQTKDTGTVK 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LEALADOTDA-LOSEEAAVVK 23
                                                                                                                                                                                                                 33.7%;
52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 383 amino acids
amino acid
                                                                                                                                                                                                                                   Best Local Similarity 52.49
Matches 11; Conservative
                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-715-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
PCT-US94-04173-4
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SUCTAMEN: PAPLICATION DATA:
APPLICATION NUMBER: US/08/537,715
FILING DATE: 16-PEB 1996
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,282
FILING DATE: 16-APR-1993
PRIOR APPLICATION NUMBER: WO PCT/US94/04173
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BASILAN, REVID L.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chuck, George S.
APPLICANT: Chuck, George S.
APPLICANT: Courtney-Gutterson, Neal
APPLICANT: Courtney-Gutterson, Neal
APPLICANT: Mijjar, Charanjit S.
APPLICANT: Nijjar, Charanjit S.
APPLICANT: Raiston, Edward J.
TITLE OF INVENTION: PH Genes and Their Uses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                   Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.5; DE
Pred. No. 78;
5; Mismatches
                                                                                                                                                                                                        NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 12176-34-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acid
TYPE: amino acid
                                                vumber: PCT/US94/04173
15-APR-1994
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,282
FILING DATE: 16-ARR-1993
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08537715
Patent No. 5910627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LEALADQTDA-LQSEEAAVVK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.7%;
52.4%;
                   SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 15-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.4°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-04173-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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ò g 243 LEARANQTEATLQTKDTGTVK 263

ATTORNEY/AGENT INFORMATION:

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SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,715
FILING DATE: 16-FEB 1996
CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,282
FILING DATE: 16-APR-1993
PRIOR APPLICATION NUMBER: WO PCT/US94/04173
APPLICATION NUMBER: WO PCT/US94/04173
APPLICATION NUMBER: WO PCT/US94/04173
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: Ralston, Edward J.
TITLE OF INVENTION: PH Genes and Their Uses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION: PH GENES AND THEIR USES
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REPERDECA-DOCKET NUMBER: 012176-003410US
TELECOMMUNICATON INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 43.5; D
52.4%; Pred. No. 78;
tive 5; Mismatches
                                                                                                                                                                                               APPLICANT: Dooner, Hugó K.
APPLICANT: COUTINEY-GUITERSON, Neal
APPLICANT: Keller, Janis
APPLICANT: Nijjar, Charanjit S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US94-04173-2; Sequence 2, Application PC/TUS9404173; GENERAL INFORMATION:
                                                                                                   Sequence 2, Application US/08537715
Patent No. 5910627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LEALADQTDA-LQSEEAAVVK 23
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chuck, George S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.7
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-537-715-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
                                                                                       US-08-537-715-2
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                                                                                                                                                                                                                                                                                                                Length 514;
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                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/049,282B
FILING DATE: 16-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHUCK, George S.
APPLICANT: DOONER, Hugo K.
APPLICANT: COURTINEY GUTTERSON, Neal
APPLICANT: COURTINEY GUTTERSON, Neal
APPLICANT: NIJJAR, Charanjit S.
APPLICANT: RALSTON, Edward J.
TITLE OF INVENTION: PH GENES AND THEIR USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              Score 44; DB 2;
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.7%; Score 43.5; D
52.4%; Pred. No. 78;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/049,282B
16-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             240 SIKAQRQATQLLKEEEARLVESNNA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08049282B Patent No. 5534660
                                                                                                                                                                                                                                                                                                                                                                                                   3 ALEALADQTDALQSEEAAVVKADNA 27
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bastlan, Kevin L. RECTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 12.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 382 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.4 Matches 11; Conservative
                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-960-022-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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DB 2; Length 382; Indels

4 LEALADQTDA-LQSEEAAVVK 23

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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08960022 Patent No. 5976837 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AGOTDASQIEKAAVSQGGKA 22
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                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-961-083-192
                                                                                  COMPUTER READABLE FORM:
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Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                     Maryland
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Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 527;
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Patent No. 6096717
GENERAL INFORMATION:
APPLICANT: JATVIK, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts And Proteins
FILE REFERENCE: 2087-961422
CURRENT APPLICATION UNBER: US/08/745,404B
CURRENT FILING DATE: 1996-11-08
EARLIER PILING DATE: 1993-01-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 87;
4; Mismatches
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Pred. No. 82
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STREET: 9410 Key West Avenue
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                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/320,774
                                                                                                                                                                                                NAME: Brothan, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.5%;
Best Local Similarity 51.7%;
Matches 15; Conservative
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Best Local Similarity 51.7%;
Matches 15; Conservative
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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US-08-745-404-3
                                                                                                   CLASSIFICATION:
                                                                              FILING DATE
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US-08-745-404-3
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LENGTH: 552
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APPLICANT: Spaniding, Vikki
APPLICANT: Spaniding, Vikki
APPLICANT: Spaniding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: ENCORING THEM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,022
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; Sequence 9, Application US/09320774
; Patent No. 626545
; GENERAL INFORMATION:
    APPLICAPT: Jarvik, Jonathan W.
    TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
    TITLE OF INVENTION: TAGGING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS: 47
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Harris Brotman
; STREET: La Jolla
; CITY: La Jolla
; STATE: California
; COUNTRY: US
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Perent No. 5948677
GENERAL INFORMATION:
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harris Brotman
STREET: 202 Coast Blvd., Suite 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/762,106 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Brockman, Harris F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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Pred. No. 82
                       1 SDALEALADQTDALQSEEAAVVK--ADNA 27 :11:11 | 1 | 1 | 1 | 369 ADAVEAAAAELTA-QAEEAANAKWEADKA 396
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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COMPUTER READABLE FORM:
WEDJUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
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Best Local Similarity 51.7
Matches 15; Conservative
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; FRAGMENT TYPE: internal
US-08-762-106-9
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STATE: California
COUNTRY: US
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US-09-320-774-9
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                                   GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts And Proteins
FILE REFERENCE: 2087-961422
CURRENT APPLICATION NUMBER: US/08/745,404B
CURRENT FILING DATE: 1996-11-08
EARLIER APPLICATION NUMBER: 08/000,619
NUMBER OF SED ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 2
LENGTH: 516
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APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/320,774
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 80;
4; Mismatches
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51.7%; Pred. No. 80
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STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla
STATE: California
COUNTRY: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
Sequence 2, Application US/08745404B
Patent No. 6096717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 64-7428
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence B, Application US/09320774 Patent No. 6265545
                                                                                                                                                                                                                                                                                                                                                                                     34.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
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Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                        ORGANISM: Chlamydomonas
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Best Local Similarity
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US-09-320-774-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
US-09-521-668B-18
US-09-521-668B-20
US-09-335-409-6
US-09-335-409-6
US-09-568-102-6
US-09-568-102-6
US-09-568-480-6
US-09-568-480-6
US-09-568-480-6
US-09-568-480-6
US-09-568-472-6
US-08-69-408B-9
US-08-69-408B-9
US-08-316-301A-10
US-08-316-301A-10
US-08-316-301A-10
US-09-076-137-10
US-09-076-137-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08762106; Patent No. 5948677; GENERAL INFORMATION: APPLICANT: Javvik, Jonathan W. TITLE OF INVENTION: TITLE OF INVENTION: TAGING NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: Harris Brotman STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.5%; Score 44.5; 51.7%; Pred. No. 80
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NAME: Brotman, Harris F.
REGISTRATION UNDBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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internal
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                       2890
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
    ; TOPOLOGY: lin.; MOLECULE TYPE: ; FRAGMENT TYPE: US-08-762-106-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-745-404-2

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US-08-720-774-9

US-08-745-404-3

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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REFERENCE

REMARK COMMENT

FEATURES

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NVAKUVVVVEITINILLEHIANSY NEETASPYADALAGGAPOLVASOLAMSKINIVYAQO
VVVLLGOTKGETALIPLINSKILTSSOTTPDROKAHVPEGS 11 THYTROLIKULKEPEGL
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TKRUYTOKOVNEMANSLOYNINANTILYNY ENTUNGTVETVONOKKANTENDEN
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KFICEGAVEHWLLNLEFRMRETLQEILEGAKNTADLWDSGDKGREEWVEGYNAQIALL
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ITIDVHSRDVVEKFVIQKVSEAESFAWLSQLKFYWENKPDSDMHLRQTLRFPWEKDKN
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THMHKWSVLDGDIDPEWIESLNTVMDDNKVLTLVSNDRIFLTPQMRLIFEISNLRNAT
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                                                                                                                                                                                                                                                                                                                                 Lincoln,L.M., Asai,D.J., Forney,J.D., Terrell,S. and D'Souza,M.S. Blrect Submission
Submitted (25-JUN-199) Biological Sciences, Purdue University,
West Lafayette, IN 47907-1392, USA
Sequence update by submitter
On Jun 25, 1999 this sequence version replaced gi:3309592.
                                            3 (bases I to 14941)
Lincoln, L.M., Asai, D.J., Forney, J.D., Terrell, S. and D'Souza, M.S.
Direct Submission
Submitted (18-JUN-1998) Biological Sciences, Purdue University,
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    11. 14941
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                                                                                                                                                                                                                                   West Lafayette, IN 47907-1392, USA
4 (bases 1 to 14941)
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4980 t 2490 g 2373 c ๙ 5098 BASE COUNT ORIGIN

Alignment Scores:

Length: Matches: .. Q Pred

Conservative: Mismatches: Indels: Gaps: 819 51.00 75.00% 60.00% 39.53% Percent Similarity: Best Local Similarity: Query Match:

US-09-847-539A-6_COPY_59_86 (1-28) x AF072878 (1-14941)

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Search completed: October 13, 2002, 05:41:08 Job time : 474.909 secs

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Lincoli,L.M., Gibson,T.M., Asai,D.J. and Forney,J.D.
A gene knockout reveals that dynein beta heavy chain is required in
Tetrahymena thermophila
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Tetrahymena thermophila ciliary outer arm dynein beta heavy chain
(DYH4) gene, complete cds.
AF072878
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Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 14941)
                                                                                                                                                                                                                                                    /product="lron transport protein C" /protein_id="AAG20877.1"
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Matches:
Conservative:
Mismatches:
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complement(10189, .10842)
/gene="trkA3"
/note="TrkA3"
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Tetrahymena thermophila
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Best Local Similarity:
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Pred. No.:
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AF072878
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komaavykkaleteavgsgliieavoirniklpgoyadavekkevekoniekkonsio
vakarberkryoakgeaeaneivaesikdnpelikiryiealnodnstiyvgagsgag
itlikdvubeenks"
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                                                                                                                                                                                                                                                              Direct Submission
Submitted (14-JUL-2000) Institute for Systems Biology, 4225
Roosevelt Way NE, Seattle, WA 98105, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                     1. .12423
/organism="Halobacterium sp. NRC-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein"/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:64091"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="VNG6208C"
147. .1016
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/gene="VNG6209H"
1016. .1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1543. .2808
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/note="VNG6210G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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  (bases 1 to 12423)
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JOURNAL
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                              AUTHORS
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Archaea: Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
Halobacteriaceae; Halobacterium.
El (bases 1 to 12423)
Sukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrogna, J., Shukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrogna, J., Swartzell, S., Walt, D., Hall, J., Dahl, T.A., Walti, R., Goo, Y.A., Leithauser, B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocks, D.G., Jablonski, P.E., Krebs, M.P., Angevine, C.M., Dale, H., Jsenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Dassarma, S.
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IVYPTAVHYSKPVAREKIGGISETIEGQATQAMAKLLLOKGSKRSOFGSUNSVHIRQ
EH DVWTDLWATGFTISTSRANSLNGRRIAMSTAMAVLSQVRSFFFEBAGGSKKEDIA
KALTYAEGCYDSYHTLQAENIMREMSNLQQINSLVTSWMLTLEKQGCHMLIRAGASGV
IQAMULSKPSKFSFFEBAGGSKREDIA
IQAMULSKSGSFFFENQHLECNIHPRRLHANGHIRVNYTIIVDDDNKAVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIALDRSDRSYYACDGGCLDEPVLLTQNRRQFPVKLTEPLTAILYITEDKQHMEELHH
AIHVKEVVEAPAHEQHLIALHRHGHQLGGLPTLFWVSVCAIIIVFHIFLCKLIIKEYC
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Proc. Natl. Acad. Sci. U.S.A. 97 (22), 12176-12181 (2000)
11016950
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                                                                                                                  /note="alignment with genomic scaffold AE003584"
/db_xref="FLYBASE:FBgn0031379"
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Mismatches:
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/strain="y; on bw sp'
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 g
                                                                                                                                                                                                          /gene="CG7289"
/note="Longest ORF"
                                                   /map="22B8-22B8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium sp. NRC-1.
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AE005155 AE004438
AE005155.1 GI:10584262
                                                                                                       /gene="CG7289"
                                                                                                                                                                                                                                                                   /codon_start=1
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AE005155
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PUBMED
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sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuracity this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspilced precursor RNA, and reverse transcription of unspilced precursor RNA, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitily.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton, M. Carlson, J. Carlson, J., Carlson, J., Carlson, J., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Parcleb, J., Paragas, V., Parki, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S. Direct Submission.

L. Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720, USA
Sequence Berkeley National Laboratory
This clone was sequenced as part of a high-throughput process to
SGMPSPLYPWMRSQFGKCQERKRGROTYTRYQTLELEKEFHFNRYLTRRRIEIAHAL
CLTBRQIKINFQNRRHKWMKRNKTKGEPGSGGBCDETTPPNSPQ"
12011(175368. 277582, 275741. 275774, 276161. 276630,
276896. 277114, 277173. 277294, 277348. >277531)
/gene="Sodh-1"
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                                                                                                                                                       ne Celera sequence differs
this transcript."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY061146 2151 bp mRNA linear Drosophila melanogaster LD12115 full length CDNA.
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/organism="Drosophila melanogaster"
                                                                                                                                              /note="Nucleotide sequence of the
from the published sequence for th
/product="Cr6209"
/db_xref="FLYBASE:FBan0001982"
/db_xref="FLYBASE:FBgn0024289"
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Mismatches:
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Drosophila melanogaster
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51.50
65.38%
50.00%
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Best Local Similarity:
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AY061146/c
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SNYGGYYPOESYSESCYXXNNGEQWTTOTVPPWAPATRRAABDDAASIIAAV
EERPSTLEALLTNPWKLLKYTPOFYTTVBOWKRAPAVSTRVASPAPSYDGEYVTVP
TPSASEDVDVLLDVYSPOSOTOKLKNODFATPPTTPTSLPELEGISTPPQSFGEKSSS
AVSOBINHRIVTAPNGAGDFNWSHIEETLASDCKDSKRTRQTYTRYQTLELEKEFHFN
RTTRRRIDIANALSLSERQIKIWPONRRWKSKNDFTRDSSPEHGGAGYTANLPPLE
ATTRRRIDIANALSLSERQIKIWPONRRWKSKNDFTRDSSPEHGGAGYTANLPPLE
YQHQCSYQOHPODLYHIG"
                                                                                                                                                                                                         GAGGSGGVVPSGGTNGGGGSAGAATEGANDY FPAAAAYTPNILYPNTPQAHYANQAAYG
GOGNPDMVDYTQLQPQRLLLLQQQQQQQQQAAAAAAQQQQQLAQQQHPQQQQQ
QQANI SCKYANDPVTPGGSGGGVSGSNNNNNSANSNNNNSQSLASPQDLSTRDISPK
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Ysonanhgchmpypreppydrmpychydgododdoyyrsrpdspssgyggydyda
Ygolgydyddododododododoyddoyyra
Sckloaaygglchyppeggsplyddagghhanagmtphhmghgadlfytdygydy
Teyhquhhnmgmyqqgsyppydgappgmmhgphhmghgadlfytdygydy
                                                                                                                                                                                                                                                                                                         LSPSSVVESVARSLNKGVLGGSLAAAAAAGLNNNHSGSGVSGCPGNVNVPMHSPGGG
DSDSESDSGNEAGSSQNSGNGKNPPQIYPWMKRVHLGTSTVNANGETKRQRTSYTRY
QTLELEKEFHFNRYLTRRRIEIAHALCLTERQIKINFQNRRMKWKKEHKMASMNIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ftz gene product; Nucleotide sequence of the Celera
sequence differs from the published sequence for this
                                                                                                                                                                                   /translation="MDPDCFAMSSYQFVNSLASCYPQQMNPQQNHPGAGNSSAGGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="84B1-84B4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(118482. .120767,130742. 130967,
131102. .131140, 131519, 132295,193615. .193704,
221238. .221367, 221470. .222034,222070. .222260,
222819. .223415,223431. .223587))
                                                                                                                                                                                                                                                                                                                                                                                                                            join(86526, .86589,86623, .87370,87518, .88310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="84B1-84B1"
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                                                                                                                                                                                                                                                                                                                                                                                                   YHMGPYGHPYHQFDIHPSQFAHLSA"
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Bukaryota Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryota Metazoa; Arthropoda; Diptera; Brachycera; Herygota; Neoptera; Endopterygota; Diptera; Brachycera; Herygota; Diptera; Brachycera; Herygota; Diptera; Brachycera; Herygota; Diptera; Brachycera; Mans. Enhydroidea; Drosophilidae; Drosophila; Canas, C. Calniker, S. E., Holt, R. A. Evans, C. A., Galler, R. F., George, R. A., Lewis, S. E., Richards, S., Ashburner, M., Henderson, S. N., Sutton, G. G., Wortman, J. R., Yandell, M. D., Zhang, Q., Chen, L. X., Galler, B. Brandon, R. C., Rogers Y. H. Blazej, R. G., Champe, M., Pfeilfer, B. D., Man, K. H., Doyle, C., Barter, E. G., Helt, G., Nelson, C. R., Gabor Mitos, G. L., Abrill, J. F., Abbryani, A. A. M. H. J. Borkova, D., Bendos, P. V., Berman, B. P., Bhandari, D., Bollew, R. M., Besun, A., Baxendale, J., Berladhan, B. P., Bhandari, D., Bollew, R. M., Besun, A., Baxendale, J., Butler, H., Cadleu, E., Center, A., Chandra, I., Cherry, J. M., Cawley, S., Dahlker, C., Davenport, I. B., Davides, D., Deckons, N., Debtochar, M. R., Douck, J., Brownes, M., Dugan-Rocha, S., Dunkov, B. C., Dunn, P., Durbin, K. J., Evangelista, C.C., Ferraiera, S., Pleischmann, W., Fosler, C., Gabriellan, A. E., Gargin, S., Gelbart, W. M., Glasser, K., Glabri, E., Gong, F., Gorrell, J. H., Gu, Z., Gelbart, W. M., Glasser, K., Glabri, M. K., Houck, J., Hostin, D., Houston, K. A., Howland, T. J., Methson, J. A., Ketchum, K. A., Kimmel, B. E., Kodira, C. D., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A. M., Muzny, D. M., Nelson, D. L., Nelson, D. K., Nelson, K., Nelson, R., Nelson, R., Nelson, R., Nelson, R., Nelson, D. L., Nelson, D. L., Nelson, D. R., Reinert, K., Remington, K., Soheeler, F., Shen, H., She, B.C., Siden-Kiamos, I., Staplerton, M., Stupski, M. P., Spier, F., Stapleton, M., Strong, R., Spier, F., Spier, F., Stapleton, M., Strong, R., Spier, F., Spier, F., Stapleton, M., Strong, R., Spier, F., Spier, F., Spier,
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/clone-Back32303 (D1350)
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Drosophila melanogaster BAC library, partial EcoRI in
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Mismatches:
Indels:
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Matches:
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AE003673 AE002699
AE003673.2 GI:10727114
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KEYWORDS
SOURCE
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                      Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zwori, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, K., Zhong, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Glibbs, R.A., Myers, F.W., Rubin, G.M. and Venter, J.C. The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced g1:7298860.
Location/Qualifiers
1. 309357
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Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A.,
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US-09-847-539A-6_COPY_59_86 (1-28) x AC095014 (1-170801)
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S CHINKER'S E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
HOIL, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
HOIL, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Bahzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phouannenavong, S., Pittman, G.S., Purly, Y., Richards, S., Scheeler, F.,
Stapleton, M., Strong, M., Strikas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J. C.
Sequencing of Drosophila chromosome 3R, region 83F-84A
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2 (bases 1 to 170801)

83 Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

10 Lotter,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

11 Celniker,S.E., Adams,M.D., Barzon,J.D., Amanatides,P.G., Brandon,R.C.,

12 Rogers,Y., An,H., Baldwin,D., Barzon,J.J., Beeson,K.Y., Busam,D.A.,

13 Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,

14 Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,

15 Ferriera,S., Frise,E. Gallek.R.F., Gargy,N.S., George,R.A.,

16 Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,

17 Ibegwam,C., Jahli,M., Kruse,D., Li,P., Mattel,B., Moshrefi,A.,

18 McIntosh,T.C., May,M., Murbhy,B., Palson,C., Nelson,C., Nelson,C.,

19 Phouanenavong,S., Pittman,G.S., Patel,S., Pfelffer,B.,

19 Phouanenavong,S., Pittman,G.S., Patel,S., Pfelffer,B.,

20 Explicit,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,

21 Lawrence Berkeley National Laboratory, One Cyclotron Road,

10 Berkeley, CA 94720, US

11 Sequence Berkeley National Laboratory, MS 64-121

12 Berkeley, CA 94720, US

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Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Ditera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Location/Qualifiers
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                                      AC095014.1 GI:15624856
                                                                                                          fruit fly.
Drosophila melanogaster
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E accounter, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H.,

Roll, R.A., Evanas, C.A., Googne, J.D., Amanalides, P.G., Brandon, R.C.,

Holt, R.A., Evanas, C.A., Googne, J.D., Amanalides, P.G., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dletz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

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(a (bases 1 to 190642)

(b) Caliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

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Pacleb, J., Paragas, V., Park, S., Patel, S., Peiffer, B., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Direct Submission

L. Submitted (15-SEP-2001) Berkeley Drosophila Genome Project, MS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ACO95015 190642 bp DNA linear INV 15-SEP-2001 Drosophila melanogaster, chromosome 3R, region 84A-84B, BAC clone BACR32J03, complete sequence.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                           Db 170223 GACGCTTTAAAAGCGTTTTCTTCACAGACTGAT---TTGAGCCATCCGATGAGTGATATT 170279
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2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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SEQUENCING IN PROGRESS ***, in ordered
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Acetyltransferase (GNAT) family, score 36.20, E-value
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Neoptera; Endopterygota; Diptera; Brachycera;
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/gene="SCBAC36F5.05c"
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/db_xref="GI:14575550"
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HTG; HTGS_PHASE2.
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Pterygota; N
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ORGANISM
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AC012724
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of AE001572 from base 200001 (AE001572 Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the submitter. may e-mail to
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                                                                   45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal
                                                                                                                              flyecolera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                                                  This sequence was identified as CDM:10209782 For further information on this sequence you
                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
7273 c 7242 g 10573 t
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Mismatches:
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Mismatches:
                                                                 Submitted (03-NOV-1999) Celera Genomics,
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               1 (bases 1 to 35031)
Adams, M. and Venter, J.C.
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                                                                                    Rockville, MD, USA
                                                   Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Begin
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                                                   Direct
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AE001572_2
AE001572_3
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AE001572_2/c
WPCOMMENT
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AC095014
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                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in codons is given for each CDS.

Usually the highest scoring match found by fasta - o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at hittp://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="SCBAC36F5.01"
'note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-JUN-2001) Streptomyces coellcolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, (3) John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SCBAC36F5.01"
/note="SCBAC36F5.01, possible secreted phosphatase
/note="SCBAC36F5.01, possible secreted phosphatase
fragment), len: >296 as; similar to C-terminal region of
SW:PPBD_BACSU (EMBL:U49060) Bacillus subtilis alkaline
phosphatase D precursor (EC 3.1.3.1) Phob, 556 as; fasta
scores: opt: 277 Z-score: 319.4 bits: 68.0 E(): 3.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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                                                                                                                               A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                             1 (bases 1 to 32608)
Redenbach,M., Kleser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 32608) Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
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/db_xref="taxon:1902"
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                                                                                                  Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                               Saunders, D. and Harris, D. Unpublished
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                                                                                                                                                                                                                                                                                                                                            PGAPLGRELQIAĒLLRFVKHRRITGTVWLTADVHHTSAQHYOPSRAĀFGDFEPFWEFV
SGPLSAGAFPASELDGTFGPERVFVKAPTASNVSPAGGYQFFGEVDIDGGTAEMTVRL
REQDGTVLFTKVLRPGOVGO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAGFLTAPOKASTALLAVADVAARYYOPOLRASLDPVVTGSGDRLKFESFSGCGGVY
ARLDVLEAGLDGGEVGHGTTNVDVNNPLREALSRIGADDPLHLRVGPEELAVTTLDGP
VVEKKVPLPDRWLRGFAEAQVIAAGFDLRAELDAABAVRFLRALPRGGRSAATGLRWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPAGRSLRPTTRAVPGAVCLPGPERLVALQRVLRHATALRVYGPAVASGAAATASAWE
VLLPGWRUTTTLSPDAARGESGEGVLDALAYDBAAADAELSYLLAMEPRIDTADLA
AASGLTAERVRAALVRLGTSGRVGYOTVABAYFHRELPYDAERVERHNPRLRSARALV
AAGGVVLDGPLGTYVAEDGHVHRVREBAGVLSGSCLWWAKYRGGRGPCKHALAVRWVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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LASDAMPTVASHAQSVLGALALAGELSPRRLAQVTEAVLFRTEKKLVRAQLVLLGKVL
TKNRSAAGELLPAAARAFGHEDSDAQERALKLVERHVGKVTAAEVREELAGAAEQLIP
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VAVEERALDCIVRHAHLDRDALLEALEPVVARRWARGEPRHGHRSDDFFARRHELFD
DPRAPDILLATTYGKVRTDTLHRVYHGGLTNSGCAHNSLARPEBARWEVAHRLRTDP
OPFILATTFWGTGILLEPGELVBLDAYRAGARVSAVDFGQALLRYRRDNRPALAA
ERAAALGTEEGERLARRLLTERAAPSVTRRTADTRILVELGEVPDLRAEEFPAALRL
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LPHLADADGEAGEAVHLSVAYGLGARHAEDRLAAVDALLVLAARGRLEAGRLGADLGQ
LVRRGAVKPARLADAVRTAAATGANATVWAVLRQVLPVLLADLSTGGATTSSARGLGE
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/cterminal part similar to TR:09FC4 (EMBL:AL591515)
Streptomyces coolicolor putative acetyltransferae
SC4B10.23, 163 aa; fasta scores: opt: 287 Z-score: 300.0
bits: 63.3 E(): 4.2e-09; 42.867% identity in 133 aa
overlap. Contains Pfam match to entry PF01842 ACT, ACT
domain and PF00583 Acetyltransf, Acetyltransferase (GNAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1042. .2445
/gene="SCBAC36F5.02"
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258% identity in 271 as overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SCBAC36F5.03"
2454. .5177
/gene="SCBAC36F5.03"
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/gene="SCBAC36F5.04"
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/gene="SCBAC36F5.04"
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2454. .5177
                                /codon_start=1
/transl_table=11
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/chromosome="3R"
                                                                                                                                                                                                                                                                        Submitted (22-APR-1997)
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65.38%
50.00%
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Best Local Similarity:
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VERSION
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence nalysis of an insertion element, IS1131, isolated from the nopaline-type Ti plasmid of Agrobacterium tumefaciens Gene 114, 229-233 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC001654 11v 21-JUL-1998
Drosophila melanogaster DNA sequence (Pl DS00189 (D16)), complete
                                                                                                                                                                                                                         BCT 26-APR-1993
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukerygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 12976)
Celniker, S. E., George, R. A., Galle, R. F., Hoskins, R. A.,
Svirskas, R. R., Harris, N. L., Agbayani, A., Arcaina, T., Baxter, E.,
                                                                                                                                                                                                                                                                                                                                      Bācteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Subclones in sac from P1 clone DS00189
                                                                              3 AlaLeuGluAlaLeu---AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
                                                           1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAla-----LeuGlnSerGlu 17
                                                                                                                                                                                                                      Agrobacterium tumefaciens insertion element IS1131. M82888
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13
5
6

    2888
    /organism-"Agrobacterium tumefaciens"

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AC001654 L48712 L39780 L39782 L39781 L39783
AC001654.1 GI:2342707
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                                                                                                                                          US-09-847-539A-6_COPY_59_86 (1-28) x AC056141 (1-850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                    insertion element IS1131; transposase.
Agrobacterium tumefaciens DNA.
Agrobacterium tumefaciens
                                                                                                                         18 GluAlaAlaValValLys----AlaAspAsnAlaAla
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Matches:
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/note="regulatory signal"
794 c 882 g 580
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156. .164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2888)
Wabiko, H.
                                                                                                                                                                                                                                                                      M82888.1 GI:142231
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72.00%
52.00%
39.92%
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Best Local Similarity:
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AC001654
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Berkeley, CA 94720
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://fruitfly.berkeley.edu/sequence/) or send
email to drosophila@mhqc.lbl.gov.
Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomotan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefil,A.R., Moshrefil,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,E., Snir,E., Twomey,B., Man,K.H., Whitelaw,K.R., Sequencing of antennapedia complex, homeotic genes
                                                                                                                                                                                                                                                   Martin, C.H., Arcaina, T.T., Bondoc, M.M., Chlang, A., Critz, P.A.,
Davis, C.A., Doyle, C.M., Ericsson, C.L., Ferfan, D.E., Gunning, K.M.,
Houston, K.A., Jaklevic, M.A., Kadner, K.E., Kim, K., Kim, S.F.,
Ko, C.L., Lewis, K.D., Li, M., Lindquist, K.J., Lomotan, M.A.,
Lustre, V.M., Machrus, M.U., Mayeda, C.A., Miguel, T.M., Miller, C.A.,
Mok, M.S., Pacleb, J.M., Patel, S.G., Santos, R.F., Subramanian, S.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="This sequence has not changed since its original submission on 04/22/1997. It was resubmitted in order to include all secondary accession numbers for the subclones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCBAC36F5
Streptomyces coelicolor cosmid BAC36F5.
Streptomyces coelicolor cosmid BAC36F5.
AL592292.
AL592292.
AL592292.
AL592292.
AL592292.
ASSOC family transcriptional regulatory protein; cation efflux system protein; exonuclease, hydrolase; integral membrane protein; lyase; regulatory protein; secreted phosphatase; siderophore binding protein; sugar acetyltransferase; transcriptional
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Streptomyces coelicolor.
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="84A6-84B2"
/clone="Pl DS00189 (D16)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        belonging to this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
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4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys

US-09-847-539A-6_COPY_59_86 (1-28) x RME603646 (1-303100)

23

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PHAYVDADNEOMIRLSVARLIERGHRRIALLNPKEQFAYGVVRLESYRRALEKAGLPY
DPALVAHGRITPAFGRENVYTMSALADPPTAYTCANEATALGAESGFHARGLYHGRDA
VINATDDLAVVGYFAAPPITSYYLPIGEPSALLGKFILRRMEGEPPDALQTLLMPDLIE
RSDDRLRPER"
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DDPGKRAARWLRIADELQALLVGTLWTGETFAARLANDPERTLPGESLIQFWPLLLGSR
LPAAMCRQLVARLVEGAFITDWGPATESPRSPFYEDDGYWRGPIWAPTTYLLWDGLRR
QGEGALAREIAQKFCALANAHGWAENFDARSGRGLRDRAFAWTSAVYLLLAGSLRDEK
PVKS"
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/db_xref="G1:15140991"

/db_xref="G1:15140091"

/db
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RYLAVAANGALLDKVIGDALGWAGLESLPDLGDLRVTRRGNLRFAFNFGRIPAEVPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGEGTFEGNVDFFRALPPPEGPGSFEBAHAAVTAEFGAWYRS FPAGYPCQEEAGRLAA
YLLWANTVPAEGVLTRPAIYWSKNGMINIWSWDNAFSALGVAAFDEELAFGQFAAIFD
HQDASGLLPDYVNDREALFAFTKPPVHGWAVSCMARENPAFLTPERRAYLRDAIGRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental /product="putative transcriptional regulator, lacI family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="putative sugar uptake ABC transporter permease
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/note="Product confidence : hypothetical
Gene name confidence : hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           small molecules;
                                                                                                                                                                                                                                                                                                                                                                                           /function="MISCELLANEOUS; Not classified regulator"
/note="Product confidence : putative"
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/gene="SMb20969"
/function="CELL PROCESSES; Transport of carbohydrates, organic acids, alcohols"
/note="Product confidence : putative Gene name confidence : hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303100
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Matches:
Conservative:
Mismatches:
Indels:
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/gene="SMb20968"
complement (6468. .8180)
/gene="SMb20968"
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                                                                                                                     complement(5426. ,6460)
/gene="SMb20967"
                                                                                                                                                                                                                                                 complement(5426. .6460)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
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52.00
77.27%
50.00%
40.31%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                   gene
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Giardia intestinalis clone MJ2161 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-APR-2000) to the EMBL/GenBank/DDBJ databases. Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                                                                                                                                                                             Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Glardia: a model for ancient eukaryotic genome analysis"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                               Giardia intestinalis
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This record contains 1 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                850
7
6
5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .850
/db_xref="taxon:5741"
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/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           850: contig of 850 bp in length.
                                                                                                                                                                  20-APR-2000 (Rel. 63, Created)
20-APR-2000 (Rel. 63, Last updated, Version 1)
                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                standard; DNA; HTG; 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone-"MJ2161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.1
51.50
66.67%
45.45%
39.92%
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Best Local Similarity:
Query Match:
                        38550 CACGAC 38545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                      HTG; HTGS_PHASE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preserved.
24 AlaAsp 25
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                                                                                                            AC056141;
                                                                               AC056141
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1-850
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1-850
                                                    RESULT 29
                                                                    AC056141,
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/product="putative exported enzyme, similar to
/product="putative exported enzyme, similar to
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LYSTASTHLLSAILTKVGGKPTLALAREWLDPVEGFRIGAWFSRNWANS
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DKEHYLRVGDPDQPAFNHDLYRAVGRRVWVMEQQPGPVNMAAHNQSPADGMYRLWTW
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RGKAQVAIVLDYESRWATHVLPQGRSYSASAVALDWYSTVARLGVDVDFIGGHSDIAG
YKLILAPDLVIAEEATVERLTRADAKVYFGARSGSKTRDMHPEGLPPGPLAKLIDIS
VSRVESLPEFHSETVLYGNEAYFAGGWRETVRTSETVIASFDGETRNGAPALVGSDKA
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CFSSRRYRSEAARITEAMARRYGEHIYVHAWQTDNEYGDHDTIYSYSAEAVGAFRLWL
AERYGSIDELNRAWGTSFWSMRYDSFEEIDLPNNLVEEPSPTHGVDFIRFSSDQVKSF
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RAIDSIQLTAKHQVATPANWQOGEDVIITAAVSNEDAVQRFGSFDTVLPYLRKTKQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARSLLAFGELYRNRGRTADGRQVVPADWVELSWRPRTASRFTGDGYGYGWFTRRIGDE
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DQVQGSGSTPSQHRLVLPSECAIYAAVAERCQRARAKACKTYLLGQPAKIYPQIGKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVYYAWGYGGQMLYIVPSLNLTVVMTSDESGPSARNGYRDALHGVLAEIISTAKAD"
complement(3296..5236)
/gene="lac22 ON SMD20966"
complement(3296..5236)
/gene="lac22 ON SMD20966"
/EC_number="3.2.1.23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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/protein_id="CAC49489.1"
/db_xref="GI:13140976"
                                                                                                           /evidence=not_experimental
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/protein_id="CAC49488.1"
/db_xref="GI:15140975"
/function="MISCELLANEOUS; Not classified regulator"
/note="Product confidence : putative"
                                                                                                                                                                                                                                                                                                                                                                                                                             /function="CELL PROCESSES; Protection responses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Product confidence : putative
Gene name confidence : hypothetical"
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Gene name confidence : hypothetical"
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Gene name confidence : putative"
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Rhizobium meliloti (Sinorhizobium meliloti) 1021 complete pSymB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finan, T.W., Weidner, S., Wong, K., Buhrmester, J., Chain, P., Vorholter, F.J., Hernandez-Lucas, I., Becker, A., Cowie, A., Gouzy, J., Golding, B. and Puhler, A.
From the Cover: The complete sequence of the 1,683 kb psymb megaplasmid from the N2-fixing endosymbiont Sinorhizobium mellicti States of America. 98 (17), 9889-9894 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted on behalf of Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld, Germany and Department of Biology, McMaster University, 1280 Main Street West, Hamilton, Ontario, L88 4K1 Canada mailto:Stefan.Weidner@Genetik.Uni-Bielefeld.DE
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4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-JUN-2001) Weidner S., Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld,
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AL603646 AL591985
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Sinorhizobium meliloti
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2 (bases 1 to 303100)
Weldner, S.
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Matches:
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Mismatches:
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/db_xref="FLYBASE:FBan0027515"
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KAHSTTADCSAIKQKTTEASIADIYTVQLNSAMRASGNLGAAKDSFLNNNNGONGAA
NAPPPNYEAKCYIEHGRINFGKLITDEIMSADYKLVEQAKRATNIAGTTALIAIVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLIVANVGDSRGVMYDWRGIAIPLSFPHKPQOVRERKRIHDAGGFIARGVWRYAĞVL
ATSRALGDYPLKDKNLVIATPDILTFELNDHKPHFLILASDGLWDTFSNEEACTFALE
HLKEPDFGAKSLAMESYKRGSVDNITVLVIVFKNDVYKIGSSAGKAGEESLKVPAKSO
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/gene="BoDNA:LD21794"

/note="BoDNA:LD21794 gene product [alt 2]"
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/gene="Rackl"
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3451. 3754)
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complement(<4497. .>6106)
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                                                                                                                                                                                                                         <421, .>4223
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/note="CG7115"
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                                                                                                                                                                                                                              gene
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Db 117572 CTGGAAGCTCTGTTCAAGCAGGTGGAGTCTCTCCAAGGCCGCAGTTGCTCTCTTGTGGCA 117631

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E (Dases 1 to 16942)

S Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

Holt.R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Burandon,R.C.,

Rogers,Y., An.H., Baldwin,D., Banzon,J. Beson,R.Y., Busam,D.A.,

Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,

Rogers,Y., An.H., Baldwin,D., Bovenport,D., Farfan,D.,

Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,

Gonzalez,M., Houck,J., Hoskin,R.A., Hostin,D., Howland,T.J.,

Neclntosh,T.C., May,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J.,

Phouanenavong,S., Pittman,G.S., Patel,S., Pfeiffer,B.,

Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,

Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.

Sequencing of Drosophila chromosome 2L, region 28B-28B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jun 7, 2001 this sequence version replaced gi:7143379. Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley, National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "(bases I to 169427)
Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Cisesiolka.L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Selli,H., Snir,B.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
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35853 c 34873 g 47640 t
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Matches:
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/db_xref="taxon:7227"
/chromosome="2L"
                                                            Drosophila melanogaster
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Query Match:
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9
                                                         ORGANISM
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JOURNAL
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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KEYWORDS
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4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23

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join(421. .927,1513. .1971,2323. .2899,2959. .3222,3299. .3351,
                               Drosophila melanogaster genomic scaffold 14200013386055 section 12 AE003619 AE002690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 281993)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7297302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                             AE003619.2 GI:10728652
                                                                                             fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome=
        24 AlaAspAsn 26
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                                                    DEFINITION
                                                                                                    ORGANISM
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JOURNAL
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                              RESULT 27
AE003619
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Fueryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Fueryota; Menophera; Endopteryota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila

1 (bases 1 to 133155)

8 Mazny, D.M., Adams, C., Balley, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

Burkett, C., Burrows, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, J.H.,

Bodota, B., Bouck, J., Benadazo, D., Ding, Y., Domen, Rashid, N.,

Burkett, C., Burrows, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, J.H.,

Burkett, C., Horsk, H., Jackson, L.E., Jackson, L., Jackson, R.,

Hollowsy, C., Horsk, H., Jackson, L.E., Jackson, M., Morris, S.,

Relly, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G.,

Parish, B., Paxton, S., Payton, B., Perez, L., Pulle, L., Quilles, M.,

Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E.,

Shen, H., Simon, M., Sparks, A., Stamps, A., Worley, K., Wren, J.,

Weinstock, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, R.,

By Direct Submission

M. Onpublished to 133155)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC011910 133155 bp DNA linear HTG 16-OCT-1999 Drosophila melanogaster clone RPC198-2017, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.
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Submitted (16-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 7x 77030, USA
* NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the places
* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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the accession number will be preserved.

Location/Qualifiers
1. 36993
/organism="brosophila melanogaster"
/db_xref="taxon:7227"
9781 a 8675 c 8725 g 9812 t
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AC007416 169427 bp DNA 11near INV 07-JUN-2001 Drosophila melanogaster, chromosome 2L, region 28B-28B, BAC clone BACR08101, complete sequence.
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/note="push3420 P element insertion site"

join(370. 513,695. 789,913. 1325,1581. 3747,3808. 4335,

4404. 10389,10447. 10651,10701. 11393,11455. 13118,

3175. 13657,13715. 15650,15706. 17302,17366. 17584)
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4404. .10389,10447. .10651,10701. .11393,11455. .13118,
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VLTRKDSLTNERIAVLTKLLEPYRETLOHODOWILVVRCILEYFDLLLPSINENCMLY
STGCHKRAPAALERHULLEQSFQYPDOLMFATGSQEGAFBVRAMYSGDQGOTIKH
LLSSGVVRRYAFCCLSSPHGRQDLAVSHKGKVTILQLSALLKQADASKRKITITOL
SSAPIACTVISLAANPCNEDCLAVCGLKECHILTFSSSGSTRRHIVVNRQLEBONYIK
KAVWLPGSQTLLAVVTSDYKIIYDLAVDTYSPKYYLLAVGCH
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RHDIEENFRKSAGEYGSSIRPTFYSLVMGDPETSYWAOEFKLDGLAWNFILCTPDKLK
YPLLVDALTDILSITDMSMYSKEKDKEASMHNLCAIOYCFTIAWKLNLGLPPSTSHVE
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DGSLRIFSAQPEYTSFWLSPQVQPFGNQLYSSTLMAKGGGSGSTSKSKSNTASGKMTS
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PIPTREEMMCOSKLLKVYRRAPDPBHYTLLDCIEVYGKSREUKWBDSEDVYVRG
SSAPAVSSQASSANFEGERNCITQLDRWARHILEVMOCALHLLGSGYPASMRQKAVK
TASALLLLFTPNPVQTQARYVLATLYGTRALYHYKDGVLLQFVNRELQSMQPKLEKL
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DEPVNIVKRGLCQPETIVHCLVEIMYGFALADPGQVGRMTKYFIDLLKHDASVISHSA
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NVATDGSTLRTSPAEPAGSGGSESGGSGVESIGGTSARSSNFGDHANASPPRQGSTKD
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ASDDKESPKEBIKRSRDLESVILOQLIAPLEBCKMTWPVESEVTDCTEQILANVE
YEQEOMGVDTLLDVCYSLPILNYTRSKYMETINGGKBIYLPTTOVEATAVKSSNNHML
TDLTILSQAQALIEMQPLTPSRIERLSMCGIAALYNAVLTSIATSVLGMSQASSSGKO
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HLCYGSWLLISGIQGAMGASGSGGSSSDSASKSASKATKSGSEAGTAPTTPIARVNLF
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AADIFCFLDQFLANRHAYMQRYVKAGVSDQQMLLMANIIKDFDRDWRNETDQGSGNA
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STDTNTWPLQVYPSTLSVLVQILLLKPTQEKEAACLSVWHRLINTLVEGVCSSNTASD
SDYEDLNIEHAQLLLFLFHSLNLWQKKSILLLTAGGVIRCAEVCRGISEDRPVKNSQI
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                                                                                                                                                                                                                                                                                              AQKYCVESRTSFBELSKIVQKVKACRSELVAYDRQQODQPPVNPGSTTGÅENPTING
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KLKVIFBELFISNCRTL
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                       VQCHTISKLIVRIADLKRTKMVRTINVYYNNRSVQAVVELKNRPALWHKARSVSLQSA
                                                                                                                                                                                                                               QTELKIDFPLPITACNLMIEFADFFETVSGSSENLQCPRCSAAVPAYPGVCGNCGENV
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PGNEVRLALLSLFGVLMGKTKSKOTGTTSPPHQFKDNSSFVASTTANVLSKSGAFVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was identified as CDM:10212995 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila
1 (bases 1 to 36993)
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Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
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HTG; HTGS_PHASE2.
fruit fly.
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LLSSGVVRRVAFCCLSSPHGRRQQLAVSHEKGKVTIIQLSALLKQADASKRKLTITGL SSAPTACTVSLAANBCNEDCLAVCELKECHTILTSSSGSTRHBIVVNRODLENGNYIK KAWULLGSQTLLAVYSDVYKIYDLAVDTYSPKYYYJVAGKIKBOTFVYQDGGNYNMI TFASSGYIYTQQLDQQSLAVHGDFYVTNTLELSHOHIKDIAGHIGGGGVSIYYSHTLQ LLFSYSGCRSRFFSPLTNVSBCWKGIYHLDPRASKGASKGPLQPLQVOWTEVTGPGL VASAQTSNYPILLATPERIYDEKAGGNSRNSRIADVYGRHAVAGVEKTTLLLLCE DGSLRIFSAQPEYTSFWLSPQVQPFGNQLYSSTLMAKGGGSGSTSKSKSNTASGKMTS TASALLLLPTPNPVQTQARYVLATLYGTRALYHNYKDGVLLQFVNRELQSMQPKLEKL ETLREIDPEAFYRLVLMVRGIANARPQSLAKICVENNYDIVPTLMGIVLELHKVTPTL DEPVNIVKRGLCQPETIVHCLVEIMYGFALADPGQVGRMTKYFIDLLKHDASVISHSA DGSVGGGGLPEPNADAEGAAVGVGGVGQQMLNLEAFMGGGFPRLLGLPEDADDEAIM DIAIALSLQQHGGDANALQSLQQGLANLQGIRQATAMAAAVNAAANVSLGGSDDDEGS NVATDGSTLRTSPAEPAGSGGSESGGSGVESIGGTSARSSNFGDHANASPPRQGSTKD DQEQPGPSGVAGSGGVAVLSAMSSSEDNEANEDDKLSKLHDLRITVLESIIQHLGTFD LCNGLQAIPLIQVILMLTTDLNGNNBRDQQVLHDLLTALVGLCGNWKRGAAARWETKC PGNEVRLALLSLFGVLMGKTKSKQTGTTSPPHQFKDNSSFVASTTANVLSKSGAFVYA LEALNTLLVHWKNVLGDPYAAGGLASQSAQASGGASGPGVQLLKPIKHGPKPDISIL
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

[ bases 1 to 17595]

Yager, J., Richards, S., Hekmat-Scafe, D.S., Hurd, D.D., Sundaresan, V., Caprette, D.R., Saxton, W.M., Carlson, J.R. and Stern, M. Control of brosophila perineurial glial growth by interacting neurotransmitter-mediated signaling pathways

11517334

11517334
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LLLVRFAWERSFHDDAGGGGPOSNMHFVPYLLFYSVYLLLSSRSAARDSKTLLTYLOA
PPSEKWILEGGTBUDGPLEMATTISLSHENEMKRIALAKERTANAGGHNSPSPVLG
PPSEKWILEGGTBUDGPLEMATTISLSHENEMKRIALAKERTANAGGHNSPSPVLG
PREDARQVYRYRFELMMALVDLIYDNLFKTVSTPKEEDMPTSLFDYLKKND
EALLKSTDSTLQTLFBEFELPGTSFVEFCDVAGLLHLIEHPDNFTEETLAALPSTSSN
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/gene="push"
/note="putative"
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Drosophila melanogaster
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/gene="push"
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Matches:

YPGVCGNCGENVPQCHKCRAINYDEKDPFLCHSCGFCKTAKFDFSMYARVCCAVDPIE SAEDRYWTVS1LHSSLERABRYRYDLLTHKQMLELLIQWCABHRSSDRWPEDNMASVH STSQVNKIIQLLAQKTCVESRTSFEBLSKIYQKVKACRSELVAYDRQQQDQPPVNPGS TTGAENPTTNRCYGCALASTEQCLTLLRAMAYNYDCRVCLYSQGLVSELAEHNLRRGT PLIQEPKTRALLYVLTKONARACMHLLLQLYTTRKYMALMGSIFDISLERAWYDENTLLE VLLGQDDICWEYKLYYTEREFISORLPRGPYTAVLHPCLRTMQNILCPYLDGSKPNO KVATTDLCSMKMFEGGNTVDYRAMLNSDRNHEYAMSKRMFSNNQAKLKNAKDQNVAAS WPDESEDVANTE STATEMENT OF THE STATEMENT DASKRITLTQLISSADPLACTY SELAMPENEDELLAVCELKECHILTESSSGSTENNEHLY
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2940

3148 g

3028 c

d 3257

BASE COUNT ORIGIN Length:

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Alignment Scores: Pred. No.:

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Drosophila melanogaster pushover (push) mRNA, complete cds.
AF096897
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Shrect Submission .
Submitted (06-007-1998) Biochemistry and Cell Biology, Mail Stop 140, William Marsh Rice University, 6100 South Main, Houston, TX
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Mismatches:
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Comprehent(2013)

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COMPLEMENT (7513. . 8424)
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/proteln_id="AAG05723.1"
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                                                                                                                                                                                                                                                                                                                                                                                            /gene="PA2333"
complement(5800. 7416)
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SGADRKTHLIDMNGNEYKRWYPGFPAAVIDPALNGGKRGHVLLQLADLAAPDKLASP
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PRPVDQISGQHDAHLIPEGLPGAGGNLLVFDNQGDAGYPSVPRGLVSGSRVLEIDPLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-AUG-1998) C. Montell, The Johns Hopkins University School of Medicline, Department of Biological Chermistry, 725 N. Wolfe Street, Baltimore, MD 21205-2185, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 DD 10151 GAAGCGGTAGCTGAGCTGAGCAGAGCGGACGGACGACTGACGCTGTGCAGCCGATGTCGCC 10092
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12373 bp mRNA linear Drosophila melanogaster mRNA for calossin protein. Y17920 Y17920 Galo non-
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/db_xref-"taxon:7227"
1. 3316
/organism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
/map-"28E1-2"
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J. Biol. Chem. 273 (47), 31297-31307 (1998)
99030403
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                                                                                                                                                                                                      Conservative:
                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                               Length:
Matches:
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/product="CALO protein"
                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="retinal"
/dev_stage="adult"
2. .12352
                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 10091 GCTGTGGTAGGGGGCGACCCTGCC 10068
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50.00%
40.70%
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Query Match:
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                               MTVWARYGSKVPAKVVAWNHVGGSGLTVAPEIADVRQLGGKSVAIPFWYSIHNVVLQQ
LLENDRGLRAWSRAVGAALADEVNILVYLPSDDNPPALASKR HGYTVYRDFRALAENL
KVGRYQRFFGDVWRHACCYVFWHEIDLERRPQWSGKYVNA VKAQIWTREHRAEAAO
LLSKAGANRYTPHAPEVLGRVLAPGAEEQQAYLASGAIRHADWQERRIDFQPYPYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGAGGTLADAVERVAAVAARSLTAAFVFWGGRAFIEYLLQSFWQELRORLLGDLLAG
RLAGATGLSRAMKELSGIEALQVVAHAEBAGWRLDGRLPWWTNLRSGOFVVAAAIEHG
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RVRRAFLGLCCCMAIGLARRALDEVQRHLGGSRSLLDGELAAQRETLDGHVAAHAGL
ASGEFASQPARLFRIRIGLARAAAANAVLELQASGGRAYLSEHGAGFARRWRESAFVP
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LLDPARQPHVLADATRQARVDQATAAVGLEHARARYPAGLSGGMAQRTALARCLARQPKV
LLLDPRFGALDEVTRADMQQLLLRATHERGFAVVLTHPIDEALLLSBRILLLGDSPA
RTLGFBFFGALDEVPRELVEELGALRIELLKTLRRASRTHAHPTAQPEASHVPGRPDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"probable ATP-binding component of ABC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2279. .3115)
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                                                                                                                                          complement(1114. .2313)
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                                                                                     complement(1114. .2313)
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/transl_table=11
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4894. ,5799
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                                                                                                                                                                /gene="PA2328"
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                                                                                                              /gene="PA2328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagroud, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University of Washington, Box 32145, Seattle, Wa 88195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE004659 12411 bp DNA linear BCT 30-AUG-2000 Pseudomonas aeruginosa PA01, section 220 of 529 of the complete
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LLSLGELLERRELYEHVLVSLKRVLLGLFLALLVGVPLGLLVGASRNLEAATTPAFQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 173045 CTGGAGGCTCTGCTGGACAGGACAGGCACAGGAAGTAGCCTTG 172992
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/product="probable permease of ABC transporter"
/protein_id="AAG05715.1"
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                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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/note="assembly_name:Contig52"
130343. .140588
/note="assembly_name:Contig53"
/note="assembly_name:Contig54"
149362. .149361
                                                                                                                                                                                                                                                                                                                                                                                    Indels:
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Nature 406 (6799), 959-964 (2000)
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complement(353, 1117)
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AE004659.1 GI:9948361
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149262 149361: gap of unknown length 149362 162349: contig of 12988 bp in length 162350 162449: gap of unknown length 162450 173772: contig of 11323 bp in length. Location/Qualifiers 1173772 /organism="Homo sapiens" /db_xref="taxon:9606" /chromesome="RPCI-II"		ture 25273572 /note="assembly_name:Contig22" /note="assembly_name:Contig23"		\n \n \n \	/ 10 / 10 / 10			
sequence ** sequence ** number will ** FEATURES **	misc_feature misc_feature	misc_feature	misc_feature misc_feature	misc_feature misc_feature misc_feature	misc_feature misc_feature	misc_feature misc_feature misc_feature misc_feature	misc_feature misc_feature misc_feature misc_feature	misc_feature misc_feature misc_feature compared to the compare
A, but the exact sizes of the gaps are std will be updated with the finished sis it is available and the accession nurved.  1282: contig of 1282 bp in length 1382: gap of unknown length 2426: contig of 1044 bp in length 1572: contig of 1046 bp in length 1572: contig of 1046 bp in length 1572: contig of in 1646 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp in 1640 bp	6159: contig of 2487 bp 14 6259: gap of unknown leng 8183: contig of 1924 bp 14 8283: ago of unknown leng	8284 11014: contig of 2731 bp 13 1015 11114: gap of unknown leng 1115 12517: contig of 1403 bp 1 2518 12617: gap of unknown leng	2618 14315: contig of 1698 bp in 4316 14415: gap of unknown leng 4416 17095: contig of 260 bp in 7096 17195: gap of unknown leng 7796 19263: contig of 2068 bp in	9264 19503: 9ap of unknow 2746: contig of 338 2747 22846: 9ap of unknow 2847 24580: contig of 173 4581 24680: 9ap of unknow 4681 27136: contig of 245 7137 27236: 9ap of unknow	7237 30151: contig of 2915 bp in 10152 30251: gap of unknown leng 0252 33090: contig of 2839 bp in 3091 33190: gap of unknown leng 1391 36912: contig of 3722 bp in 1619 57012: gap of unknown leng 07372 bp in 1619 57012: gap of unknown leng 07372 bp in 1619 57012: gap of unknown leng 1013 40616: contig of 3604 bp in 1619	0617 40716; gap of unknown length 44848 44947; contig of 4131 bp in 44848 44947; contig of 4131 bp in 44848 50238; contig of 5291 bp in 0239 50338; gap of unknown length 53196; contig of 2858 bp in 3197 53296; gap of unknown length 57538; contig of 4242 bp in 7539 57638; gap of unknown length 7539	7639 62554: contig of 4916 bp in 2555 62554: gap of unknown lengt 2655 66368: contig of 3714 bp in 6569 71647: contig of 3100 bp in 1448 74947: contig of 3200 bp in 4948 75247: contig of 3200 bp in 6548 79238: contig of 4191 bp in 65339 79338: gap of unknown lengt 6548	f 5495 b f 4807b n 602b n 602b n 602b n 602b f 6499 f 6499 n 702b n 702b n 702b n 702b n 702b n 702b n 702b n 702b n 702b n 702b

EST AA909108 (NID:93048513) om32d11.s1"

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18011. 18146
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31598. 33237
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21983 22295
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On puritations 1 to 173772)
Waterston, R.H.
Direct Submission
Submitted (O2-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 18, 2001 this sequence version replaced gi:12745114.
                                                                                                                                                                                                                                                                                                       ACO87862 173772 bp DNA linear HTG 19-FEB-2001 Homo sapiens chromosome RPCI-11 clone RP11-724H13, WORKING DRAFT SEQUENCE, 37 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173772)
Waterston, R. H.
                                                                                                                                                                                                          Db 96844 CTGGAGGCTCTGCTGGACAGACAGACAGGGCCACAGAGCAAGAAGTAGCCTTG 96897
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                                                                                                                                                                                     4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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Center code: WUGSC
  117309
11
                                                                                                                                             US-09-847-539A-6_COPY_59_86 (1-28) x AC007274 (1-117309)
                       Matches:
Conservative:
Mismatches:
Indels:
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  Length:
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HTG; HTGS_PHASE1; HTGS_DRAFT.
3.46e+03
53.00
77.78%
61.11%
41.09%
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AC007274 117309 bp DNA linear PRI 14-OCT-2000
Homo sapiens BAC clone RP11-105L10 from Y, complete sequence.
AC007274
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Submitted (09.ARR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 117309)
/note="3 base direct repeat bordering transposon Tn5714. Note difference - TCA in Streptomyces coelicolor plasmid SCP2. TGA in Streptomyces coelicolor plasmid SCP1." complement(7784. .7794)
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Sulston, J. E. and Waterston, R. Toward a complete human genome sequence Concerns 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                       23713 GCCGAGGGGCCGCCGACCGCGAGACGGAGCCGTCCAGTCGGAGGCCGCCGGGCC 23654
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Submitted (14-OCT-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Oct 14, 2000 this sequence version replaced gi:6624109.
                                                                                                                                                                                                                                                                                                                                                                                                                   3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
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                                                              complement(7784...7794)
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/note="Similar to In5714 from SCP1"
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The sequence of Homo sapiens BAC clone RP11-105L10
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Matches:
Conservative:
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is RP11-305H21; the clone sequenced to the right is RP11-109F19, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-105L10; actual end is at base position 24605 of RP11-109F19.

Location(VP11-109F19.

1. 117309
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between nelghboring data submissions.
                                                                                                                                                          all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                    The position of this clone was established as part of a collaboration between the Human Chromosome Y Mapping Project (Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen, and David C. Page at the Whitehead Institute for Blomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO
                                                                                                                                       This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="Y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-105L10"
/clone_lib="RPCI-11"
733. .1035
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/rpt_family="MaLR"
4654 .4753
/rpt_family="MIR"
4917. :5048
/rpt_family="MIR"
6100. .6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alu" 3460. 3864
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8066. .8419
/rpt_family="ERV"
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/rpt_family="L2"
7363. ,7578
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/rpt_family="ERV1"
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9185. .10437
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8961. .9178
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/rpt_family="Alu"
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1967, .2286
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6920. .7254
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7586. .8065
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                                                                                                                                                                                                                                                                                                     restriction digest.
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/note="Similar to Agrobacterium rhizogenes Riorfi36 protein, hypothetical integrase TR:BAB1625 protein, hypothetical integrase TR:BAB1625 protein, hypothetical integrase cores: E(): 7.5e-18, 31.6% id in 326 aa, and to Pseudomonas pavonaceae putative integrase intP TR:O9RDU9 (EMBL:AJ250371) (379 aa) fasta scores: E(): 4.8e-08, 28.28, id in 383 aa, and to Bacteriophage P1 recombinase Cre SW:RECR.BPP1 (P06956) (343 aa) fasta scores: E(): 0.0001, 24.7% id in 304 aa. Contains Pfam match to entry PF00589 Phage_integrase, phage_integrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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/protein_id="CAD12000.1"
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ETVAAIAASVADSTRRAYGTDRAAFAAWCAEEDRTAVPASAETWAEWVRHLTVTPRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="QHEGAAAFARGVYVAIRNPIAHELGDELKEHEALEQLAAFSLLA
RWVDDATVETAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTPGPPGRNAVLGVGAEGGRMTIVVLRELRKELSEDFGPGDAVD
RIEAVHAAPADSDVSGDPDDRTFCGKPTLDMERVNYQPVGPGAPWLPPNMHAWECRDC
ALAQEAEEAGGRSPYDVTLIDAAPSLGLVTVAALTAADEALVPIKVGGLDMKAMASLH
                    KTLRSVORKTNPKLSVGAVLLTAWDKSTFAROLATKVSEDYPEAAVVPIRRSIRASEA
PLSEEPIRLYAPEAAPAGDYDQAAAVLLPGRAAA*
complemet (4190. 4534)
/gene="parA"
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PPMTRRGRVIGDPAGRMTAEAAAEVIERLAVAAGLSGDWSGHSLRRGFATAARAAGHD
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/note="Partial CDS, unknown. May have been disrupted by
                                      /product="hypothetical protein (fragment)"
/protein_id="CAD12002.1"
/db_xref="GI:17026166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLEIARAGGWVDGSRVLARYMDDVDRVKNSPLVGIGL"
7201. .7386
                                                                                                                                                                                                                                                                                                                                                                                            /product-"hypothetical protein"
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/db_xref-"G1:17026165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5935, .7050)
/gene="SCP2.07c"
complement(5935, .7050)
/gene="SCP2.07c"
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/gene="SCP2.09c"
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/gene="SCP2.08"
7201, .7386
/gene="SCP2.08"
/note="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                    5557. .5886
/gene="SCP2.06"
/note="Unknown"
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                                                                                      misc_feature
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                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCP2.02"
/note="Identical to Streptomyces coelicolor putative
/Inote="Identical to Streptomyces Scolor in Streoby28
/EMBL-AL022861) (152 aa) fasta Scoros: E(): 0, 99.3% id in 152 aa. Complete protein may be translated via a frameshift from the upstream CDS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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/product-*hypothetical protein"
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/db_xref="c01:17026161"
/translation="MSRRSIALPSTRSTEPDDADELEAAPEEKLAAARSAGVVASLTG
ABLSTPLIVAOLPTPYDVAETYTAPLHOGRORYLLOVEQALEHGFRKSVVAGKALEVI
NRGRLY RETHETFANYTEWDMRRAHAYRNI EGWRPADLVSPIGDI NEGGARELAVI
LKEYGPEVTVTLYRGVKELRGDRRVTAADLSEARAALPPPRHLARPDQVRDVLLVAAA
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/protein_id="CAD11995.1"
/db_xref="GI:J7026159"
/translation="MGRGDLTNREWSLLEPHLPPLGGRGGRWNDHRTVVNGILFRVRT
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GGRPATRPDHYSGDAXYSSRRNRYLBRRRIHHTPPERDQRANRRRGREGGRPAGF
DRDHYRRRNEYFRINKLKARRAVATRYDKRAYVFHGTVTAAAIRLWLRQ"
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/translation="MTESPRAALPSLNSPPGDRLEIVNGWDADTPYQSWRPQILVPPTFRQASAPRVFVVVNQKGGAGKTTTTVELAAAWAAAGHRVRVIDADHQEAALSAWLLPQ
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YPEGSERHSLRSVFFEDCTLAEATYPTLFAGVDVVPSSVDLQRVEXERPIGAEQGLAA
                                                                                                                                                                                                                                                                                                                                                                                         GVPWRDLPERYGSWKTIYERHRRWSADGTWDRILQSYQADADLAGRIDWSMYGYDSTS
CRAHQHAAGARKTRPRYPKKGQRPGTTAPTRDSDGPGAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGRAPRLAPAEPKVPAQAADEHQAEGVDEGGVSODGVDEGAEATATLEAAVAQQRQIY
DRVGGGTLAAALLXDPGRGDHLRRELRQYAQRTAYRARDTSGEGVADDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (266 aa)
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/note="Similar to Caulobacter crescentus chromosome
partitioning protein ParA SW:PARA_CANCR (005189) (266 aa
fasta scores: E(): 13e-21, 36.2% id in 257 aa, and to
Streptomyces coelicolor ParA TR:09RPM1 (EMBL:AF187159)
(357 aa) fasta scores: E(): 2.6e-19, 36.1% id in 263 aa.
Contains Pfam match to entry PF00991 ParA, ParA family
                    /gene="SCP2.01"
/note="Identical to Streptomyces coelicolor putative ISIG68 transposase SCIS8.15 or SC6A9.36 TR:069927 (EMBL:AL023861) (141 aa) fasta scores: E(): 0, 100.0% in 141 aa. Contains Pfam match to entry PF01511 Transposase_6, Transposase. Complete protein may be translated via a frameshift into the downstream CDS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry PF01511 Transposase_6,
Transposase, score 12.30, E-value 3.6e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative partitioning protein ParA"
/protein_id="CAD11998.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3033, .4010)
/gene="SCP2.04c"
complement (3033, .4010)
/gene="SCP2.04c"
/note="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4007. .4939)
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914. 1372
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/gene="SCP2.01"
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GMEPPYLVAWEGRFVGEVHRHGPAYLHSWYVLPYGDDEEPTAEAPDFNGRPFGTARAA
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GFATLGKARLETVGVUDVGILVLIALDLLMARIRRPIGWVRFPVWILLTGASA
APSAGAWTALDXVATFAHAVVVLFTATVEVGRATVDRVVRPDAHNGPGVPLYKHWELA
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2140. 2179
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/transl_table=11
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BARADEAAAERRAREBEAALTAAEDEARTAAAEASTEEARARASQAQRDAABAEGQAA
BARHRAAEAERRAVEAEDELTLSPRDRVVRKVARMILAEGAGHPENLPLESVWTACSV
SOTTAGESTRSAALCLAEGYTPEAR"
1 2999 c 2583 g 979 t
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Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
Submitted (14-NOV-2001) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CBIO ISA E-mail: barrell@sanger.ac.uk Plasmid supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 19-NOV-2001
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Haug, I., Brolle, D., Welssenborn, A., Kieser, T., Wohllebens, W. and
Altenbuchner, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bidA regulation; GntR-family regulator; IS1648; partitioning protein ParA; plasmid transfer; Tn5714; TraA; TraB; transposase;
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    .31317
/organism="Streptomyces coelicolor"
/db_xref="taxon:1902"

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Indels:
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Matches:
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ISBN 0-7084-0623-8,
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CDS

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gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces,
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Wilkinson.C.J., Hughes-Thomas,Z.A., Martin (nee Rowe),C.J.,
Mikinson.C.J., Hughes-Thomas,Z.A., Wheatcroft,M., Wirtz,G.J.,
Staunton,J. and Leadlay,P.F.
Increasing the efficiency of heterologous promoters in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORF1; ORF2; ORF3; ORF4; ORF5; ORF6.
Streptomyces coelicolor.
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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1. .7686
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1261. .1713
                                                                                                                                                                                                                                                                                                                        /note="CG7901 gene product [alt 2]"
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Streptomyces coelicolor plasmid 2 (SCP2*).
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Conservative:
Mismatches:
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/gene="CG7901"
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J. Mol. Microbiol. Biotechnol. In press
2 (bases 1 to 7686)
Wilkinson, C.J.
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Query Match:
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gene

CDS

mRNA

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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotta, Metaacoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryotta; Metaacoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 224866)

8 Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Asaburner, M., Henderson, S.N., Button, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfelffer, B.D., Wan, K.H., Doyle, C., Batter, E.G., Helt, G., Nelson, C.R., Gabor, Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Beson, R.Y., Baxendale, J., Bayaraktaroglu, L., Beasley, E.M., Beson, R.Y., Botchan, M.R., Bouck, J., Brokstein, P., Botshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Botshakov, S., Burtis, K.C., Busho, D.B., Buller, H., Cadleu, E., Center, A., Chanfar, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., Chunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabziellan, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic scaffold 14200013386035 section 46 AE003721 AE002708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 13996 GAGGAGGAAGCTGACGAGGACGCCGCCGCCGCCGCAGCAGGAGGATGCCGCAGCCGCCTGCCGCC 13937
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Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
153590: contig of 924 bp in length
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154319: contig of 649 bp in length
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155502: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pBACe3.6"
41735 a 34360 c 34802 g 41426 t 3517 others
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Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Drosophila melanogaster
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66.67%
50.00%
41.86%
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154824
155423
155503
                                          153591
153671
154320
154400
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Best Local Similarity:
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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/gene-
//gene-
Guan, P., Harris, M., Harris, N.L., Harvey, D., Hehman, T.J.,
Mernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J.,
Med., M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z.,
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Li, J., Li, Z., Liang, Y., Lin, X., Mutchi, B., Murlosh, T.C.,
McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C.,
Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L.,
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Simpson, M., Skupski, M.P., Smith, T., Spier, B., Spradling, A.C.,
Stapleton, M., Strong, K., Sur, K., Wassarman, D.A.,
Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T.,
Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T.,
Weinstock, G.M., Zhan, M., Zhang, G., Zhao, O., Zheng, L., Zheng, X., H.,
Glbbs, R.A., Myers, E.M., Rubin, G.M. and Venter, J.C.
The genome sequence of Drosophila malanogaster
S. Johase, Iro, 224866,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitsed
Rockville, MD, USA
Location/Qualifiers
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Drosophila melanogaster chromosome 3 clone BACR48113 (D522) RPCI-98 48.1.13 map 90E1-90F10 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 38 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa; Arthropoda; Tracheata; Brachycera; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E l (bases 1 to 155840)

S Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butchhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L., Hokle,A., Hoskins,E., Galle,R., George,R.A., Harris,N.L., Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfelifer,B., Hoblards,S., Schti,H., Srirskas,R.R., Wan,K.H., Webster,D., Hoolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
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Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Chamee,M., Chavez,C., Chew,M., Ciestolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kan,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Buck,S., Pytrskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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12
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54.00
66.67%
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                   contig of 667 bp in length
gap of unknown length
contig of 541 bp in length
gap of unknown length
contig of 6337 bp in length
gap of unknown length
gap of unknown length
contig of 5481 bp in length
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contig of 121170 bp in length
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gap of unknown length
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (Dases 1 to 151610)

Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., An, H., Baldwin, D., Manatidos, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J. Besson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Forfsett, V., Doup, L.E., Doyler, C., Dresnek, D., Farfan, D., Feritora, S., Frise, E. Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Petelfer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Saupetcon, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G. M. and Venter, J.C., Stephylon, Sequencing of Drosophila chromosome 3R, region 908-908
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC009462 151610 bp DNA linear INV 06-SEP-2001
Drosophila melanogaster, chromosome 3R, region 90E-90E, BAC clone
BACR57604, complete sequence.
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Submitted (23-3407-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Sep 6, 2001 this sequence version replaced 91:13384332.
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ALKGWYTIATKLGYDYQDLYDAFAALKNQLLNNLDNENSLFETQTASHDSAVAQFNAD
ISNYNGQINDARQALNDLINDSLINTYQNLQDAQQALQDWTDALNAAEBALANNERALYQ
VATARYSNADQYJIAVEKLQASGSHYDNALGSFSFYQIKNTFVSFAQKWTEATKGM
NAKHQLFVKPVVQAMMQVKNNTSQSSLQTAIKALQDLGAYFQRTFSDLTNEYYSFTQN
VQSTIDGLNQIIDILQNQVIPGYEAQISSLQAQIQQVEDALALAQQNLQDAQNALDAE
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Submitted (16-70V-1999) Celera Genomics, 45 West Gude Drive,
Submitted (16-70V-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10212984 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
                        /note = "Ca2+ binding protein; translated as a proprotein;
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                               /product="granule lattice protein 5 precursor"
/protein_id="AAC27989.1"
/db_xref="G1:3366655"
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/db_xref="taxon:7227"
7110 c 6761 q 9151 t
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                                                                                 /codon_start=1
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AC014470.1 GI:6436865
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/gene="GRL5"
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PVGTFKYGSLSLWWGFRYDYDTGISIARKYTANGKTLGFQDFGKASLLCHARCAEARAEA
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EADGEADAIKKRAQAEADAIKLRGEALRQVPNVMELEAINKWNGGLPQYWTEGANTPF
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/gene="HCM2.0007c"
/gene="HCM2.0007c"
/gene="HCM2.0007c"
/note="HCM2.0007c"
/note="H
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Tetrahymena thermophila granule lattice protein 5 precursor (GRL5)
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/gene="HCM2.0006c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site"
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Matches:
Conservative:
                                                    /product="putative lipoprotein"
/protein_id="CAD09873.1"
/db_xref="GI:16505987"
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Best Local Similarity:
Query Match:
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Complement(1647. 2489)

Gene="HCM2.0006c, possible lipoprotein, len: 280 aa;

//doce="HCM2.0006c, possible lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipoprotein lipid attachment site"
                             /translation='WKILMESASTDYDYPLEMVKCDGLNDEELQAAIERNLVEYTG
MDADSVYVDDGVCWHNGSCWYVDDTMTVSDEDAAHLERILGISTFE"
complement(58..65)
//note="possible RBS"
complement(719. .1129)
/gane="HCM2.0004c"
complement(719. .1129)
/gane="HCM2.0004c,"
/gane="HCM2.0004c,"
/note="HCM2.0004c, hypothetical protein, len: 136 aa;
/note="HCM2.0004c, hypothetical protein len: 136 aa;
/sone="HCM2.0004c, hypothetical protein from plasmid
pwr1 (136 aa), fasta scores; E(): 0, 97.8% identity in 136
aa overlap and TR:068762 (EMBL:AF074611), Y1116, Yersinia
pestis KIM5 hypothetical protein from plasmid pwr1 (136 aa),
postis KIM5 hypothetical protein from plasmid pwr1 (136 aa),
poverlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1113. .1484)
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complement(1113. .1484)
/gene="HCM2.0005c"
complement(1113. .1484)
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SEDEADWORFIRMYAEEVGPTPTAEQAMLLKYFKEAGENLPVDDTPHWFHAAWRKFDV
IYTRGMGSKDMVVWHLMHIDKAVDRTLEKFFPPA"
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complement(1492. 1497)
/note="possible RBS"
1565. 1621
/note="repeat 1; 57 bp repeat"
complement(1647. 2489)
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/transl_table=11
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/protein_id=1cab09872.1"
/db_xref="G1:16505986"
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/db_xref="G1:16505985"
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/gene="HCM2.0005c"
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'db_xref-"GI:16505984°
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I (bases 1 to 106516)

RS Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Waln, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T. G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18

L Nature 413 (6858), 848-852 (2001)
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plasmid pHCM2.
AL513384.1 GI:16505981
/product="Cation EFFLUX SYSTEM PROTEIN"
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AQVVVQITYPRQSPRIVQEQVTYPPLVSTEMSTANIDTVRGISSYESGLIYIFKDGVN
LYWARDRVLEQLNRVSNLPKDAKVEIGSDSTSIGWAYQYALSSDSKNLSDLKVLQDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKTLQYIVPVSVFIIFILIVFALKNLTNSLLCFFTLPFAFLGGLIFMNLMGFNMSVAA
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
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69.57%
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SOURCE
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Complement(29. 334)

/gene="HCM2.0002c", possible periplasmic protein, len: 101
aa; similar to TR:CAB5528 (EMBL:AL17211), YPMT1.46c,
Yersinia pestis hypothetical protein from plasmid pWT1
(111 aa), fasta scores; E(): 2.88-26, 95.5% identity in 67
aa overlap. The N-terminal 37 aa are highly similar to
YPMT1.46Ac (EMBL:AL17211) Yersinia pestis hypothetical
protein from plasmid pWT1 (59 aa) (86.8% identity in 38 aa
overlap) which lies immediately upstream of YPWT1.46c in
PMT1. Contains a possible N-terminal signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(375. .650)
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/fone="HCM2.0000c"
/fone="HCM2.0003c, hypothetical protein, len: 91 aa;
/highly similar to TR:CAB62371 (EMBL:AL117211), YPMT1 46BC,
Yersinia pestis CO-92 hypothetical protein from plasmid
pMT1 (91 aa), fasta scores; E(): 0, 94.5% identity in 91
pestis KIM5 hypothetical protein from plasmid
pestis KIM5 hypothetical protein from plasmid
aa), fasta scores; E(): 0, 94.5% identity in 91 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKTVLDTLLLIVSIAFVLDCIFTGAIRKALAPVNGAMVVDSGEQ
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                                                                                                                                                                                                                                                                                                                                                                       /gene="FKM2.0001c"
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/note="FKM2.0001c, hypothetical protein, len: 68 aa;
/note="FKM2.0001c, hypothetical protein, len: 68 aa;
/note="FKM2.0001c, hypothetical protein from plasmid persila pestila co-92 hypothetical protein from plasmid pwr1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity forsina pestils KIMS hypothetical protein from plasmid pwr1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity in 60 aa overlap. Spans the end of the sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .232
/note="95.7% identical to Yersinia pestis CO-92 plasmid pMT1 (EMBL.ALI1211) bases 48304. .48535"
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Location/Qualifiers
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on the World Wide Web
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Diane E. Taylor are with the University of Alberta Department of Medical Microbiology and Immunology, Edmonton, Alberta, Canada, T66 2H7 and the Canadian Bacterial Diseases Network. All other authors are with Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Putative identifications, sequence alignments, and name and sequence search capabiblity are available at ARCB's World Wide Web site. (URL: http://www.astra-boston.com/hpylori).
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gene

CDS

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NGDY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA linear BCT 20-JAN-1999 section 109 of 132 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (Jan. 128 Sidney Street, Cambridge, MA 02139, USA Address all correspondence to: hp@arcb.us.astra.com or Richard A. Address all correspondence to: hp@arcb.us.astra.com or Richard A. Aid. Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, Mary Co. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills, Rene Gibson, and Gerald F. Volsia are with Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
Nature 397 (6715), 176-180 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                            /hote="similar to GB:M26073 SP:P13511 PID:141928 percent identity: 31.32; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 12526)
Alm,R.A., Ling,L.S., Moir,D.T., King,B.L., Brown,E.D., Doig,P.C.,
Smith,D.R., Noonan,B., Guild,B.C., deJonge,B.L., Carmel,G.,
Tummino,P.J., Caruso,A., Uria-Nickelsen,M., Mills,D.M., Ives,C.,
Gibson,R., Merberg,D., Mills,S.D., Jiang,Q., Taylor,D.E.,
Vovis,G.F. and Trust,T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S041 ATACAAGCCTTACAAGAGCAAATTGACGCTTTAAGTTCTCAAGAAAAGTCGTTAGCAAG 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValLys
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2 (bases 1 to 12226)
King, B.L., All, R.A. and Trust, T.J.
Direct Submission
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Mismatches:
Indels:
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Matches:
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Helicobacter pylori, strain J99
genome
                                                                                                                                                                                                                                                                                               /transl_table=11
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Helicobacter pylori J99
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AE001548 AE001439
AE001548.1 GI:4155845
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57.00
69.57%
52.17%
44.19%
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AUTHORS
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REMARK
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KEYWORDS
SOURCE
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AE001548
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YYFRSKQYYNYDMFSIALSIPLPIYGKQAKLVEQKKKESLVFKSEVENTKNKTHHLAL
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gene

CDS

gene CDS

gene

23

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LLNVFENMVFLELYKQPRYZELYSHDNGIFILRENSTNKLALIAHAFPTPHFLEKQLL
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BEKLIGGNTAFGLLKRFPHIQTIIKGDETIAQIAMASYLAKAFKOREMLELHALFKEY
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complement(2676. .2927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GB:L77117 PID:1592175 percent identity: 30.81; identified by sequence similarity; putative"
                            Submitted (06-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA 3 (bases 1 to 12496) White, O. Direct Submission Submitted (17-MAR-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical ATP-binding protein"
/protein_id="AAD08366.1"
/db_xref+"GI:2314490"
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/protein_id-"AAD08375.1"
/db_xref-"GI:2314499"
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                                                                                                                                                                                                                                                                                                                                             /organism="Helicobacter pylori 26695"
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/gene*"HP1324"
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/gene="HP1323"
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/transl_table=11
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/transl_table=11
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/transl_table=11
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/1452. 2067
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/gene="HP1321"
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/gene="HP1321"
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/gene="HP1322"
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                                                                                                                                        /codon_start=1
/protein_id="AAA29758.1"
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/protein_id="160671"
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GFLNGKNGKGNKYEDLQEEGEGENDBEHSNEEESDNDEENEIVGQDEAPKSDEAEA
IKSDEAEALKSDEAEARKSDEAEALKSDEAEARKSDEAEARK
                                                                                                                                                                                                                                                                                                                                             SDEAEALKSDEAEALKSDEAEARKSDEAEARKSDEAEARKSDEAEARKSDEAEALKSD
EAEARKSDEAEARKSDEAEALKSDEAEARKSDEAEARKSEAGTEGPKGTGGPGSEAGT
EGPKGTGGPGSGGEHSHNKKKSKKSIMMMLILM"
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Hellcobacter pylori 26695 section 112 of 134 of the complete
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2 (bases 1 to 12496)
Tomb,J.-F., White,O., Kerlavage,A.R., Clayton,R.A., Sutton,G.G., Tomb,J.-F., White,O., Kerlavage,A.R., Clayton,R.A., Sutton,G.G., Fleischman,R.D., Ketchum,K.A., Klenk,H.P., Gill,S., Dougherty,B.A., Nelson,K., Quackenbush,J., Zhou,L., Kirkness,E.F., Peterson,S., Loftus,B., Richardson,D., Dodson,R., Khalak,H.G., Glodek,A., McKenney,K., Fitzegerald,L.M., Lee,N., Admas,M.D., Hickey,E.K., Berg,D.B., Gocayne,J.D., Utterback,T.R., Peterson,J.D., Welley,J.W., Cotton,M.D., Weldman,J.M., Fujii,C., Bowman,C., Watthey,L., Wallin,E., Hayes,W.S., Borodovsky,M., Karp,P.D., Smith,H.O., Fraser,C.M. and Venter,J.C.
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Helicobacter pylori 26695
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
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14
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7
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                                   antigen signal peptide"
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Indels:
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                                                                665. .1594
/note="S antigen precursor"
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/product="S antigen"
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1 bp upstream of EcoRI site.
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AE000634.1 GI:2314489
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/note="S a
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sig_peptide
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REMARK
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AE000634
LOCUS
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KEYWORDS
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/goods the subtilis | spip19670|MUA2_BACSU | note="Mest blastp hit = spip19670|MUA2_BACSU | note="Mest blastp hit = spip19670|MUA2_BACSU | UDP-N-ACETYLGLUCOSAMINE | -CARBOXYVINYLTRANSFERASE | CUDP-N-ACETYLGLUCOSAMINE | ENOLPRRUYL TRANSFERASE | CUDP-N-ACETYLGLUCOSAMINE | ENOLPRUYL TRANSFERASE | CEPT | sqi12127262|pir|1032354 | UDP-N-ACETY1glucosamine | -carboxyvinyltransferase | Sci1683567|cheb|CASSP672| | (249782) | UDP-N-ACETY1glucosamine | -carboxyvinyltransferase | Bacillus subtilis| sqi12636235|emb|CASB5727.1| (299122) | UDP-N-ACETY1glucosamine | -carboxyvinyltransferase | Bacillus subtilis| sqi12636247|emb|CASB5738.1| (299123) | UDP-N-ACETY1glucosamine | -carboxyvinyltransferase | Bacillus subtilis| subtilis|
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DALGSEERAAVVKADNASDALEALADQTDALGSEEAEVVQSDNAASDAMEKAAPPIAL
DVKKŢKDTKPVVĶKEERQNVNŢLPŢŢGEESNPFFTAAALAIMVSTGVLVVSSKCKEN"
  /product="protein GRAB (protein G-related alpha 2M-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFASA7 3838 bp DNA linear INV 26-APR-199
PlasGmodium falciparum (1solate NF7) S antigen gene, complete cds.
M10130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Twenty degenerate tandem repeats of twentyfour base pairs each start at position 953 and end at 1432.

Location/Qualifiers
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Plasmodium falciparum
Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 3838)
Cowman, A.F., Saint, R.B., Coppel, R.L., Brown, G.V., Anders, R.F.
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l_carboxylnyltransfersse"
/protein_id="AAK34186.1"
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Conservative:
Mismatches:
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/db_xref="taxon:5833"
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complement(6939. .8198)
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Best Local Similarity:
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Pred. No.:
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ACCESSION
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PFASA7
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KEYWORDS
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MYRCIEKAVIGNRIGDIGAAVQEYAESFGYGVVRDLVGHGVGPTMHEEPMVPNYGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVTHYDTFTVATMINHALSNIRIKTDLKTVEQVMIPITDYGYLCEDSSVEEFNTLIKK
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COMPLEMEN (5148. . 5690)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introgreement (18856. 5139)

Complement (18856. 5139)

Gane="Spy1355"

Complement (18856. 5139)

/gene="Spy1355"

/note="Best Blastp hit = pir||A69999 hypothetical protein ytol = Bacillus subtilis >9112293258|gb|AAC00336.1|

AF008220) Ytol [Bacillus subtilis]

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/note-"Bast Blastp hit - sp|0929J4|AMPM_BACHD METHIONINE
AMINOPEPTIDASE MAP) (PEPTIDASE M)
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(identity of 81% to B. subtilis) |Bacillus halodurans)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SPy1356" 5690)
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                                                                                                                                         complement(2980. .3840)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSP SYNTHASE) SAL1075724|ptr||552580 3-phosphoshikimate | carboxyvinyltransferase (EC 2.5.1.19) - Lactococcus | lactis > 94|683583|emb|CAA55180.|| (X78413) - Lactococcus | lactis > 94|683583|emb|CAA55180.|| (X78413) - Lactococcus | lactis > 94|683583|emb|CAA55180.|| (X78413) - 164010pruvylshikimate-3-phosphate synthase [Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAFPLIVIAANIFPYLNIDIADLLRLMKQNLPKDIFRPASAIVENIFSKPSGSVLGVA
TLTGLMTMSRSLTSLQKAINKAYGASQHRDFFIGHLVGLLTSLIILFLLAFALIFSIF
SKAAIQVLDKHYHLSDNITTIFLLLIQPITVLIIFVGLMLLYFLLPNVKIKKIRYILP
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//Acce="Best Blast | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Access | Acce
Yuan,X., Clifton,S.w., ncc,c....

Direct Submission

Submitted (10-APR-2001) Department of Microbiology and Immunology,
University of Oklahoma Health Sciences Center, 940 SL Young Blvd,
Oklahoma City, OK 73104, USA

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Best Blastp hit = sp|P43905|AROA_LACLA 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table-11
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/gene="arok"
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                                                                                                                                                                                                                                                                                                       /serotype="M1'
                                                                                                                                                                                                                                                                                                                                                                                                     /gene="aroK"
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                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MOKEIKYKCFLRRSAFGLVAVSASVLVGSTVSAVDSPIEOPRII
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1 (bases 1 to 10029)
Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Seatete,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Oian,Y., Jia,H.G., Najar,F.Z., Ren,O., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 TCAGATGCCTTAGAAGCATTAGCGGATCAAACAGACGCTTTACAATCAGAAGCAGCGGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100. .273
/note="Region: alpha2-macroglobulin-binding A domain"
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                                         pyogenes"
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/note="Region: repeat motif"
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/protein_id="AAD26338.1"
/db_xref="GI:4589079"
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                                      /organism="Streptococcus
/strain="ATCC700294"
/db_xref="ATCC:700294"
/db_xref="taxon:1314"
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Streptococcus pyogenes M1 GAS
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/codon_start=1
/transl_table=11
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/product-"GRAB"
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/note-"Region:
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Streptococcus pyogenes
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Streptococcus pyogenes strain AP49 GRAB precursor, gene, partial
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/note="Region: alpha2-macroglobulin-binding A domain"
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Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates pacterial surface by binding alpha2-macroglobulin J. Biol. Chem. 274 (22), 15336-15344 (1999)
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          Rasmussen, M., Muller, H. P. and Bjorck, L.
Direct Submission
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Pathogenesis, Scelvegatan 39, Lund 221 00, s
1. 717
/organism="Streptococcus pyogenes"
/strain="KTL9"
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2 (bases 1 to 804)
Rasmussen.M., Muller,H.P. and Bjorck,L.
Direct Submission
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/note="Region: repeat motif"
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/note="Region: cell-wall att
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/note="grab"
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AF124403.1 GI:4589086
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VVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE"
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Rasmussen.M., Muller, H.P. and Bjorck, L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the
bacterial surface by binding alpha2-macroglobulin
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcacese;
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/note="Region: alpha2-macroglobulin-binding A domain"
Biology, Molecular
Sweden
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Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular
Pathogenesis, Scelvegatan 39, Lund 221 00, Sweden
Location/Qualifiers
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/note="Region: cell-wall attachment"
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                                                                                 /organism="Streptococcus pyogenes"
/strain="AP49"
Submitted (28-JAN-1999) Cell and Molecular Pathogenesis, Soelvegatan 39, Lund 221 00, Location/Qualifiers
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Mismatches:
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/codon_start=1
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Rasmussen, M., Muller, H.P. and Bjorck, L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin
J. Blol. Chem. 274 (22), 15336-15344 (1999)
   Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin 37. Biol. Chem. 274 (22), 15336-15344 (1999)
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Streptococcus pyogenes strain KTL9 GRAB precursor, gene, partial
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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/product-"GRAB"
1. .15
/note-"Region: alpha2-macroglobulin-binding A domain"
<1. .>469
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Rasmussen, M., Muller, H.P. and Bjorck, L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular
Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden
1. 469
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/note="Region: repeat motif"

343. 469

/note="Region: cell-wall attachment"

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Mismatches:
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/db_xref="taxon:1314"
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                       1 (bases 1 to 468)
Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin
9.274 (22), 15336-15344 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"VDSPIEOPRIIPNGGTLTNLLGNAPEKIALRNEERAIDELKKQA
IEDKEATTAIEAASSDALEALADOTDALQSEEAAVVKADNAASDALEALADOTDALQS
EEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE"
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Bacteria; Firmlcutes; Bacillus/Clostridium group; Streptococcaceae;
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/note="Region: alpha2-macroglobulin-binding A domain"
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Brasmussen, M., Muller, H.P. and Bjorck, L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden
Location/Qualiflers
Location/Qualiflers
/organ.sm="Streptococcus pyogenes"
/strain="KTL3"
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Rasmussen,M., Muller,H.P. and Bjorck,L.
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Streptococcus pyogenes
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/note="grab"
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-MODEL-frame+_pin.model._UDEV=xlh
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-Q-/cgn2_1/USPTQ_spool/US09847539/runat_10102002_093105_4992/app_query.fasta_1.526
-Q-/cgn2_1/USPTQ_spool/US09847539/runat_10102002_093105_4992/app_query.fasta_1.526
-Q-/cgn2_1/USPTQ_spool/US09847539/runat_nred
-UDECALIGN-200 -LOPE-TAR_score=pot -THR_MAX=100 -THR_MIN-0 -ALIGN-40 -MODE-LOCAL
-UOTENT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09847539_GCN_1_1182_erunat_10102002_093105_4992 -NCPU-6 -TCPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6 -FGAPDEXT=7
                                                                                                     ; Search time 274.909 Seconds
(without alignments)
2131.407 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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129
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Maximum Match 100%
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AF124400 Streptoco
AF124402 Streptoco
AF124403 Streptoco
AF124399 Streptoco
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AE011548 Helicobac
AE011394 Salmonell
AF0311321 Tetrahyme
AC014470 Drosophil
AC009462 Drosophil
AC006495 Drosophil
AE003721 Drosophil
AL44671 Streptomy
AL64771 Streptomy
AC07274 Homo sapil
AC09724 Homo sapil
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AC011910 Drosophil
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AL592292 Streptomy
AC012724 Drosophil
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AC006495
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AF124401 468 bp DNA linear BCT 14-AUG-2000 Streptococcus pyogenes strain KTL3 GRAB precursor, gene, partial

Streptococcus pyogenes

AF124401 AF124401.1

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CC The present invention provides a number of single exon nucleic acid
C probes which may enable used to measure gene expressed in the human
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX
SO Sequence 544 BP; 124 A; 113 C; 135 G; 172 T; 0 other;
Alignment Scores:
Breach No.:
CC strip probes of the invention.
SO Sequence 544 BP; 124 A; 113 C; 135 G; 172 T; 0 other;
Alignment Scores:
Breach Similarity:
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                                                                                                   measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                             probe of the invention.

Note: The sequence data for this patent did not form part of the parinted specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                        2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer-------
                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                  Claim 1; SEQ ID NO 10489; 639pp + sequence listing; English,
                                                                                         probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe SEQ ID NO: 10499.
                                                                                                                                                                                                    Sequence 544 BP; 124 A; 113 C; 135 G; 172 T; 0 other;
                                                                                                                                                                                                                                     544
13
                                                                                         a single exon nucleic acid
                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6_COPY_59_86 (1-28) x ABA62184 (1-544)
                                                                                                                                                                                                                                     Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK10508 standard; DNA; 544
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                   85.9
45.50
55.56%
48.15%
35.27%
                                                                                       The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
         WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52.
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                          Alignment Scores:
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                             290 GACATITIGGAACAGACTGCAGCTCAGGTGGATGCCTTGCAGGGCCATCTTCAACAAATG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                            SEQ ID NO: 10499; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                       Sequence 544 BP; 124 A; 113 C; 135 G; 172 T; 0 other;
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13
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7
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 GluGluAlaAlaValValLys 23
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2000US-0207456.
2000US-0608408.
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20000S-0234687.
20000S-0236359.
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45.50
55.56%
48.15%
35.27%
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                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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   exon
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                                              Example 4;
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Single
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DB:
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Penn SG, Hanzel DK, Chen W,
03-AUG-2000;
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                                                                                                                                                                                                                                                             Query Match:
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                                                                                                                                                                                                                                                                                                                                                                              RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #23858 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow .
                                                                                                                                                                             Example 4; SEQ ID NO: 23882; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                       234
13
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                                                                                                                                                                                                                                                            61 G; 57 T; 0 other;
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Matches:
Conservative:
Mismatches:
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                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                       17 GluGluAlaAlaValValLys 23
                                                 20000S-0632366,
20000S-0234687,
20000S-0236359,
                                                                                                                                                                                                                                                             Sequence 234 BP; 61 A; 55 C;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                  2000US-0207456.
2000US-0608408.
        30-JAN-2001; 2001WO-US00668
                         2000US-0180312
                                                                              2000GB-0024263
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45.50
55.56%
48.15%
35.27%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic disorder; ss.
                                                                                                                Hanzel DK,
                                                                                                                                WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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                                                  03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                   26-MAY-2000;
30-JUN-2000;
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                         04-FEB-2000;
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                                                                                                                Penn SG,
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foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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13
2
7
1
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Mismatches:
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                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 23858; 654pp; English.
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                                                                                                                                                             Penn SG, Hanzel DK, Chen W, Rank DR;
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                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000, 2000US-0207456.
30-JUN-2000; 2000US-0631408.
03-AUG-2000, 2000US-0531366.
21-SEP-2000, 2000US-0234687.
27-SEP-2000; 2000US-0234597.
04-OCT-2000; 2000GB-0024263.
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                   21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0236359.
04-OCT-2000, 2000GB-0024263.
2000US-0632366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 GluGluAlaAlaValValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.6
45.50
55.56%
48.15%
35.27%
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Best Local Similarity:
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid norther invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 22983; 639pp + sequence listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 234 BP; 61 A; 55 C; 61 G; 57 T; 0 other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                               21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                      04-FEB-2000; 2000US-0180312, 26-MAY-2000; 2000US-0207456, 30-JUN-2000; 2000US-0608408, 03-AUG-2000; 2000US-0632366.
                                                                                   30-JAN-2001; 2001WO-US00669
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45.50
55.56%
48.15%
35.27%
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Best Local Similarity:
                                          WO200157277-A2
                     Homo sapiens
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                                                               09-AUG-2001
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple solerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                              for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 23145; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone marrow expressed single exon probe SEQ ID NO: 23882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer------
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72
72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                              exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                             26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060B40B.
03-AUG-2000; 2000US-0632566.
21-SEP-2000; 2000US-02346B7.
27-SEP-2000; 2000US-02346B7.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 234 BP; 61 A; 55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                                                                                    30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GluGluAlaAlaValValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 GAGCAGGAAGCCCTGGTGAAG
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45.50
55.56%
48.15%
35.27%
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                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483446/52
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WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40200157276-A2
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                                          09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                              Penn SG,
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98US-0103794

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09-OCT-1998;
30-APR-1999;
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                                                                                                                                                                                                                                                      sequences from the Corynetorm bacterium Corynebacterium glutamicum. Resequences from the Corynetorm bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, massuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacterium coryneform bacterium of a gene derived from coryneform bacterium, Coryneform bacterium of a gene derived from coryneform bacterium, Coryneform bacterium of a gene derived mino acids, nucleic acids, vitemins, saccharides and organic acids, in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 225435 ATTGAGGCTTACGCACCTGAGGCAGGACGAGGGCGAGGCGAATCTACAAG 225494
                                                                                                                                                          mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification;
                                                                      Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N. meningitidis B full length genome DNA sequence SEQ ID NO:1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 349980 BP; 80289 A; 91081 C; 97378 G; 81232 T; 0 other;
                                                                                                                                                                                                              Disclosure; SEQ ID NO: 7060; 246pp + Sequence Listing; English.
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9
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Mismatches:
                                                                     S, Hayashi M,
Ozaki A;
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                                                                      Mizoguchi H, Ando
Senoh A, Ikeda M,
                                          (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.41e+05
46.00
62.50%
37.50%
35.66%
07-APR-2000; 2000JP-0159162. 03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                      European Patent Office.
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                                                                                                               WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                     Nakagawa S
Tateishi D
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82144

CC represent specifically claimed Neisseria meningitidis genomic DNA c sequences: AAA81260 to AAA81303 and AAB25620 to AAB2565 represent CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA8132 represent PCR primers used in the cisolation of Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to composition of Neisseria meningitidis DNA sequences; and AAA8132 to composition of Neisseria meningitidis DNA sequences, and antibodies composition on be used in the manufacture of a composition on be used in the manufacture of a composition on be used in the manufacture of a composition on be used in the manufacture of a composition of the reating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection due to composition against all pathogenic some of the identificat proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of biological probes, particularly organism-specific probes. Attempts to make efficacious condorcoccus B vaccines have also facilitate production of biological probes, which each antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
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                                                                                                                                                                    Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1437668 BP; 344338 A; 353206 C; 385074 G; 355045 T; 5 other;
                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                 Tettelin H, Venter JC;
Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #22983.
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 866-1272; 1760pp; English.
                                                                                                                                     Peterson J,
C, Mora M,
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46.00
65.38%
42.31%
35.66%
99US-0132068
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                                                                                                                                 Hickey E,
Galeotti
                                                                                                                                                          , V, Gale...
R, Pizza Μ;
                                                                  (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                       WPI; 2000-318079/27.
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Best Local Similarity:
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                                                                                                                                                                                                    Rappuoli R,
                                                                                                                                     Frazer CM,
                                                                                                                                                                        Masignani
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AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis Menb polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism specific probes. Attempts to make efficacious Meningococus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully
                                                                                                                                                                                                                                                                       Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V;
Rappuoli R;
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 69936 BP; 16512 A; 19259 C; 17399 G; 16763 T; 3 other;
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Scarlato V,
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Matches:
Conservative:
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Galeotti C, Mora M, Ratti G, Scarselli M, {
Frazer CM, Grandi G;
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46.00
65.38%
42.318
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Neisseria meningitidis B (NMB). The sequences in AAP71544 and AAP21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21548 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21588 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have attained activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases can be used in a search to identify open reading frames (OKPS) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computers, computer memory, computer storage medium or computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 111891 GCTTTGGAAGCGCGTTTGGAAAAACTTCGAAAAGCCGGGAAAATCCCGAAAAATGGGGCAGCATTG 111950
                                                      Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 349980 BP; 84410 A; 84863 C; 94187 G; 86520 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349980
                                                                                                                                                                  full length genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C glutamicum coding sequence fragment SEQ ID NO: 7060.
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                  present invention describes the
                                                                                                                         Claim 7; Appendix A; 692pp; English
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65.38%
42.31%
35.66%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium;
                 WPI; 2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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99JP-0377484

16-DEC-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a /*tag= a /*tag= a /*tag= a /*tag= a /*tag= a /*note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
3721..3780
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                                                                                                                                                                                                                                                                                                                                                                                                                             Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
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                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus contig SEQ ID #174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
121..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon PJ,
                                                                                                                                                                                           AAV74485 standard; DNA; 4549 BP
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                                                                           576 TTCGAGACGCT 565
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                        24 AlaAspAsnAla 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
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S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyellits, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the Saureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA813103 and AAB25620 to AAA825650 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                             1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ďC;
                                                                                                                                                      Seguence 4549 BP; 1387 Å; 858 C; 698 G; 1421 T; 185 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. meningitidis partial DNA sequence gnm_27 SEQ ID NO:27.
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Ratti G, Scarselli
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112
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Conservative:
Mismatches:
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C, Mora M,
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                                                                                                                                                                                                                                                                                                                                                                              2765 TCAGATATATTGGAAGCGGTA---
                                                                                                                                                                                                                                                                                                                                                                                                                              21 ValValLysAlaAspAsnAlaAla
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AAA81479 standard; DNA; 69936
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99US-0132068
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60.71%
42.86%
35.66%
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                                                                                                                        computer readable medium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-318079/27.
                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                        Alignment Scores:
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30-APR-1999;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamine, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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Tateishi N, Senoh A, Ikeda M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                C glutamicum coding sequence fragment SEQ ID NO: 555
                                                                                                                                                  AAH65520 standard; DNA; 2115 BP
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organic acid synthesis; ds
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209 GCCTATAAAGCTGAT 223
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07-APR-2000;
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Ochiai K, Yokoi H;

Mizoguchi H, Ando S, Hayashi M, Senoh A, Ikeda M, Ozaki A;

Nakagawa S, Tateishi N,

WPI; 2001-376931/40.

(KYOW ) KYOWA HAKKO KOGYO KK

16-DEC-1999; 99JP-0377484. 07-APR-2000; 2000JP-0159162. 03-AUG-2000; 2000JP-0280988.

03-AUG-2000;

18-DEC-2000; 2000EP-0127688

Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.

Corynebacterium glutamicum

EP1108790-A2

20-JUN-2001.

C glutamicum coding sequence fragment SEQ ID NO: 556

(first entry)

26-SEP-2001

AAH65521;

ВР

AAH65521 standard; DNA; 2160

AAH65521, ID AAH6

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly Liysine. The present sequence is a nucleic acid described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO: 556; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621 G; 508 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-847-539A-6_COPY_59_86 (1-28) x AAH65521 (1-2160)
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Best Local Similarity:
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4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23

US-09-847-539A-6_COPY_59_86 (1-28) x AAH65520 (1-2115)

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2115 9 6 9 0 0

Conservative: Mismatches: Indels: Length: Matches:

46.00 62.50% 37.50% 35.66%

Percent Similarity: Best Local Similarity:

Alignment Scores:

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Aspergillus niger EST SEQ ID NO:3866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 4044185 TTGATGGACGCGCGACCTGCTGGAAGGCGAACAGGTAACCATCGTCGATATGGACAAC 4044126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed ication, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                           determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
                                                                                                                                                                                                                                                                                                                                                                                                            Evaluating strain variation of Mycobacterium tuberculosis, comprises
                                                                               Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn
                                            Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
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Mismatches:
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Best Local Similarity:
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expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the Fr cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be consible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be considered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore adapt to changes in culture conditions, environmental stress, spore congineering. Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the canalysis of the results. AAF11248 to AAF11247 represents ESTS from Aspergillus ongers: AAF11854 to AAF11248 to AAF11487 tom Aspergillus organisation.

C all specifically claimed in the present invention.
Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryxae; Trichoderma reese!; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monitoring differential expression of genes in filamentous fungal cell uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NORDISK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shuster JR,
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(first entry)

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AAI99683 standard; DNA; 4403765 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences second. DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (hub.), which data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 29017.
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11-JUL-2000; 2000US-0614150
23-MAR-2001; 2001WO-US09231
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ABL25848/C
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AAI99683/c
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4036256 TTGATGGACGCCGCCGACCTGCTGGAAGGCGAACAGGTAACCATCGTCGATATCGACAAC 4036197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
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                                                          Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
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9
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Mismatches:
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36.43%
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                                                                                                                                                         Mycobacterium tuberculosis
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ID AA1996
XX
AC AA1996
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660 11 3 12 0

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G66 bp mRNA linear EST 19-APR-2001 GH02073.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH02073 5prime, mRNA sequence. A1062753 A1062753.1 GI:3338592 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Metazoa; Anthropoda; Tracheata; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 666)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS06378
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/do_xnef="taxon:727"

/do_xnef="taxon:727"

/clone="GH02003"

/clone_1ib="GH Drosophila melanogaster head pOT2"

/dev_stege="adult"

/lab_host="DH5" - alpha"
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Mismatches:
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Matches:
Conservative:
Mismatches:
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BDGP/HHMI Drosophila EST Project
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High quality sequence stop: 566.
Location/Qualifiers
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Contact: Stapleton, M.
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Query Match:
                                                                                       148
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Percent Similarity:
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KEYWORDS
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                                                                                     BASE COUNT
ORIGIN
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                                      Anote "Vector: pBluescript II SK-; Site_I: ECORI; Site_2:
XhoI: This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA MRNA was purified from each sample, pooled and CDNA
Synthesized. The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcorN (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIG33216
SD2724.5prime SD Drosophila melanogaster Schneider L2 cell culture p072 Drosophila melanogaster CDNA clone SD27244 5 similar to CG7289: FBan0007289 GO:[] located on: 2L 2288-2288:: 05/23/2001,
      /clone_lib**C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture pOT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 660)

1 (bases 1 to 660)

1 Lewis, S. and Rubin, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,

BOGP/HINI Drosophila EST Project

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       507 GAGAAGATCGAGCTGCTGGTGGACAGAGACCGACCTGCGCAACCAGGCGGAGCAGTT 566
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 498
http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003584; arm:2L [1824960,2149443]
estimated-cyto:2284-2292: 05/23/2001
Plate: SD.272 row: D column: 8
High quality sequence stop: 529.
Location/Qualifiers
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD27244"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
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B1633216
B1633216.1 GI:15535426
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Best Local Similarity:
Query Match:
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VERSION
KEYWORDS
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BI633216/c
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JOURNAL
COMMENT
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1...643

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="Lib"LD Drosophila melanogaster embryo BlueScript"
/scx="male and female"
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/Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
ECORI and XhoI in BlueScript SK(+/-)"
              Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
Plate: 101 row: F column: 12
High quality sequence stop: 463.
Location/Qualifiers
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                                              Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota: Neptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 633)

1 (bases 1 to 633)

1 Lewis, S. and Rubin, G. M.

1 Ewis, S. and Rubin, G. M.

1 BDGP/HHMI Drosophila EST Project

Uppublished (2001)
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 643)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.

BOGF/Hilly Drosophila EST Project
Unpublished (2001)

Contact: Stapleton, M.
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LD10172.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD10172 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS06378
hit genomic sequence DS06378
Plate: 21 row: G column: 1
High quality sequence stop: 567.
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Conservative:
Mismatches:
                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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                                    fruit fly.
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Chiamydomonadacaes, Chiamydomonas.

I (bases 1 to 650)

S Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chiamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular plants; project phase 2
Unpublished (2000)

L Unpublished (2000)

DCMB Box 91000

Duke University

Durham, NC 27708-1000, USA

Tel: 919 613 8164

Fax: 919 613 8174

Email: chiamy@duke.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                894047D11.yl C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii CDNA, mRNA sequence.
BE337641. GI:9210726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                            2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
643
11
12
0
                                                                                                                                                                      US-09-847-539A-6_COPY_59_86 (1-28) x AA391497 (1-643)
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Indels:
                        Matches:
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442 GTAGTG 437
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Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (22 (bases 1 to 622))

Rakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hariamoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Makesuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,K., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Riken Mouse,Ests (Arakawa,T., et al. 2001)

AL Onpublished (2001)

AL Departory for Genome Exploration replaced gi:8866254.

Contact: Yoshihide Hayashizaki,Y.

AL Departory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama institute of Physical and Chemical Research Group, Riken)

1.7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tea: 81-45-503-9222

Email: genome-reségsc.riken.go.jp,

Wil.http://genome.gsc.riken.go.jp,

Garninci,P., Shibata,Y., Hyayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subfraction of captrrapper-selected cDNAs to prepare full-length cDNA ilbraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

Watchiki,M., Yoneda,Y., Ishikawa,T., Okazaki,Y., Muramatsu,M., Innoue,Y., Anakaura, S., Kawai,J., Okazaki,Y., Muramatsu,M., Innoue,Y., and Hayashizaki,Y.

Hayashizaki,Y., Muramatsu,M., Innoue,Y., Anakaura, Brakizaki,Y., Muramatsu,M., Innoue,Y., and Hayashizaki,Y., Muramatsu,M., Innoue,Y., and and Hayashizaki,Y., Muramatsu,M., Innoue,Y., and and Hayashizaki,Y., Muramatsu,M., Innoue,Y., and and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and they and th
                                                                          /note—Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
Drote—Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
Drote_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

155 c 148 g 140 t
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Mismatches:
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Matches:
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/clone_lib="RPCI-23"
                               /sex="Female"
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462 GTAGTG 457
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alu62828
GH02173.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH02173 5prime, mRNA sequence.
Al062828
                                                                                                                 encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo.S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Computational Analysis of Full-Length Mouse cDNAS Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Fplease visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                        Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A430036B19"
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                                                                                             Computer-based methods for the mouse full-length cDNA
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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Unpublished (1999)
Other GSSS: RPCI-23-224F10.TJ
Cother GSSS: RPCI-23-224F10.TJ
Cother GSSS: RPCI-23-224F10.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhaodetigr.org
Clones are derived from the mbuse BAC library RPCI-23. For BAC
Library avallability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ698116 615 bp DNA linear GSS 24-JAN-2001 RPCI-23-224F10.TV RPCI-23 Mus musculus genomic clone RPCI-23-224F10 DNA sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 613)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
Mouse BAC End Sequences from Library RPCI-23
                              /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="ib="GH08128"
/clone=lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/sex="male and female"
/lab_host="alult"
/lab_host="lb="3"
/note="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2: Xno1; Sized fractLonated cDNAs were directly ligated into pot1; Plasmid ORA library."

a 146 c 146 g 144 t.
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Mismatches:
Indels:
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/clone="RPCI-23-224F10"
Location/Qualifiers
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53.85%
42.31%
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Best Local Similarity:
                                                                                                                                                                                                                            129
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                                                                                                    A1108834 587 19-APR-2001 GH08128.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster consecuence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 583)
1 (bases 1 to 583)
1 Lewrvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., BDCP/HHMI Drosophila EST Project
Unpublished (2001)
 Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS06378
Plate: 81 row: C column: 4
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Matches:
Conservative:
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Indels:
                 Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
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AI108834.1 GI:3477369
                                                                       Contact: Stapleton, M.
BDGP
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                                                    Unpublished (2001)
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Best Local Similarity:
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/organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDC1011306"
/db_xref="BDGP_EST:BDC1011306"
/db_xref="LD12115"
/clone_1Dp="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/dev_stage="0.to 24 hours mixed sta
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                                       Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydrolda; Drosophilidae; Drosophila.

[ Dases 1 to 569)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,

Lewis,S. and Rubin,G.m.

BORP/HHMI Drosophila EST Project
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hit genomic AE003584: arm:2L [1824966,2149443]
estimated-cyto:2284-2202: 04/10/2001
Plate: Lb.121 row: B column: 3
High quality sequence stop: 527
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 581)
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                                                                                                                                                                                                                                             Unpublished (2001)
On Jan 19, 1998 this sequence version replaced gi:2792678
Other ESTs: LD1115.3prime
Contact: Stapleton, M.
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Conservative:
Mismatches:
Indels:
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Best Local Similarity:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa; Arthropoda; Tracheata; Hachycera;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 568)
1 (bases 1 to 568)
1 (bases 2 to 568)
1 (bases 3 to 568)
1 (bases 4 to 568)
1 (bases 5 and Rubin, 6.M.
1 (BDGP, HHMI Drosophila EST Project
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hit genomic sequence DS06378
hit genomic sequence DS06378
Plate: 88 row: A column: 4
High quality sequence stop: 511.
Location/Qualifiers
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Indels:
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Matches:
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                                                                    167 GTACGAGGAGATCGTGCC 150
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                     22 ValLysAlaAspAsnAla
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                       fruit fly.
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AA392809/c
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AI109571/c
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KEYWORDS
SOURCE
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BI637415 ST 10-SEP-2001 SD19430.5prime SD Drosophila melanogaster Schneider L2 cell culture porz Drosophila melanogaster cDNA clone SD19430 5 similar to CG7289: FBan0007289 GO:[] located on: ZL 22B8-22B8;: 05/19/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon,7227"
/dlone="1501943"
/clone=lib="SD Drosophila melanogaster Schneider L2 cell
culture porg"
/lab_host="DH5-alpha"
/note="Vector: por2; site_1: EcoRI; site_2: Xho1; Sized
fractionated conAs were directly ligated into por2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophilldae; Drosophila.

1 (bases 1 to 567)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubla, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                 Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003584: arm:2L [1824960,2149443]
estlmated-cytc:2284-2202: 05/19/2001
Plate: SD.194 row: C column: 6
High quality sequence stop: 479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       567
111
12
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     00531
                   Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
                                                                                                                US-09-847-539A-6_COPY_59_86 (1-28) x AI388B71 (1-567)
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                                                                                Gaps:
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BI637415.1 GI:15539625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                              167 GTACGAGGAGATCGTGCC 150
51.00
53.85%
42.31%
39.53%
                                                                                                                                                                                                                          22 ValLysAlaAspAsnAla
               Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                                                                                                                   RESULT 24
BI637415/C
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KEYWORDS
SOURCE
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             /clone_lib="GH Drosophila melanogaster head por2"
/sex="male and female"
/sex="male and female"
/dev_stage="adult" = alpha"
/lab_host="DHS" = alpha"
/note="Organ: head; Vector: por2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
por2. Plasmid plasmid = 138 t.
161 c 141 g 138 t.
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Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 567)

2 (bases 1 to 567)

2 (bases 1 to 567)

3 (bases 1 to 567)

4 (bases 1 to 567)

5 (bases 1 to 567)

6 (bases 1 to 567)

6 (bases 1 to 567)

7 (bases 1 to 567)
                                                                                                                                                                                                                                                                                                                                                                                                                  Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC005749
Plate: 199 row: B column: 1
High quality sequence stop: 566.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         2 AspalaLeuGlualaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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/organism="brosophila melanogaster"
/clone="GH19913"
                                                                                                                                                                                                                                                              Conservative:
Mismatches:
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 /clone="GH03030"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 GTACGAGGAGATCGTGCC 151
                                                                                                                        port. Fir-
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53.85%
42.31%
39.53%
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Best Local Similarity:
Query Match:
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Pred. No.:
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AI388871/c
LOCUS
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ORIGIN
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VERSION
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JOURNAL
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Percent Similarity:
Best Local Similarity:
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AI063297/c
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Drosophila melanogaster

Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota: Metazoa: Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 563)

2 (aperan, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, G., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Peacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S. E., Cellinker, S. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 19-APR-2001
                                                                                                                                                                                                                                                                                                                           /clone_lib="unpublished oligo-capped cDNA library, stage
L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF486089
AT20267. prime AT Drosophia melanogaster adult testes poTB7
Drosophila melanogaster CDNA clone AT20267 5 similar to CG7289:
FBan0007289 located on: 2L 2288-2288;: 04/09/2001, mRNA sequence.
                   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11569390.
                                                                                                                                                                                                                                                                                                                                                                                                                          1 others
                                                 Comparing the Company of the Company genome Unpublished (2001)
Contact: Yuli Kohara
Contact: Yuli Kohara
Contact: Yuli Kohara
National Institute of Genetics
Yata Illi, Mashima Shizuoka 411, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                     /organism-"Caenorhabditis elegans"
//dsrain-"N12"
//db.rref-"taxon:6239"
/clone-"yk858e11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                   /sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
a 146 c 142 g 105 t
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Matches:
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                                                                                                                                                                                                Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .558
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68.00%
36.00%
39.53%
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   (bases 1 to
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Query Match:
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LOCUS
DEFINITION
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ORGANISM
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ORIGIN
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AUTHORS
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JOURNAL
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JOURNAL
COMMENT
REFERENCE
AUTHORS
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KEYWORDS
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003584: arm:2L [1824960,2149443]
estimated-cyto:22B4-22D2: 04/09/2001
Plate: AT.202 row: F column: 7
High quality sequence stop: 562.
Location/Qualifiers
1 563
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="AT20267"
/clone="AT20267"
/sex="male"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1063297 EST 19-APR-2001 GH03030.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH03030 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                           //dev_stage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 567)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS06378
Plate: 30 row: C column: 6
High quality sequence stop: 454.
Location/Qualifiers
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11
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0
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/db_xref="taxon:7227"
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One Cyclotron Rd, Berkeley, CA 94720, USA
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Mismatches:
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 GTACGAGGAGATCGTGCC 151
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Fax: 510 486 6798
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478 GAGGATGAC 470
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Best Local Similarity:
Query Match:
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                                RESULT 19
BM431282/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORRWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                          Buvidae; Buvineria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bos.

1 (bases 1 to 548)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Keele, J.W.
                                                                                                                                                                EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.548
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="WARC 1BOV"
/tissue_type="pooled"
/tissue_type="pooled"
/ndb_host="bHi0B"
/note="vector: pCW SPORT6; Site_1: Xbai; Site_2: Xhoi;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
a 143 c 151 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
                                                                                                                                                       амъэчъв
96120 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW659168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTCCCAGTCACGACG
Plate: 83 row: M column: 13
Seq primer: ATTTAGGTGACATARG.
Location/Qualifiers
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                                                                                    151 GTACGAGGAGATCGTGCC 134
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51.00
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Best Local Similarity:
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24 AlaAspAsn 26

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovidae; Bos.

E (bases 1 to 553)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon y.P.M. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)

Contact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of ARNS, University of Alberta
410 Ag1/For, Dept of ARNS, U of A, Edmonton, AB, TGG 2P5, Canada Tel: 780 492 4165

Fax: 780 492 4165
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
    EST 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9913"
/clone_lib="Bos taurus Duodenum #1 library"
/tlone_lib="Bos taurus Duodenum #1 library"
/tcloue_lype="Simple columnar epithelial"
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/note="Organ: Intestine/duodenum; Vector: Uni-2ZAPXR;
Site_1: EcoRI; Site_2: Xho I"
a 124 c 139 g 132 t
  553 bp mRNA linear EST 31-JAN-Bos taurus Duodenum #1 library Bos taurus CDNA, mRNA
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AU206045 unpublished oligo-capped cDNA library, stage L1
Caenorhabditis elegans cDNA clone yk858ell 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smoore@afns.ualberta.ca
Insert Length: 553 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .553
/organism="Bos taurus"
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                                                     seguence.
BM431282
BM431282.1 GI:18453004
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EST.
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276 GCGCGGATACGCCGCC 293
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53.85%
42.31%
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57.69%
50.00%
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Best Local Similarity:
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AA540164/c
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH25307"
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/lab_host="GH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUJO1404 Rice panicle shorter than 3cm Oryza sativa cDNA clone 200571, mRNA sequence.
AUJO1404 I GI:9865654
EST.
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1 (bases 1 to 529)
Sasaki, T. and Yamamoto, K.
Rice cDNA from panicle (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic sequence AC005749 plate: 253 row: A column: 7 High quality sequence stop: 465. Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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/clone=1830571"
/clone=1b="Rice panicle shorter than 3cm"
/dev_stage="shorter than 3cm"
/note="Organ: panicle"
163 c 198 g 89 t
                                                                                                                                                                                                                                                                                                                       491
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Nipponbare"
/db_xref="taxon:4530"
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
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42.31%
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Best Local Similarity:
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Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 195 row: E column: 7
High quality sequence stop: 411.
Location/Qualifiers
1. 535
/organism="Drosophila melanogaster"
/db_xref="BEOF_EST:BDCIN018642"
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/clone="LD19555"
/clone="LD19555"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 19-APR-2001
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LD19555.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD19555 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fruit fly.
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 535)
1 (bases 1 to 535)
Lewis, S. and Rubin, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                  3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
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Mismatches:
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  Length:
Matches:
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI405338.1 GI:4248425
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   Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                               AA423358 454 bp mRNA linear EST 16-OCT-1997 ve38f01.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE1820441 5', mRNA sequence.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
          IMAGE Consortium (infortmesserver)
MGI:488721
His chome was previously sequenced on the 5' end only, this new data is from the 3' end stop: 348.
High quality sequence stop: 348.
Location/Qualiflers
1. 387
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                              /organism="Mus musculus"
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/clone="IMAGE:820441"
/clone_lib="Soares_mammary_gland_NbMMG"
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Conservative:
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Indels:
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/lab_host="DH10B"
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Best Local Similarity:
Query Match:
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/note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                              A1405338 491 bp mRNA 11near EST 19-APR-2001 GH25307.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH25307 5prime, mRNA sequence.
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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pteryota: Metazoa: Endopterygota: Diptera: Brachycera:
Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.

[ (basea 1 to 491)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,Lewis,S. and Rublin,G.m.
EDCP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C578L6"
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/issue_yppe="mammary_gland"
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/lab_host="DH10B"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
MGI:488721
Seq primer: -28ml3 rev2 ET from Amersham.
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Matches:
                                                                                  /organism="Mus musculus"
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                                          Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
   Unpublished (1997)
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279 GTAGTG 274
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi:
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi:
1 (bases 1 to 383)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Eax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Insert Length: 333 Std Error: 0.00
Plate: 5 row: A column: 2
High quality sequence stop: 333.
High quality sequence stop: 333.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 333)
                                                                                                                                        Kopczynski, C., Serano, T., Rubin, G. and Goodman, C. BDGP/HHMI CK Drosophila EST Project Unpublished (1996) Other. ESTS: CK00525. 3prime Contact: Stapleton, M.
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AI552971.1 GI:4485334
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Best Local Similarity:
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AI552971/c
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/note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1467576 387 bp mRNA linear EST 09-MAR-1999 ve38f01.x1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE1820441 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:488721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="ImAGE:820441"
/clone=lib="Soares_mammary_gland_NbMMG"
/sex="male"
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Indels:
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                                                                                                                                                                                                                                                                                                                                                           /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Matches:
Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 346.
Location/Qualifiers
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AI467576.1 GI:4320913
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51.00
68.18%
50.00%
39.53%
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Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.

1 (bases 1 to 24)

2 1 (bases 1 to 24)

3 Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harria, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)

On Dec. 6, 2000 this sequence version replaced gi:11579867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 29-NOV-1998
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    FBan0007289 located on: 2L 22B8:1: 04/08/2001, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: AT.104 row: C column: 1
High quality sequence stop: 235.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Mismatches:
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                                                                                                          Drosophila melanogaster
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                                                                                    fruit fly.
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L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremeleux, CP 5706, 31057 EVRy cedex, FRANCE. (E-mail:

seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Kluyveri, Zygosaccharomyces rouxii,
saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenli var. hansenli, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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                                                                                                                                                                                                                      2 (bases 1 to 1163)
2 (bases 1 to 1163)
2 (bases 1 to 1163)
Soucier, Ju., Algle, M., Artiquenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Mappertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekalan, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Mincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 407 (1), 3-12 (2000)
                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotlna; Saccharomycetes; Saccharomyceteles; Saccharomyces. 1 (bases 1 to 1163).
Neuveglise, C., Bon, E., Lepingle, A., Wincker, P., Artiguenave, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts: 9.
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FEBS Lett. 487 (1), 56-60 (2000)
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/db_xref="taxon:4934"
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/clone_lib="AU0AA"
/note="end : T3"
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                   Saccharomyces kluyveri.
Saccharomyces kluyveri
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BE056346 1inear EST 08-JUN-2000 00257 leafy spurge Lambda HybrizAP 2.1 two-hybrid vector cDNA Library Euphorbia esula cDNA clone 25D 5' similar to Arabidopsis Unknown Protein (accession# AAF24521), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSO6NI7 1163 bp DNA linear GSS 17-JUN-2001 T3 end of clone AUOAA012D04 of library AUOAA from strain CBS 3082 of Saccharomyces kluyveri, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 553)
Anderson,J.V. and Horvath,D.P.
Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)
Unpublished (2000)
Contact: Anderson JV
Plants Science Research
                                                                                                                                                                                                                                                                                                                                               Euphorbia esula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I; Malpighiales, Euphorbiaceae, Euphorbia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Euphorbia esula"
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                                                      231 AACGATCGGCGGAATCATATAGAAGACCACACAGACCAGAGGAGGAGCAGGAGGAACAAGCG 172
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                      1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla
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/dev_stage="3-day induced (decapitated)"
117 c 116 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA/ARS, Blosciences Research Lab
1605 Albrecht Blvd., PO Box 5674, Fargo, ND 58105,
Tel: 701 239 1263
Fmai: andersjvéfargo.ars.usda.gov
Seq primer: pAD5.
Location/Qualifiers
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 438)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,

Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA941632
LD25873.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD25873 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                              Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
Plate: 258 row: G column: 1
High quallty sequence stop: 226.
Location/Qualifiers
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/db_xref="taxon:7227"
/clone="LD5873"
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/sex="male and female"
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/lab_host="%11 Blue"
                                                                                                                                                                                                                                                                       5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLySAla
                                     47 others
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/clone="BACR32D16"
/note="end : T7"
329 c 226 g
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Best Local Similarity:
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                                             ISM Orgidas latipes

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygil; Neopterygil; Buteleostel; Neoteleostel;

Acanthomorpha; Acanthopterygil; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyidae; Oryzlinae; Oryzlas.

CE (bases 1 to 615)

RS Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.

Medaka EST project in Takeda's lab

Unpublished (2001)

Contact: Tadasus Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mashima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ013747 624 bp mRNA linear EST 05-DEC-2001 BJ013747 MF01SSA CDNA Oryzlas latipes CDNA clone MF01SSA155A09 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostel; Neoteleostel;
Acanthomorpha; Acanthopterygli; Perconcrpha; Atherlnomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.

I (bases 1 to 624)
Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab
Unpublished (2001)
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/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 -
a 137 c 234 g 109 t
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes/strain="Hd-rR"
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BJ013747
BJ013747.1 GI:17363622
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Olrect Submission

Direct Submission

Submitted (02-Jun-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCT-98 and was constructed by partial EcoRI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pli and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR32D16 of RPCI-98 library from Drosophila melanogaster (fruit ALD); genomic survey sequence.
ALD71361
ALD71361.1 GI:4951201
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                            /organism="Oryzias latipes"
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/clone=lib="MF01SSA cDNA"
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/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
i a 139 c 232 g 108 t 1 others
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/db_xref="taxon:7227"
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Conservative:
Mismatches:
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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US-09-847-539A-6_COPY_59_86 (1-28) x BM396025 (1-861)
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Location/Qualifiers
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
a 219 c 121 g 199 t l others
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Hymenostomatida: Tetrahymenina: Tetrahymena.
I (bases 1 to 861)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
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Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

    . 861
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    /organism="Tetrahymena thermophila"

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[ (Dases 1 to 613) | Chordata; Cryzinae; Oryzias. Kohara; Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medaka EST Project in Takeda's lab (Dupblished (2001) | Contact: Tadasu Shin-i Center For Genetic Resource Information (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: Tadasu Shin-i (Contact: 
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Fri J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cel.: Conteat: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago University of Chicago 920 E. S8th Street, Chicago, IL 60637, USA Tel: 773 702 4374

Fax: 773 702 4372
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-MODEL-frame+p2n model -DEV-xlh
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BM396025 5009-0-15
                                                                                                                                                                      ; Search time 332.257 Seconds (without alignments) 1137.418 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27472414
                                                     Compugen Ltd
                                                                                                                           - nucleic search, using frame_plus_p2n model
                         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
                                                                                                                                                                                                                                                                             US-09-847-539A-6_COPY_59_86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM400696
BM396025
                                                                                                                                                                         October 13, 2002, 02:12:56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss:*
em_gss_hum:*
em_gss_inv:*
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seq length: 2000000000
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em_esthum:*
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em_estro:;
em_estco:;
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Match Length DB
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861
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41.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                           OM protein
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Maximum DB
                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                           Run on:
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                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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231450
10
6
10
       Length:
Matches:
Conservative:
Mismatches:
                                         Indels:
                                                 Gaps:
      6.37e+03
51.00
61.54%
38.46%
                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
      Pred. No.:
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US-09-847-539A-6_COPY_59_86 (1-28) x AL596163 (1-231450)

g ò

21 ValValLysAlaAspAsn 26 ò

43400 GGAGTAGAAAAAGAAAC 43417

Search completed: October 13, 2002, 03:04:30 Job time : 503.262 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIDMEVGGETOYRGTTVHFTPDPQIFTETTEPDFDTLFTRTRELAFLNRGLTISIEDK
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PARFPNLLVNGSSGIANGMATNIPTHHLGEVIDGVLALSHDPEISIRDLMEHIPGPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVODFGSOGOORTTALSVKLAEIDLIHEETGEYPVLLLDDVLSELDDYRQSHLLGAIË
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTAGMIMGRSGIRRAYESGRGSITVRGRVDIEEKKNGKETIVITEIPYOVNKARLVER
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Tierrez.A., Vazquez-Boland,J.A., Voss,H., Wehland,J. and Cossart,P. Comparative genomics of Listeria species Science 294 (5543), 849-852 (2001)
                                                                                                  (bases 1 to 231450)
Glaser, P., Frangeul, L. and Rusniok, C.
Direct Submission
Submitted (09-JUL-2001) Glaser P., Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
                                                                                                                                                                                                                                                        E-mail: pglaser@pasteur.fr
Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
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1868. .3013
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                                                                                                                                    AUTHORS
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Gene name confidence : hypothetical
predicted by Goodn_usage
predicted by Homology
predicted by FrameD"
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Listeria innocua Clipil262 complete genome, segment 1/12.
AL596163 AL592022
AL596163.1 GI:16412421
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
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Conservative:
Mismatches:
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4227. 5081
                                                                                                                                                                                                                                                                    complement(3365, .4138)
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Glaser,P., Frangeul,L.,
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Best Local Similarity:
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SOURCE
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Gene name confidence : hypothetical
predicted by Codon_usage
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Direct Submission

E. Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMCN CNRS I18 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGY, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex. Andoratoire de Genetique Cellulaire Christian.Boucher@toulouse.inra.fr
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Gene mame confidence : hypothetical
predicted by Codon_usage
predicted by FrameD"
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Location/Qualifiers
1. 202050
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Unpublished
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/db_xref="G1:16409367;"
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IHAIPNNTNEKLPRLSKRIAHLITSIEPIKGNKIEILTNGEETFPVLLDALRKAENHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQAVIELQESFLNDWYYMENQAGAADGFISESGSKQYFSPVDMGDEWAQVIYGGPYDK
KEWYBOSMLDLIDSAKESVWIYSPYPDEESLAVIRRVAMSSOVDRYITPGKGORGI
SFHGSNAYKKTMIEGAKMYAYADDSFYNAKAMLVDGTRAAIGTANFOVRSFRLNHEL
WYFLYDESEAMHHLKRDFKKDFEDSRLFTWKDMENKPLLTRIKRVLSSLLSPIL.
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FDPIASPWIVRTANLRNHRKIVVIDGQIGFTGGLNIGEEYRSNTPDFRVWRDTHIKIT
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Salamoubac,M., Genin,S., Artiquenave,F., Gouzy,J., Mangenot,S.,
Arlat,M., Billault,A., Brottler,P., Camus,J.C., Cattolico,L.,
Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N.,
Gaspin,C., Lavle,M., Moisan,A., Robert,C., Suurin,W., Schiex,T.,
Siguler,P., Thebault,P., Whalen,M., Wincker,P., Levy,M.,
Weissenbach,J. and Boucher,C.A.
Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 51231 GCTGAAACAAAAGAACAACTAAGTGATGAAACAGATCGACTTGACCGAGAAGATGCAGGT 51290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia solanacearum GMI1000 chromosome, complete sequence; segment 9/19.
AL646065 AL646052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
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Bacteria; Proteobacteria; beta subdivision; Raistonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to cardiolipin synthase"
/codon_start=1
/transl_table=11
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/gene="lmo0008"
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Best Local Similarity:
Query Match:
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AUTHORS MEDLINE REFERENCE

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/LEGISLALOH-WHIESTULRNFRNYENLELEFSPSVNVFLGENAQGKTNLLEAVL
MLALAKSHRTTNDKDFIWMEKEBAKNEGRIARHGOSVPLELATTOGGKRAKVNILLEOK
KLSQYGNLINVVIFAPEDLSLYKGAPGIRRFLIMMETGQMQPIYLHNLSEYORILLOGR
NOYLKMLOWKRKVDFILLDILTEQFADVAINITRRRADFIOKLEAYAAPTHQISRGL
ETLKIEYKASITLNGDDPEVWRADLLQKMESIKQREIDRGVTLIGPHRDDSLFYINGO
NVODFGSQGQQRTTALSIKLARIDLIHEETGEYPVLLLDDVLSELDDYRQSHLLGAIE
GKVQTPVTTSTSGIDHETLKQATTFYVEKGTVKKS"
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   RIDSLTYOPGIAFGAASSMFAGONIGAGKIDRVREGFWSGIKVVTAISIGITILVOLF
ARQFLLLFVDSSETEVINIGVSYLLIVSLFYVVVGILFVVRETLRGTGDAMVPLAMGI
FELVSRLVIGFVLSLYIGYVGLMMATPVAMITATILGVWRYKSGAWQKKAVIRRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MAETVKINSEFVTLGQLLQMIDVVSTGGMAKAYLSENTIYINGE QDNRRGKKLRNGDVILVPGVGKVKIEQGK"
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VIFTVLHAGGKFGGGGYKVSGGLHGVGASVVNALSTSLEVYVHREGQKYYQRFERGDV
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LVDGHGNFGSVDGDMAAAMRYTEARMSKISMELLRDINKDTIDYADNYDGSEREPVIL
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                                                                                                                                                                                                                                                                                                                                          B. subtilis YaaA protein"
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/transl_table-11
/product-DNA gyrase subunit B"
/protein_id="CAC9821.1"
/db_xref="GI:16409365"
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/protein_id="CAC98222.1"
                                                                                                                                                                                      join(4631. .4637,4644. .4865)
/gene="lmo0004"
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/db_xref="GI:16409364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAC98219.1"
/db_xref="G1:16409363"
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                                                                                                                                                                                                                                                                                                                                          /note="similar to
/codon_start=1
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                                                                                                                                                lmo0004"
                                                                                                                                                                                                                                                                  4644. .4865
/gene="lmo0004"
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8048. .8053
/gene="gyrA"
8065. .10593
/gene="gyrA"
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/gene="RecF"
4869. .5981
/gene="RecF"
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/gene="gyrB"
6030. .7970
/gene="gyrB"
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/gene="gyrB"
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4856.
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/gene="RecF"
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/gene="lmo0
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                                                                                                                     Laster, P., Frangeul, L. and Rusniok, C.

States, P., Frangeul, L. and Rusniok, C.

Direct Submission

NI Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE

E-mail: pglaserefpasteur.fr

Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.

1. 200050

/organism="Listeria monocytogenes"
/strain="EGD-e"
/strain="EGD-e"
/db_xref="taxon:1639"
305. 1673
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APNHEYDMLEKSYTQFIANILQETTGRLEDVRFIDGEBENFEYTVIKBNPALDEDG
IEIGKHMLNPRYVEDTFVIGSGNRFAHASLAVAEAPAKAYNPLFITGGQCGLGKTHLM
HAVGHYVQOHKDNAKVYLSSEKFYNEFISSIRDNKTEEFRYKYRWDVLLIDDIQFL
AGKEGTQEEFFHTFNTLYDEQKQIIISSDRPPKEIPTLEDRLRSRFEWGLITDITPPD
GLARALKOTIFKKARAGCLDIPNEWULINQIDSNIRBLEGALRYVAXSILVNKDITA
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SRELTDASLROIFGRASCOYTIISGTQBANGFTANDVLKNDLAEIEKNLRRAQNM
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GSDSDSISTEREPLILENDEVTVEVPESFGGTVLGSKYFGDLVBYRRLPERENVETEVTSNY
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VLTGVNWIIKENKLSAVATDSHRLAIRRIPLEDEDIDEENNIVPIGKSLSELNKLLDDA
SESIENTMANOLIEFKLKDLLFYSRLLLGSYPDTRAIPTVRELVINSKRFLDDA
RASLLARENNNNVILETATLENGOVEDVSKNYSENVFSGLVINSKRFLQAID
MADALRAFEGDDIQISFSGTWRPFVLRPKDAANPNELLOLITPVRTY*
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AITITVAGVLAKPLAILLEPRANILDDSTIFTTIETGIBSLYNBAINBAALIKALGN
AITPLIFILLSSLANTALDFLEVYNDMGVRGAALATVLSGTAAALAVF
MRIERAKFKLSTPLLKEMVRIGLPSGLQGSFISIGNMALQSLINGFGSSVVAAYTAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Chromosomal replication initiation protein DnaA"
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Tierrez,A., Vazquez-Boland,J.A., Voss,H., Wehland,J. and Cossart,P. Comparative genomics of Listeria species Science 294 (5543), 849-852 (2001) 21537279 2. (2005) 2. (bases 1 to 200050)
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/gene="lmo0003"
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318. .1673
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1856. .1860
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1867. .3012
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/gene="dnaN"
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Db 130651 GTACGAGGAGATCGTGCC 130668
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AC092244.1 GI:14578125
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Celniker, S. B., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dove, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Gargy, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hoskin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Location/Qualiflers
1. .175115
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Matches:
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Best Local Similarity:
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Refittedb. 7. E., Moy. M. Nurphy. S. Nelson. C. Nelson. K. A., Munco. J., Pholatenestry C., Moy. M. Nurphy. S. Patell. 2. Picificar. S. Steller. F. Pholatenestry S. Steller. F. Pholatenestry S. Steller. F. Pholatenestry S. Steller. F. Steller. F. Steller. F. Pholatenestry S. Steller. F. Stelle
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CNKDPSCSGNIETVIIDMNYTPVARYHFDLSGTAFGAMAKPGLNDKLRHSGTIDIQF
RYPCNYPGLKINFHVEEGSNPVYFAVLVEYEDLDGDVVQVDLMESKSAYGGATGVWT
PMRESWGSTWRLDSNHRLQAPFSLRIRSDSGKTLVANNVIPANWSPNSNYRSIVQFS"
23102. . 23121
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DNVFYHASCEAMAATVPAIIVSLDYRLAPEHHLPAAYVSTVLMLCDAAAGDPWIAASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:8118430 (Oryza sativa) (Proc Natl Acad Sci U S A 94 (12), 6559 6564 (1997)); EST AU062937, C72255, AU161321 from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVAGYGAVAVGCLALSSILPYSGRHHSSPPPPLRPAAQAEREKREREGDREKW

Complement(29843. .29879)

\rangle Trpt_family="(GA)n"

30600. .30652

\rangle Trpt_family="(GGAGA)n"

\rangle Complement(32120. .32144)

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\rangle Trpt_family="AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-"identical to beta expansin EXPB6 GB:AAF72987
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complement(27602. .27629)
/rpt_family="GC_rich"
27980. .28118
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/gene="OSJNBb0014111.15"
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Education Drosophila metanogater archeata; Hexapoda; Insecta; Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Preryota; Neoptera; Endopterygota; Diptera; Brachycera; Pterygota; Neoptera; Bradopterygota; Diptera; Brachycera; Muscamorpha; Bphydroidea; Drosophila.

12. (Dases 1 to 175115)

S. Celniker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Carlson, J. M., Center, A., Champe, M., Davenport, L. B., Dietz, S. M., Carlson, J. W., Center, A., Champe, M., Davenport, L. B., Dietz, S. M., Dodson, K., Dorsett, V., Doup, L. E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R. F., Gargin, S., George, R. A., Houck, J., Hock, M., Murphy, B., Melson, C., Nelson, K.A., Nunoo, J., McIntosh, T. C., Moy, M., Murphy, B., Patel, S., Petelffer, B., Pateler, F., Stapleton, M., Strong, R., Patel, S., Petelffer, B., Phouanenavong, S., Pittan, G. S., Patel, S., Petelffer, B., Phouanenavong, S., Smith, B.O., Rubin, G. M. and Venter, J. C. Sequencing of Drosophila chromosome Zi, region 22C-22C

M. Unpublished (1998)

E. (Dases I to 175115)

E. Chakes I to 175115

Callsker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Bulsam, D. A., Carlson, J. W., Center, A., Gocayne, J. D., Amanatides, P. G., Brandon, R., Carlson, J. W., Center, A., Gocayne, J. D., Amanatides, P. G., Brandon, R., Dodson, K., Dozett, V., Doup, L. E., Doyle, C., Dresnek, D., Farfan, D., Farfan, S., Fitse, E., Galle, R.F., Gargy, N.S., George, R.A., Gonzalez, M., Houck, J., Houck, J., Hostin, B., Netteris, B., Molled, T. J., Paragas, V., Park, S., Patel, S., Petel, E., B., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Shukh, H., O., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster, chromosome 2L, region 22C-22C, BAC clone BACHIF10, complete sequence.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
4 (bases 1 to 135509)
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Genes were identified by a combination of several methods: Gene prediction programs including Genscan and Genscan+ (Chris Burge, http://wcm.ed.nt.edu/GENSCAN.html), GeneMarkhm (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark), Fgenesh (http://www.softberry.com/), and GeneSplicer (Mihaela Pertea and Steven Salaberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/rdb/rgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted similarity but protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE) implering ob prediction brotesins dense encoding tRNAs are predicted by simple repeats are identified by repeatmasker (Arian Smit, http://tp.genome.washington.edu/RW/Repeatmasker.html).
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/gene="05JNBb0014111.1"
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92 (20), 9245 9249 (1995)); EST AA751536, AU030829 from
this gene"
join (3920. .4103,4207. .4316,4453. .4637,4983. .5310)
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15881 .17602

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BAC clone OSJNBb0014111 is from Oryza sativa chromosome 10 The orientation of the sequence is from SP6 to T7 end of the BAC

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Berkeley Drosophila Genome Project
Lawrence Berkeley, National Laboratory, MS 64-121
Berkeley, CA 94720
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Library locations: 42-67, 59-42.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105823 bp DNA linear HTG 03-JAN-2000 r, *** SEQUENCING IN PROGRESS ***, in ordered
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DS03995 (D277) is a bridge clone extending from Pl end at bp 57,688 to bp 96,288 minimally overlapping its proximal neighbor DS064 (D269)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was identified as CDM:10211226 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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Matches:
Conservative:
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Drosophila melanogaster,
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51.00
53.85%
42.31%
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fruit fly.
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Query Match:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 9628B)

Scelniker, S. E., George, R.A., Galle, R.F., Hoskins, R.A.,
Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, S.H., Lee, B., Lomoran, M.A., Mak, J., Mesda, P., Moshrefi, A.R.,
Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E.,
Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M.,
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Solir, E., Twomey, B., Man, K.H., Aphayani, A., Arcaina, T.F., Baxter, E.,
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Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, M.,
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(657 aa), fasta scores; opt: 479 z-score: 421.7 E():
3e-16, 28.2% identity in 333 aa overlap. Contains possible
N-terminal signal sequence"
                                                                                                                                                                                                                                             /tragslation-*MFANVPTVLTPLRARLLLVLAVLLAVLTPTAPEALAAGKPETGA
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DAPGATSALEADFNRQNHALAAELKRVGARHVTTHFYGPGTHGWAYRERELHASLPML
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64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
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Drosophila melanogaster
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Mismatches:
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Sequence submitted by:
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6183. .6186
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KEYWORDS
SOURCE
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YLVLSHATGDVHEDRREDAAAVYNKATASLNLRSHAAVLDLFGDFSLVEPGILVRTDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MYGTPREDID'SKPHPARVYDMLLGGKDNYPVDQRVGETLPAE
ARGNAARNRAEMHRAAAWLAKNGVDQFLDIGTGIPTEPNLHGIVQAISPAARIVYADN
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PDDEDPYRVYSTLVGTPRGSYLLLSHGTADQHPEIKQETESAYKKGAIPLRMRTRSE
VEPFFCGLELVKPGLVFATEWYQEEPAPVRERSGFYAGVARIP"
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TALDRASADELAAELRRDGFEARVEEYTPATADYRGGTLGWRVR.IGTFDSQTAATA
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PSWYYGWVHKRNPRTVAGVDAAGRTVLYTADGRSTDSLGLSIGESAEVARSLGLRDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SCIF3.04, unknown, len: 261 aa; similar to upstream gene SCIF2.03c,E(): 0, 48.8% identity in 260 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKLRKRRLCAATGVVLGALTALAALPPAAVASPHPGGHPPTARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCIF2.06, probable secreted protein, len: 342 aa; some similatity to secreted antigenic proteins 85A, 85B and 85C from Mycobacteria e.g. A85B_MYCLE (327 aa), fasta scores; opt: 325 z-score: 247.2 E(): 1.6e-06, 28.5% identity in 319 aa overlap and to secreted antigenic protein PSI from Cornebacterium glutamicum CSPI_CORGL
                                                                                                           /note="SCIF2.03c, unknown, len: 300 aa; similar to upstream gene SCIF3.04, E(): 0, 48.8% identity in 260 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SC1F2.05, probable secreted protein, len: 552 aa; contains N-terminal signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4908. .4991
/note="12_degenerate repeats of AGGCAC(C /A)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLDGGGSTTMVAEGAVLNSPSDAAGERPVGDALLILPHRHRTRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="possible RBS upsteream of SCIF3.04"
2308. ;3093
/3en="SCIF3.04"
2308. ;3093
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/note-"possible RBS upstream of SCIF2.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein SCIF3.04"
/portein_id="CARA1045.1"
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/db_xref="SPTREMBL:086541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"putative secreted protein"
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                                  complement(1275, .2177)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPEEARRPDAPPIGIYGGVARKDA"
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3223. .4881
/gene-"SCIF2.05"
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/gene="SCIF2.06"
5014. .6042
/gene="SCIF2.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2308, .3093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                      /codon_start=1
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                                          CDS
                                                                                            In Codons 15 given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Kroph et al., Nucleic Acids Research, 22(22):4766-478(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1994) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon daty, tig or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the noist upstream initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced chone. It may be shorter because we arrange for a small overlap between neighbouring submissions. Cosmid 1F2 lies between 8A6 and 4G2 on the ASBI-A genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codoc_start="""
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/translation="ABHFAAYAAVAKELGABLLIKTTEEYGPRKLYVTENGSSFP
DLVRPDGSVDDPERRGEYLTAHLAAAASAARGABALAGYFAWSLLDNFEWAYGYDKRFG
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Beal-1,3-glucanase II from oerskovia xanthineolytica (435 ba); fasta scores; opt: 100 2-score: 207.7 E(): 0.00025, 38.3% identity in 60 aa overlap. There is no start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="SCIP: 01, probable beta-glucosidase, partial CDS, len >311 aa; similar to mnay e.g. BGLS_AGRSP beta-glucosidase (EC 3.2.1.21) (459 aa), fasta scores; opt: 784 z-score: 986.7 E(): 0, 42.5% identity in 315 aa overlaps on extends SCBA6.25. Contains Plam match to entry PF00232 glycosyl_hydrol, Glycosyl hydrolases family 1, score 350.20, E-value 2.2e-101*
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SC1F2.01"
/note="nominal overlap with cosmid 8A6 from 37344 to
37445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //octe-"Pfam match to entry PF00232 glycosyl_hydrol, (glycosyl hydrolases family 1, score 350.20, E-value 2.2e-101
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/strain="A3(2)"
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CDS

FEATURES

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CDS

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Direct Submission
Submitted (21-AUG-1998) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycesaes 1 to 30561)
1 (bases 1 to 30561)
Seger, K. J. and Harris, D.
Unpublished
2 (bases 1 to 30561)
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Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach, M., Kieser, H.M., Denapalte, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                    /gene="cyss"
/note="MPN356(new), 481(Himmelreich et al., 1996)"
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ATP/GTP binding protein; beta-glucosidase; dehydrogenase; hydrolase; pseudogene; TTA Leu codon.
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Mismatches:
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Streptomyces coelicolor cosmid 1F2.
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                                               PMNPKLNSLNVSVAVGIILFGWKS"
                                                                                                                                                                     /note="H91_orf437"
complement(8671. .9984)
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                                                                                     complement(8671. .9984)
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72.73%
50.00%
39.53%
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Best Local Similarity:
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DLKGNPVGFSGRALQKTEKIKYKNSAEHQWFKKSELLFNFHRIDKNTLKLYLVEGYFD
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RIANGGIVEVDWNQAAYKNDRELFLABGSDDVYKAKHRVLINLEYLYAFKFKGFDE
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complement (6569. .7918)
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GSLKSHTENDDTNKVISLLVEVWEKKNKKKDNNSLSNKDIVNVLSKFELPDDEIIFVL
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NTLLELMPKEQSRDEK SSDIKSSNEMASDLIKQLLEDSELKNKIFNMEELKNKIDAEN
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WQKLAY PSKRCLQSHLANLE GOXIEQUITFNDDPYST IPRVVMISRFFNPQSFLTAIMQV
ISRAKAY ELNKLY I OTFETTKR ET EETGGAAK EGATVYGFILEGARMDY OLGGDLEESKP
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HKLIFLTLNVFRLMOKKIIDVAYEVAEMDFLIKCPARPGVENTLDWLPNISWDQIQGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chases 1 to 20217)
Dandekar,T., Huynen,M., Regula,J.T., Ueberle,B., Zimmermann,C.U.,
Andrade,M.A., Doerks,T., Sanchez-Pulldo,L., Snel,B., Suyama,M.,
Yuan,Y.P., Herrmann,R. and Bork,P.
Re-annotating the mycoplasma pneumoniae genome sequence: adding
value, function and reading frames
Nucleic Acids Res. 28 (17), 3278-3288 (2000)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmatecee; Mycoplasma.
1 (bases 1 to 2021)
Himmelreich,R., Hilbert,H., Plagens,H., Pirkl,E., Li,B.C. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae Nucleic Acids Res. 24 (22), 4420-4449 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"5-formyl tetrahydrofolate cyclo-11gase (H10858) homolog; similar to GenBank Accession Number D64160, from
(MPN numbers) from the origin of replication. Annotation comments and further update data are at http://www.bork.embl-heidelberg.de/Annot/MP/.
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984. .1829
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/db_xref="GI:1674177"

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/organism="Mycoplasma pneumoniae"
/strain="M129"

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/db_xref="GI:1674179"
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/db_xref="G1:1674176"
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/note="H91_orf239"
complement(1821, ,2540)
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/gene="H91_orf213"
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                                                                                                                                                                                                               /db_xref="taxon:2104"
/note="ATCC 29342"
                                                                                                Location/Qualifiers
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S (bases I to 14941)

S Lincoln,L.M., Asai,D.J., Forney,J.D., Terrell,S. and D'Souza,M.S. Direct Submission

E Unicoln,L.M., Asai,D.J., Forney,J.D., Terrell,S. and D'Souza,M.S. Direct Submission

E 4 (bases I to 14941)

S Lincoln,L.M., Asai,D.J., Forney,J.D., Terrell,S. and D'Souza,M.S. Direct Submission

E Submitted (25-JNN-1999) Biological Sciences, Purdue University, West Lafayette, IN 47907-1392, USA

Sequence update by submitter

On Jun 25, 1999 this sequence version replaced g1:3309592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lincoln, L.M., Gibson, T.M., Asai, D.J. and Forney, J.D.
A gene knockout reveals that dynein beta heavy chain is required in
Tetrahymena thermophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14941 bp DNA linear INV 21-DEC-199 (DYH4) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                            2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee,S., Wisniewski,J.C., Dentler,W.L. and Asai,D.J.
Gene knockouts reveal separate functions for two cytoplasmic
dyneins in Tetrahymena thermophila
Mol. Biol. Cell 10 (3), 771-784 (1999)
99169020
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join(1. .908,975. .2114,2177. .13257,13310. .13835,
13903. .14425)
                  /codon_start=1
/transl_table=11
/product="TRK potassium uptake system protein"
/protein_id="AAG20878.1"
/db_xref="GI:10584271"
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Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 14941)

    14941
    /organism="Tetrahymena thermophila"

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                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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/note="TrkA3"
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/gene="DYH4"
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ONPELKTIVODTTKKDMGLVAEELFVTKVVOLAEILEVRHCCFVIGPPGSGKTCVWKT
LIKSYINSGEDAEYDTLNPKAVTSDELFGAYTKTKEWKNGVIAVIMKNQVKNEEKYKA
THWRWSVLDGDIDPEWIESLNTVWDDNKVLTLVSNDRIFTPOWRLIFEISNAT
PATVSRAGVLFINETDIGMPYMNSWLERSQIVILKQOKEMANMPEYPVIDDVAKSVF
YRCFOSYFEONIDVNRNKRHICPWYDIAMIQTICTILDALLIQHLEKLKOWKEEDE
KQALBAFFIFAGLWAIGGPVGGQDDSKDMKEFNTVWKGAAKVKFPEGGLCYDYYYDI
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Siaqifkefeeavqaftsvsydimijaekkfdddfyefrskikelerrlasvitqgfd
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ERKNRPMSPDDYDQFLKAIFSNKLTIVKDNGNQIQKLVKEVLDAVKADKKQNSWKNYN
DYVNVIVIEGISTAIQTALLHLNEQINPVFIKRNDISPLFDIRLELGQSGIQFDPEIG
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KUPEPREGITTRMKEWYTKKKHUPFTEKGTODPLQQIDDANSNFIELTGRPKVK
ADITPLQAEETQNIKRDLDIEWKEVESFRKWOKLPFDYTESMGYENINNAYTHVY
KKLTALGGREALBYNNLEKLFELQKSNYKQLKDCMNDLKNLKTMMDAIALIHFQYNDWK
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EFMEDRHWSQLKQITGTVFDHNSLSFYFEDILALNLYKYENTVNEIVDVAQKEAKIEK
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KFICEGAVEHWLLNLEFRMRETLQEILEGAKNTADLWDSGDKGREEWVEGYNAQIALL
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ITIDVHSRDVVEKFVIQKVSEAESFAWLSOLKFYWENKPDSDMHLRQTLRFPWEKDKN
KNKCIIRIVDWFRFYSYEYIGNAIRLVITPLTDRCYITLTQALNLTWGGAPAGPAGTG
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RSCAMVYPDLALICENMLMSEGFTMARVLSRKFVSLYMLSREFVSKQKHYDWGLRAVK
SVLRQAGKLKRGDPDMPEDPLLMRALRDFNMPKIVTDDKVIFRRLIGDLFPKLDPPTK
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DKILKNTTAFAPSAKRFHYQFNFRELARVCEGICRTTPGQYSGGDQGKLVRLWAHEMK
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TQCTIFVLKRYLDDKLEEFNEWKAQMINVLEQOAMEHVSKICRILDMEGNALLVGVG
GSGRQSLCRLSTFIRGEIDQLVYRASFTINDLRKOTYKKIYKRIARRNSIARYFMIT
DSQIKRQFLIPINDMINSGWIFDLFPKEDMDSLVSGVRNEAKGVDVNNLTALTSYFLD
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MKNIGSPPAGVIVTARVVLILFNQGITLNDPDEKVWKKAVTFMNNPQASLIRLNLLMV
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TALDPLLQRAVKKNGNQLQEIGGDP IDVDPWRFKIPLWYKLINPHFRETAAQCTIIN
FTTTPSIGEDPIIAWVVIIEKUELBAAQDUVKKQNITAVTLDKLESDLLQSLGSBADP
ATILDNTELIQNLDKTKKTTIEITEQQOKAKVTEAEINIQREHYRVVAABGSMLYFLV
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CDS

CDS

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COMPLEMENT (10189. 10842)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mntyedtlodavtadtwatversllakllreftyeellapertt
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AGEHESIHTYIEHAISSPERGFTEPAAVVLEIVQGEGGVNPAPDAMVOBLRRTTREHD
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TVADIQSVLVAFKGHAATIEAADRTAPITTAAGGDQ*
4376. .6199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTGVGAVADTPAAHAESATLHAFLNCYLRETDAGEVVSPRAVPD
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SDEAEALKSDEAEALKSDEAEARKSDEAEARKSDEAEARKSDEAEARKSDEAEALKSD
EAEARKSDEAEARKSDEAEALKSDEAEARKSDEAEARKSEAGTEGPKGTGGPGSEAGT
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Shukla, H.D., Lasky, S.P., Mahairas, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.R., Baliga, M., Thorsson, V., Sbrogna, J., Swartzell, S., Meir, D., Hall, J., Dahl, T.A., Welti, R., Goo, Y.A., Leithauser, B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocks, D.G., Jablonski, P.E., Krebs, M.P., Angevine, C.M., Dale, H., Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Dassarma, S.
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Halobacteriaceae; Halobacterium.
I (bases I to 1242)
I (bases I to 1242)
I (bases I to 1242)
My W. V., Rennedy, S.P., Mahairas, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.P., Baliga, N., Thorsson, V., Sbrogna, J., Swatzell, S., Weit, T.D., Hall, J., Dahl, T.A., Welt, K., Goo, Y.A., Leithauser, B., Reller, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocks, D.G., Jablonski, P.E., Krebs, M.P., Angevine, C.M., Dale, H., Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., DasSama, S.
                                                                                                                                                                                                                                                                                                                                                                                                                            From the cover: genome sequence of halobacterium species NRC-1
Proc. Natl. Acad. Sci. U.S.A. 97 (22), 12176-12181 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-JUL-2000) Institute for Systems Biology, 4225
Roosevelt Way NE, Seattle, WA 98105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147. .1016
/gene="vN65208C"
/note="conserved hypothetical protein"
/codon_start=1
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                                                                     EGPKGTGGPGSGGEHSHNKKKSKKSIMNMLILM" 734. .1591
                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
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                                                                                       ptide 734. .1591
/product="S antigen" 1601 a 270 c 504 g 1463 t
1 bp upstream of EcoRI site.
                                                                                                                                                                                                                                                      Matches:
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147. .1016
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Halobacterium sp. NRC-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome.
AE005155 AE004438
AE005155.1 GI:10584262
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Best Local Similarity:
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                                                                                                                                     BASE COUNT
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                                                                                                                                                            ORIGIN
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                                                                                                          /product="LD12115p"
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PYVGNGYLGLEIAHDAFLNIKNGRAMQLPIPPOPVVSVSGGSASGGEKEATVVEYLTG
MVHRFOCFAGYFVSYTYYAHRTQPNIFMQELQITNTRNLLEDIELIMPRVNLQKLTRR
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GFLNGKNGKGNKYEDLQEEGEGENDDEEHSNSEESDNDEENEIIVGQDEAPKSDEAEA
                                                                                                                                                                                                                                                                    TVPLSEPVSVGVFTYTELEVLSGTVOLOAENPSKSIVISIVKPOMDSKLOLRÄRGTVR
IVYPTAVYTSKRVAERKIGGISETIEOOATOMAKLLOAKLGSKESNGSKSNTSTRO
EHIDVWTDLARATGETISTSKAENSLNODRINATNY AVLSQVBSFEFERAGSSKKEDIA
KALTYAEGCYDSYHTLOAENLWERNLOOLNSLVTSWMLTLEKOGCHNLIRAGASGV
IQAMVLSFSSERSRENOHLECNHIPKFHRDFHFRRANYGNTTHVDVNTIYDDDNKAVI
NIAADRSBRSYYAGOGGCLDEPVLLYONRECPVKLRENTYNYTTIYDDNKAVI
ALHVKEVVERAHEDHLIALHRHGHOLGGLPTLWVSVCAIIIVFHIFLCKLIIKEYH
ALHVKEVVERAHEDHLIALHRHGHOLGGLPTLWVSVCAIIIVFHIFLCKLIIKEYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INV 26-APR-1993
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Conserved sequences flank variable tandem repeats in two S-antigen genes of Plasmodium falciparum
genes of Plasmodium falciparum
genes of 1985)
85176931
Twenty degenerate tandem repeats of twentyfour base pairs each
start at position 953 and end at 1432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFASA7 3838 bp DNA linear INV 26-APR-199 Plasdmodium falciparum (isolate NF7) S antigen gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
Kuaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 3838)
Cowman,A.F., Saint,R.B., Coppel,R.L., Brown,G.V., Anders,R.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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11
3
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/organism="Plasmodium falciparum"/db_xref="taxon:5833"
665. 733
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Conservative:
Mismatches:
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/note="S antigen signal peptide"
                                                                                         /db_xref-"FLYBASE:FBgn0031379"
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/note="S antigen precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
79. .1992
/gene="CG7289"
/note="Longest ORF"
                                                                     /codon_start=1
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P.falciparu
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AY061146/c
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                                  / TEARS 1 & LON-*MCYTEPROMPRGKWAEDARRWVELGLSWVRIGEFAWAKIEPRSGE
/ TEARST SEARATTEAMARRYGEHIYVAMOTONEZGHDDTIYTSYSAEAVGARRHY
GFSSRYRSBEAARTTEAMARRYGEHIYVAMOTONEZGHDDTIYTSYSAEAVGARRHY
GFSSTRYRSPARTEAMARRYGERIYONEGHIYVAMOTONEZGHDDTIYTSYSAEAVGARRHWL
AERYGSIDELINRAMGTSEWSHXYDSFEEIDLPNNLYEEPSTHGYDFIRESSCOVKSF
NKAQVDITRAHSPGRPYTHNFMSQNTDFDHYRVGEDIDIASWDYYPMGGLLNGRLAAK
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LAYHGVDWYSYFRRRQAPRADCHAGGLLLPNSEADOGYLEGVAEVARLEGGEV
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YKLILAPDLVIAEBAFVELGIAANAKVYGRASGSKTRDMHIPEGLEPGGLPGGLAGGIJG
SVSRVESLPEFHSETVLXGUNAX BAGGWRETVYRTSETVIASFOGEYRKARTIDIS
SVSRVESLPEFHSETVLXGUNAX BAGGWRETVYRTSETVIASFOGEYRKAPATUGSDKA
RYLAVAANGALLDKVIGDALGWAGLESLPDLGDLRVTRRGNLRFAFNFGRIPAEVPAG
ASAEFYVGGRTLKFVDVAINNE*
COMDIEment (5426. 6460)
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HQDASGLLPPYVNDRRALFAFTKPPVHGWAVSCWARENPAFLTPERRAYLRDAIGRGY
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DDPGKAARWRIAIDEGYFHGNDSGWNASFPAEGGPYLSPDLPVFLILACEALANLLE
LDAAMCRQLVARLVEGAFITDWGPAFESPRSPFYEDDCYWRGFIWAPTTYLLMGLRR
GGEGALAREIAQKFCALANAHGMAENFDARSGRGLRDRAFAWTSAVYLLLAGSILDF
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/product-"putative transcriptional regulator, lacI family
protein"
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/gene="SMb20968"
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/note="Product confidence: hypothetical
Gene name confidence: hypothetical
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//note="Product confidence : putative
Gene name confidence : hypothetical"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="MISCELLANEOUS; Not classified regulator"
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/codon_start=1
/transl_table=11
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complement(8184, .8996)
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I (bases I to 1121).

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Chawez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungali, C.J., Nunoo, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.

Direct Submission

L. Lawrence Sarkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
Sequence submitted by:

Barkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene collected to integrity checks for sequence accuracy, presence of a polya tall and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clones that may attifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcribtase errors that result in sequence information about this sequence. Including its location for there are proverse transcribtase errors that result in sequence.
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VLLLATWMIPWDVKMIPLYMEFNWLGWINTLKPLIVPAYFADAFFVFLLRQYIMTIPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INV 08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38610 ATGGATGATCTGGCCGACGGACGGACGATTCGGTCGATGAGCGCGCGTGATGCGG 38551
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AY061146.1 GI:16768949
FLI_CDNA.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2151).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY061146 2151 bp mRNA linear Drosophila melanogaster LD12115 full length cDNA.
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                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualiflers
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                                                                                                                                                            5.72e+03
52.00
77.27%
50.00%
                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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us-09-847-539a-6_copy_59_86.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPSQADPRINDITIGNILSMQAGLGRWSGPNYGRWYSSRNWYRFALAQPFDDEPGGRW
LYSTASTHLLSAILTRYGGRPTLALAREWLDPVBGFRIGAWERDPGGIYLGGNQMAMS
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CTTELGAMAGIEPEFRKRGKIGISVPPLGEDRDL
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/db_xref="GI:15140974"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence-not_experimental
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/note="Product confidence : putative"
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/note="Product confidence : putative
Gene name confidence : hypothetical"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="MISCELLANEOUS"
/note="Product confidence : putative
Gene name confidence : hypothetical"
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complement(2189, .3187)
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1412. 2071
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                                                                                                                                                                                                                                                             1002. .1307
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/gene="SMb20963"
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Rhizobium meliloti (Sinorhizobium meliloti) 1021 complete pSymB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinorhizobium meliloti.
Sinorhizobium meliloti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 303100)
11 (hases 1 to 303100)
Vorholter,F.J., Hernandez-Lucas,I., Becker,A., Cowle,A., Gouzy,J.,
Golding,B. and Puhler,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             From the Cover: The complete sequence of the 1,683-kb pSymB
magaplasmid from the N2-fixing endosymblont Sinorhizobium mellloti
Proceedings of the National Academy of Sciences of the United
States of America. 98 (171), 9889-9894 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted on behalf of Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld, Germany and Department of Biology, McMaster University, 1280 Main Street West, Hamilton, Ontario, 188 4K1 Canada mailto:Stefan.Weidner@Genetik.Uni-Bielefeld.DE pEXO, pSymB.
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/plasmid="ByymB"
/strain="1021"
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                                                                                                                                                                                                                                                                                                             4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-JUN-2001) Weidner S., Universitaet Bielefeld,
     MIVVKYGVVLVDSIKEDAGEDLQVCGTALFMHLLGKAVVSSTT"
                                                                               281993
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                                                                                                                                                                                                                                                             US-09-847-539A-6_COPY_59_86 (1-28) x AE003619 (1-281993)
                                                                             Length:
Matches:
Conservative:
Mismatches:
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complement(167. .967)
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/evidence=not_experimental
                                                                                                                                                                                  Indels:
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AL603646 AL591985
AL603646.1 GI:15140973
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2 (bases 1 to 303100)
                                                                          5.3e+03
52.00
65.22%
47.83%
40.31%
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                                                                                                                             Percent Similarity:
Best Local Similarity:
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MDDELEDKVFYQTYVSHMKILSKFAVGFSSINSPLAYIWKLCRL
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2 (bases 1 to 281993)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Blrect Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced 91:7297302.
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Alignment Scores:
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I (bases 1 to 169427)

Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenportt, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferrieras, S., Frise, E., Galle, R.F., Garg, N.S., George, K.A., Gonzalez, M., Houck, J., Hoskin, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Staplecon, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C., Williams, S.M., E., J., Phoses I to 160477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jun 7, 2001 this sequence version replaced gi:7143379. Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                      Drosophila melanogaster, chromosome 2L, region 28B-28B, BAC clone BACROB101, complete sequence.
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequaira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophia melanogaster BAC library, partial EcoRI in
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/db_xref="taxon:7227"
/chromosome="2L"
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/note="Alternate"
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Bukaryota, wetacara Arthropoda; Tracheate; Hexapoda; Insecta;

Petrogota; weoptera; Endopteryotaca: Direchycera;

Muscomorpha, Beptaca; Endopteryotaca: Direchycera;

Muscomorpha, Ephydroidea: Drosophilidae: Drosophila.

El 10, 10 281931

AdamsAM.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Adamstides, F.G., Seheer, S.E., Lilp.M., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Holt, R.A., Holk, I.A., Mandell, M.A., Holk, Bacach, S.B., Mandell, M.D., Zhang, O., Chen, L.X.,

Banandida, R.C., Rogers, M.H., Blazel, R.G., Champe, M., Pielifer, B.D., Man, K.H., Doyle, C., Baldwin, D., Ballew, R.M., Basu, A., Barachada, P.C., Baldwin, D., Ballew, R.M., Basu, A., Barachada, D., Bayerkerrogulu, L., Basaley, E.M., Bescon, K.Y., Barachada, D., Bayerkerrogulu, D., Basley, E.M., Bescon, K.Y., Buchler, N., Cawley, S., Dahlke, C., Daune, S., Durkov, B.C., Dunn, P., Durkin, M.Y., Cawley, S., Dahlke, C., Daver, D., Dew, J., Dietz, S.M., Benchan, M. M., Calle, E.K., Downes, M., Dugan, Rocha, S., Durkov, B.C., Rentison, J.A., Retchun, K.A., Kalush, F., Karpen, C., Ferriac, C., Ferriac, C., Ferriac, C., Kraft, C., Kratt, E.S., Kulp, D., Lall, M., Malushon, M., Rosher, D.M., Melson, D.L., Merkulov, G., Milshina, N. W., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Merkulov, G., Milshina, S. M., Moonter, M., Strong, W., Zhang, G., Zhan, W., Shuger, D., Wall, M., Welson, D.L., Well, M., Welson, M., Strong, M., Shuger, B., Shrad, M., Shang, A., Wenter, S., Shangson, M., Shuger, B., Shang, A., Wenter, S., Man, Shang, A., Welley, M., Nelson, D.L., Well, M., Welson, M., Strong, W., Zhang, S., Yang, S., Shangson, M., Strong, W., Zhang, W., Zhang, W., Zhang, W., Zhang, W., Zhang, W., Zhang, 
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Drosophila melanogaster genomic scaffold 142000013386055 section 12
                                                                                                                                                                                                                                                                                                                                          Db 117572 CTGGAAGCTGTTCAAGCAGTGGAGTCTCCAAGGCCGCAGTTGCTCTTGTGGGA 117631
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Mismatches:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophila.

1 (bases 1 to 13315)

8 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Bundot, J., Buroks, A., Bundo, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
Burkett, C., Durbin, K.J., Fernandez, C., Ferraguto, D.,
Fordun-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L. C.,
Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hoques, M.,
Holloway, C., Hosak, J., T., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R.,
Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S.,
Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Martinez, C., McLeod, M.P., Naudyen, S., Oswal, G.,
Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E.,
Taylor, T., Vasquez, L., Vinson, R., Wolley, R., Watlington, S.,
Weinstock, G., Weinstock, I. R., Williamson, A., Worley, K., Wren, J.,
Direct Suhmission
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                                                                                                                                                                           This sequence was identified as CDM:10212995 by the submitter
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                                                                                                                                                                                        **NOTE: This is a 'working draft' sequence.

**NOTE: This is a 'working draft' sequence.

**This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

**Location/Qualifiers

**Lorganism="Drosophila melanogaster"

/db_xref="taxon:7227"

9781 a 8675 c 8725 g 9812 t
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophiliae: Drosophila.

1 (bases 1 to 3693)
Adams, M. and Venter, J.C.
Direct Submission
Submitted (09-DBC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
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Best Local Similarity:
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KEYWORDS
SOURCE
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                                                                        AUTHORS
TITLE
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REFERENCE
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                                                    REFERENCE
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Direct Submission

Submitted (16-007-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

* NOTE: This 1s a "working draft" sequence. It currently

* consists of 39 contigs. The true order of the pleces

* is not known and their order in this sequence record is
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                                                                                                                           * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1641 bp in length
2068 bp in length
1381 bp in length
1378 bp in length
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3011 bp in length
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1247 bp in length
1548 bp in length
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841 bp 1
843 bp 1
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950 bp 1
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JOURNAL PUBMED

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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/note="push3420 P element insertion site" 3747,3808. .4335, join(370. .513,695. .789,913. .1325,1581. .3747,3808. .4335, 4404. .10389,10447. .10651,10701. .11393,11455. .13118, 13175. .13657,13715. .15650,15706. .17302,17366. .17584)
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YPLLVDALTDILSITDMSMYSKEKDKEASMHNLCAIQYCFTIAWKLNIGLPPSTSHVE
SLKAERSPNLHSLMWSIRLPLASSHYLVVSSLIKQGMYTQYAETLWTHVGDIGADIKY
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SSSSSNAQPPTWMATVSAWBISDQLDPWEISTDCTAAGGGSRWPOTGGAAANTSQ
ILSIWQAAQPDPSEESSQACOHESDERNGALLLSFVKSLVKDQSKASQIAPPLFOALL
OLGQTLISPPOEGCDFADVLQIMITLADASPARGHVALFNTTLWLELAKLQLEDPKHL
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CSDNSEEDDSESYLGHWFKETLSPETHDDNANTSTQERAEQKSALVPKLDEPHEYLDL
AADIFCFLDQFLANRHAYMQRYVKAGVSDQQMLLMANIIKDFÖRDVMRNETDQGSGNA
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STORWWPLOYVPSTLSVLVOTLLLERPOEKERAACLSWWHELINTLWEGYCSSRTASD
SDYEDLAIBHAQLLLEFFEHSLNLAORKSILLLTAGGYTRCAEVCRGISEDRPVKNSOL
MLLSRLLLFLEFLEYMKHLYNAPPELLDOVRWNLFSVSSMPDTOKITDLLNCRTKLNSYC
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ARGOSAGTSITSSSNDPELTSSNES IDDOKLKADDDGKLSDSDLGKYDLOVNELWYKLM
NSYOLLSSV Y VRGOMKKOLSSSTPEKALNL YP I VSDKFAIMLELHAAFLKLLPHEDKO
LIANEWPKCLMYNDFAFNGKOHPVEPY I LINY I DAHI I ELTRGSNY STLHTLKHCLKSI
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HLCYGSWLLISGIQGAMGASGSGGSSSDSASKSASKATKSGSEAGTAPTTPIARVNLF
KVQGFGELNAAIANHSIKLLSELIEDLKVEAACGQSLESTELPEPAQFDILQNYSSL
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LEKPVAVQAMROFFKDORSGSLTTLLLSFTGTSLPVSYARKMLOFVNRLFQLSLQADS
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TKWLLGALKMLCEGRECPASASSSMFDYNAVANVLKSCKHPESTTKSIMPSSSSSGSG
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TDLTILSQAQALIEMQPLTPSRIERLSMCGIAALYNAVLTSIATSVLGMSQASSSGKQ
                                                                       2 (bases 1 to 17595)
Richards, S., Hekmat-Scafe, D.S., Hurd, D.D., Caprette, D.R.,
Saxton, W.M., Carlson, J.R. and Stern, M.J.
Direct Submission
Submitted (06-OCT-1998) Biochemistry and Cell Biology, Mail Stop
140, William Marsh Rice University, 6100 South Main, Houston, TX
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4404. .10389,10447. .10651,10701. .11393,11455. .13118,
13175. .13657,15706. .15715)
Natl. Acad. Sci. U.S.A. 98 (18), 10445-10450 (2001)
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Proc. Nat
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PGNEVŘÍJALÍSÍPGVLMGKTKSKQTGTTŠPHQFKDNSSFVASTTANVLSKSGAFVYA

LEALMYLLYNYDIFRANKONYAAGGGABASORQAGASORGVOLLKPITHGRKDDISIL

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CGTFVHQIFRYACDALIRFVRIFLLENNITQLRWQAHSFWTGLFFHANERQREKLLN
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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AQKYCVESRTSFEELSKIVQKVKACRSELVAYDRQOQDQPPVNPGSTTGAENPTTNRC
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ETLREIDPEAFYRLVLMVRGIANARPGSLAKICVENNYDIVPTLMGIVLELHKVTPTL
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VQCHTISKLIVRIADLKRTKMVRTINVYYNNRSVQAVVELKNRPALMHKARSVSLQSA
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KLKVIFELFISNCRTL"
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Matches:
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Mismatches:
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17558. .17563
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17584
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LLLYEHWYGYCYRMLKEFAADIRQPQAAGPSGGAPLDQDRAMFNESMLFAVLKTMFKM
LEKPVAVQAMQFFKDQRSGSLTTLLISFTGFISPVSYARKMAFVNELRQLSTQDS
QQHBDLVECFSELATVDNARLKQMIATTGFISPVSTSRAMGFVNRLFGLSTQDS
SSSSSNAQPPVMATVSAMPSISDQLDPMELEYDCGTAAGGGESNAGTPGTANTSILQP
LISLWQAAQPDPSEESSQACDHSDSERNGALLLSFVKSLVKDQSKASQIAPPLFQALL ETLREIDPEAFYRLVLMVRGIANARPOSLAKICVENNYDIVFTLMGIVLELHKVYPTL BEPVNIVKRGKLQPETIVICIVEIMYGRALADPGOVGRUTKTFIDLLKHDSVISHSA KEALILLLSPRMKRKVAIVPPAGSTPTSTSTMOALQAASSAASDIIEEAAGVVV DGSVGGGLPEPNADAEGAAVGVGGVGOOMMLEAPRGGGFPRLLGLPEDADDBAIM DIAIALALQOHGGDANALQSLQQGLANLQGIRQATAMAAAVNAAANVSLGGSDDDEGS NVATDGSTLRTSPAEPAGSGGSESGGSGVESIGGTSARSSNFGDHANASPPRQGSTKD DQEQPGPSGVAGSGGVAVLSAMSSSEDNEANEDDKLSKLHDLRITVLESIIQHLGTFD LCNGLOAIPLIQVILMLTTDLNGNNERDQQVLHDLLTALVGLCGNWKRGAAARRETKC PGNEYRLALLSLEGVLMGKYRSKQTGTTSPPHQFKDNSSFVASTTARVLSKSGAFVYA PGNEYRLALLSHWNVLGDPYAGGGLGSGGASGGGVQLKPIKHGPKPDISIL IPHYLKNYPDIFESY DGLLTEIIVRLPYQILRLSSAHPDNYDSGFCEAMTFLCEYM MLNLNTLLRRQVRKLLMYICGSKEKFFMYRDGHSLDAHFRVVKRVCNIVSSKTGAPYN RHDIEENFRKSAGEYGSSIRPTFYSLVMGDPEISYWAOEFKLDGLAWNFILCTPDKLK YELLVDALTDILSITDMSMYSKENDRASMHUNCAIOYCFITAMKLUGGLPFSYSHYE SLKABRSPNHISLAMSTRLPLASSHYLVNSSIKOGNYTQYAFTLWTHYGLDADDIK SLKQTILGVEAFNSQMNGNGTPRLSDLILFDSLVAHMQAVAWANKEGLKWPRKESEDA AGGSAGATSTISSSNDPELLSDDOKLKQDDDGKLSSDLQXYYDLW NSYQLLSVYNRGQMLSTSSNEDIDOKLKQDDDGKLSSDLQXYYDLWELWYKLM NSYQLLSVYNRGQMLSSSTPERALNILVPIVSDKRAIMLELHAAFKLLPREDKD LIANEWPKCLMVNDFAFNGKQHPVEPYILNYIDAHIIELTRGSNYSTLHTLKHCLKSI QLGQTLISPPQEGCDFADVLQIMITLADASPARGHVALFNTTLMLELAKLQLPDKHL KHAENVSAQLRYLSELLQSIGFRGSRQHNPPWDDELQTDIDELYDELAEEGEQDSLLD DSDEDTLNNKLCTFSQTQKEFMNQHWYHCHTCNMINTVGVCSVCARVCHKGHDVSYAK VASTRSNGFTLEVI NNDPNVVIVGIRVLIGTQDVQRAPQSVTILGRTIPTPVRRARWF PIPLTREBENGSDKLLKVVFRARAPDEBTVTLLCI EVYGKRELVGWPDESEDVTVPG SSAPAVSSSQASSARFGERFUT TQLDRMANHLLEVMCCALHLLGSGVPASWRGKAVK TASALLLLPTPNPVQTQARYVLATLYGTRALHINYKDGVLLQFVNRELQSMQFKLEKL ANPPMLSYDALVELTEHLRTCQEISQMRTGNWQKFCVVHEDALAMLMEIACYQLDDGV SPIIIQLLQAAVCNLPPPSGSKQAQPQPSTSSASGKLRTDREKSEDTDAYYSKFDPAQ CGTFVHQIFRXACDALIIRFVRIFLLENNITQLRWQAHSFWTGLFEHANERQREKLLN QTELK IDFPLPITACNLMIEFADFFETVSGSSENLQCPRCSAAVPAYPGVCGNCGENV FQCHKCRAINYDEKDPFLCHSCGFCKYAKFDFSMYARVCCAVDPIESAEDRVKTVSLI HSSLERADRNYRQLLTNKQMLELLIQKVAEHRSSDRMVEDNMASVHSTSQVNKIIQLL PAASAGAGTSAGASTKWQTSMIRFSGAAGRYIHNLISTSLLSEQLQSNLLQHLSISPW
STORTWPROYVESTLSVLVQTLLLFRPQEKEAACLSWWHSLINTLVEGVCSSNTASD
SDYBDLNIEHRAQLLIEFLFRSINLMQKKSILLLTAGGYIRCAEVCRGISEDRPVKNNQQI
MILSRLILLFLERYLMKHLYNAPPELLDQVRWNLFSVSSMPDTQKITDLLNCRTKLNSYC KLKVIFELFISNCRLPRGPVTAVLHPCLRIMQNLICPVLPGSKPNQKVATTDLCSMKM **FEGNTVDYRAWLNSDRNHEYAAWSKRMPSNNQAKLKNAKDQNVAASGGSDAPPKSRRE** QLLAIEISKVHRMEEYSLSSDLSLGYALRQYVELLWLLLECPNIRRTYKTRMLGPVLE TDLTILSQAQALIEMQPLTPSRIERLSMCGIAALYNAVLTSIATSVLGMSQASSSQKQ TASTSQGSGVGGSSGGQSNKDHDDFEDQACSIVNKALEIYSNIGHMFKTSARIHVYQN HLCYGSWLLISGIQGAMGASGSGGSSSDSASKSASKATKSGSEAGTAPTTPIARVNLF KVQQGFGELNAAIANHSIKLLSELIEDLKVEAACGQSLESTELPEPAQFDILQNYSSL ERIVRVLNTATLHQLFTFLATVAYRKACTLKRASAKDRTECEPISYSDSTTYFNDSLS CSDNSEEDDSESYLGHWFKETLSPETHDDNANTSTQERAEQKSALVPKLDEPHEYLDL AADIFCFLDQFLANRHAYMQRYVKAGVSDQQMLLMANIIKDFDRDVMRNETDQGSGNA JFWNLWPLVPTYGRRTAQFVDLLGYLTLSTRSITERLPEFVSRAVDVLRQQNELLCKH PNAPIYTTLESILOVNGYYLESEPCLVCNNPEVPMANIKLPSVKSDSKYTTTTMIYKL VOCHTISKLIVRIADLKRTKMVRTINVYYNNRSVQAVVELKNRPALWHKARSVSLQSA **AQKYCVESRTSFEELSKIVQKVKACRSELVAYDRQQDQPPVNPGSTTGAENPTTNRC** /GCALASTEQCLTLLRAMAYNYDCRVC1/YSQGLVSELAEHNLRRGTPL1QEEVRNLLV VRVAFLSEKYGKRWRERVLDKQRVIKPLVFNAKWIQPLLFNANSRFGRQLACSLLSSL SRTNERROQALNMLTSFLKHVGEAGEASAEYLMLYKNMATEQPWLQYLVLKGVLSQIS

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RABKKRLAMATREKOLDALGMRTNEKGOVTAKGSILOKIEKIRDETGITCFICREGYA
CQPDKVLGIYTFTKRCNVEEFELKSRKTIGYTTVTHFNVVHVDCHTSAIRLTRGRDEW
ERASLONANTRCNGILPLMGPANGEAAFSACMTRHSSYMQESTQRCDISYTSSVHDLK
                                                                                                                                                                                                     LLLVRFAWERSFHDDAGGGGPQSNMHFVPYLLFYSVYLLLSSRSAARDSKTLLTYLOA
PPASEKWLEGCYEVDGPLFWAFTISLSHKRKLAMHKRALNFKRATANGGRHVSFAVLC
PRALAPADRQVKDYYVRPELAWMALVDLTVONLFKTVSTPKEEDWPISLFVRKND
BALLKSTDSILQTLTEEFLPCTSFVEFCDVAGLIHLIEHPDNPIEEILAALPSTSSN
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                 YRMRGLLGDATEEFVETLNNKSQEQVDTEQLYRMANVLADCNGLRVMLERIGSLQRIS
RNRELIQVLLKLFLICVKVRRCQEVLCQPEIGAINTLLKVLQMCLQSENDSIQSAVTE
                                                       QLLETMET ILSKAASDTLDSFLOFSLTFGGPEYVSAL ISCTDCPNVRNNPSVLRHLIR
VLAALVYGNEVKMALLCEHFKDTLNFNRFDNERTPEEEFKLELFCVLTNQIEHNCIGG
                                                                                                  TLKDYIVSLGIVERSLAYITEHAPCVKPTLLRTDSDELKEFISRPSLKYILRFLTGLS
NHHEATQVAISKDIIPIIHRLEQVSSDEHVGSLAENLLEALSTDSATAARVQQVRDFT
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DVKNKICTDCELIALLEDDNGMELLVNNKIISLDLPVKDVYKKVWLAEGGDRDAMRIV
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Mooptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 17595)
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Mismatches:
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/bound_molety="zinc"
15995. .16135
/gene="push"
16130
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/bound_moiety="zinc"
11402. .11542
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5411, .5599
/gene="push"
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/gene="push"
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AF096896/c
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WPESEDVIYPGSSARANSSQASSARFGEGFNCTTQLDRMAHILLEVMCCALHILGS
GVPASMROKAVKTASALILLDTPNPVQTQARYVLATLYGTRALYHNYKDGYLLGFVNR
ELQSMQOKLEKLET LEEI DPREFYRLVLMYKGTANARHILLEVWCCALLHLLGS
GVPASMROKAKTASALILLLDTPNPVQTQARYVLATLYGTRALYHNYKDGYLLQFVNR
ELQSMQOKLEKLET LEEI DPREFYRLVLMYKGTANARACHILLEVWRYKDGYLLQFVNR
ELQSMQOKLEKLET LEEI DPREFYRLVLMYKGTANARACHILLEVPHMG
IVLELHKYTPTLDEVNIYKGLCOPRETYTVTDLYGTATAAAAAASAA
SDITEEAAGVYVDGSVGGGLPEPRNDAEGAAVGVGQQQMLNLEAEMGGGFPRLL
GLPEDADDEA IND IA IA LALGOHGGDANALOSPQGGTANLQGTRGATANAAANNAAAN
VSLGGSDDDEGSNYATDGSTLATSPAEPAGSGGSESGGSGVESIGGTSARSSNFGDHA
NSSPRQGSTKDDQEQPGPSGVAGSGGVAVLSAMSSSEDNEANEDDKLLSTAVDYVEIG
KRGAAARETKCPGNEVALLILYHWKNYLGDPYAAGSGGASGGSGSGSGSGSGSGSGVUSIGLTAVDYVEIG
KRGAAARETKCPGNEVALLLESTEVVLAGDPYAAGSGGASGGSGSGSGVASTTA
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TIPTPVRRARWFDIF LLREEMLQSDKLLKVVFAKAPDPEHVTLLDCIEVYGKSKELVG
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TYKTRMLGPVLESYLALRSLVVQRTRLIDDAOEKLLEMLEDMTSGTEEETRAFMEILI
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LKYILRFLTGLSNHHEATQVAISKDIIPIIHRLEQVSSDEHVGSLAENLLEALSTDSA
TAARVQQVRDFTRAEKKRLAMATREKQLDALGMRTNEKGQVTAKGSILQKIEKLRDET
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LEBEGBOSILLDDSBEDTLUNKLCTFSQTQKERMOHWYHTVROWSYCSYCAR
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PGTGGAAANTSQILSLWQAAQPNPSEESSQACDHSDSERNGALLLSFVKSLVKDQSKA
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Yager, J., Richards, S., Hekmat-Scafe, D.S., Hurd, D.D., Sundaresan, V., Caprette, D.R., Saxton, W.M., Carlson, J.R. and Stern, M.
Control of Drosophila perineurial glial growth by interacting neurorransmitter mediated signaling pathways
Proc. Natl. Acad. Sci. U.S.A. 98 (18), 10445-10450 (2001)
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PISLFDYLRKNDEALLKSTDSILQTLTEEFLPCTSFVEFCDVAGLLHLIEHPDNFIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFU96897 16135 bp mRNA linear INV 15-OCT-2001
Drosophila melanogaster pushover (push) mRNA, complete cds.
AF096897
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Submitted (06-OCT-1998) Biochemistry and Cell Biology, Mail Stop
140, William Marsh Rice University, 6100 South Main, Houston, TX
                                                                                                                                                                                                                                                                                                                                                                                                                                     2329 CTGGAAGCTCTGTTCAAGCTGGAGGTGCTCTCCAAGGCCGCAGTTGCTCTTGTGGCA 2270
                                                                                                                                                                                                                                                                                                                                                                                                            4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 16,135)

Yager, J., Richards, S., Hekmat-Scafe, D.S., Hurd, D.D., Sundares:
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Richards,S., Hekmat-Scafe,D.S., Hurd,D.D., Caprette,D.R.,
Saxton,W.M., Carlson,J.R. and Stern,M.J.
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                                                                                                                                                                                                                                                            Conservative:
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Matches:
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Query Match:
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AF096897/c
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AUTHORS
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130342: gap of unknown length
130342: gap of unknown length
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contig of 6499 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 9057 bp in length
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contig of 9680 bp in length
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (basas I to 12373)
Xu, X. Z., Wes, P. D., Chen, H., Li, H. S., Yu, M., Morgan, S., Liu, Y. and Montell, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (11-AUG-1998) C. Montell, The Johns Hopkins University
School of Medicline, Department of Biological Chermistry, 725 N.
Wolfe Street, Baltimore, MD 21205-2185, USA
Location/Qualifiers
1. 12373
/organism="Brosophila melanogaster"
//db_xref="taxon:7227"
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/map="28E1-2"
/tissuc_type="retinal"
/de_ystage="adult"
2. .12352
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3. Biol. Chem. 273 (47), 31297-31307 (1998)
99030403
2. (bases 1 to 12373)
Montell,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                           44934. .89804.

Anote-"assembly_name:Contig47"

89905. .95932.

Anote-"assembly_name:Contig48"

96033. .102531.

7.note-"assembly_name:Contig49"

102632. .11305.
                                                                                                                                                                                                                                     111406. .120462

/note="assembly_name:Contig51"

120563. .130142

/note="assembly_name:Contig52"

130343. .140588

/note="assembly_name:Contig53"

140689. .149261

/note="assembly_name:Contig54"

149362. .162349
                                           /note="assembly_name:Contig45" 79339. .84833 /note="assembly_name:Contig46"
/note="assembly_name:Contig44"
15048, .79238
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Y17920.1 GI:3893108
calo gene.
fruit fly.
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53.00
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61.11%
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Best Local Similarity:
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Submitted (02-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                         EST AA909108 (NID:g3048513) om32d11.s1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173772)
Waterston,R.H.
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Feb 18, 2001 this sequence version replaced gi:12745114
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Center code: WUGSC
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Conservative:
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Unpublished
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                                                                                                                                                                                       /rpt_family="ERV1"
38463. 38929
4.rpt_family="MER1_type"
39354. 39609
4.rpt_family="L1"
4.2594. 4.2877
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alu"
45998. .46226
/note="similar to
47950. .48034
                                                                                                                                                                                                                                                                                   /rpt_family="Alu" 43519. .43817
                                                                                                    /rpt_family="ERV1"
34473. .35285
               /rpt_family="ERVK"
31172. .31597
                                                          /rpt_family="ERVK"
31598. .32237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
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48869. .48985
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5883. 36498
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Waterston, R.H.
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* NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 150537 bases at least Q40 consensus quality: 158418 bases at least Q30 Consensus quality: 15327 bases at least Q20 Insert size: 191000: agarose-fp Insert size: 191001; sum-of-contigs Quality coverage: 2.8% in Q20 bases; agarose-fp Quality coverage: 3.33 in Q20 bases; sum-of-contigs Quality coverage: 3.33 in Q20 bases; sum-of-contigs
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/rpt_family="ERV"
13237. 13580
/rpt_family="MaLR"
14241. 14593
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24194. 24335
/rpt_family"MaLR"
24452. 24562
24961. 25528
                                                                                                                                                                          8883. .8945
/rpt_family="Alu"
8961. .9178
/rpt_family="ERV1"
                                              /Jeb. ,8065
/rpt_family="ERV1"
8066, R417
                                                                                            8066. .8419
/rpt_family="ERV"
8762. .8877
/rpt_family="ERVI"
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21983. .22295
/rpt_family="ERV1"
23119. .23239
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10676. 10021
                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to
10829. .11250
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12809. .12925
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16242. .16534
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17189. .17450
/note="similar to
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25530. .27490
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27922. .28018
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27997, ...29042
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12808. .13247
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/rpt_family="ERV1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note-"similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="L1"
18739, .20933
/rpt_family="L1"
20934, .21246
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23639. 23924
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                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Alu"
10829. .11215
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21740. .21881
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18705. .18738
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21247, 21cc
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                  7363. .7578
/rpt_family=
7586. .8065
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27808. 2701
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B.Y., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, F.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-305H21; the clone sequenced to the right is RP11-109F19, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-105L10; actual end is at base position 24605 of RP11-105F19.

Location/Qualifiers
                                                          63108, USA
                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The position of this clone was established as part of a collaboration between the Human Chromosome Y Mapping Project (Tomoko Rawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen, and David C. Page at the Whitehead Institute for Biomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO.
                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                Direct Submission
Submitted (14-OCT-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Oct 14, 2000 this sequence version replaced g1:6624109.
                                                                                                                Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="Y"
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NEIGHBORING SEQUENCE INFORMATION:
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/clone_lib="RPCI-11"
733. .1035
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/rpt_family="Alu"
3460. .3864
4654. .4753
/rpt_family="MalR"
4917. .5048
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6100. .6400
/rpt_family="Alu"
6920. .7254
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/rpt_family="Alu"
1787. .1857
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                  TITLE
JOURNAL
AUTHORS
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                                                                            COMMENT
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AC007274 117309 bp DNA linear PRI 14-OCT-2000 Homo sapiens BAC clone RP11-105L10 from Y, complete sequence. AC007274
                                                                                                                                                                                         /product-"hypothetical protein (fragment)"

protein_id-"CAD12002.1"

/db_xref-"G172026166"

/translation-"OHEGAAAFARGVYVAIRNPIAHELGDELKEHEALEOLAAFSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases I to 117309)
Waterstoon, R.H.
Direct Submission
Submitted (09-APR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 117309)
                                                                                                                                                                                                                                                                                                                                /note="3 base direct repeat bordering transposon Tn5714. Note difference - TCA in Streptomyces coelicolor plasmid SCP2, TGA in Sr-Tseptomyces coelicolor plasmid scoplement(7784. 7794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                            /note="Partial CDS, unknown. May have been disrupted by Tn5714 insertion."
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Inverted and repeated imperfectly at complement(71285 . 11295)"
/note="Similar to Tn5714 from SCP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 117309)
Mcpherson-Wagner, C., Maupin, R. and Krasucki, Peter.
The sequence of Homo sapiens BAC clone RP11-105L10
Unpublished
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Mismatches:
Indels:
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Sulston, Land Materston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                             complement(7612. .7782)
                                                                                                                                                                                                                                                                                    RWVDDATVETAV"
complement(7781. .7783)
                                                                           /gene="SCP2.09c"
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65.38%
50.00%
41.09%
                                                        /partia]
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Best Local Similarity:
Query Match:
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SOURCE
                               CDS
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/protein.id-"cAD11999.1"
/db_xref-"c1:17026163"
/translation-"WFGPPCFANGYGAEGGRMTTVVLRELRKELSEDFGPGDAVD
RIEAVHAAPADSDVSGDPDDRTFCGKPTLDMERVNYQPVGPGAPWLPPNMHAWECRDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to Agrobacterium rhizogenes Riorfl36 protein, hypothetical integrase TR:BAB16255 (EMB.:AP002086) (383 aa) fasta scores: E(): 7.5e-18, 31.6% id in 326 aa, and to Pseudomonas pavonaceae putative integrase intp TR:09R009 (EMBL:AJ250371) (379 aa) fasta scores: E(): 4.8e-08, 28.2% id in 383 aa, and to asceriophage PI recombinase Cre SW:RRCR_BPP1 (P06956) (343 aa) fasta scores: E(): 0.0001, 24.7% id in 304 aa. Contains Pfam match to entry PF00589 Phage_integrase,
                                                                                                                                                                                                                                                       /traislation-"MTESPRAALPSLNSPPGDRLEIVNGWDADTPYQSWRPQILVPPT
FRQASAPRVFVVVNOKGGAGKTTTTVELAAAWAAAGHRVRVIDADHQEAALSAWLLPQ
YPEGSRRHSLRSVFFEDCTLAEATYPTLEAGYDVPSSYDLQRVEYERRIGAEGGLAA
ALAQEAEEAGKSPYDTLIDAAPSLGLVTVAALTAADEALVPIKVGGLDMKAMSLH
KTLRSVORKTRPKLSYGAVLLITAMDKSTFARCLATKVSEDYPEAAVVPIRRSIRASEA
PLSEEPIRLYAPEAAPAGDYDQAAAVLLDGRAAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"putative integrase/recombinase"
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/db_xref-"GI:17026164"
/db_xref-"CI:17026164"
/translation-"MCETGRQLAVVTADADVVEAELVDDETAGASVVVHTDRDRHLSP
FTVAAIAASVADSTRRAYGTDRAAFAAWCAEEDRTAVPASAETWAEWVRHLTVTPRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TORPAGPSTIERAMSAVITWHEEGGRPKPNMRGARAVLNAYKORLAVEKAEAAQAROA
TAALDPQIRAMLAGVORTIAGKRNAALVLIGGRATAARVESETYALDVDTVTEAEBGYD
VTLYRKVVRKHTMIILYGTODPATCOVPALATAALAAAGRTDGELFVYDDRWDRLA
PPMTRRGRVIGDPAGRMTAEAAAEVIERLAVAAGLSGDWSGHSLRRGFATAARAAGH
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ETGFDIDNVRSAIESNG"
partitioning protein Para SW:PARA_CAUCR (005189) (266 aa) fasta scores: E(): 1.3e-21, 36.2% id in 257 aa, and to Streptomyces coelicolor Para TR:09RFM1 (EMBL:AF187159) (357 aa) fasta scores: E(): 2.6e-19, 36.1% id in 263 aa. Contains Pfam match to entry PF00991 ParA, ParA family
                                                                                                                                                                                                                                                                                                                                                                                                                 ATERS, SCORE 56.80, E-value 4.6e-13"
5557. :S86
/gene-*SCP2.06*
5557. :5886
/gene-*SCP2.06*
                                                                                                                                                                                       /product="putative partitioning protein ParA"
/protein_id="CAD11998.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5935, 7050)
/gene="SCP2.07c"
complement(5935, 7050)
/gene="SCP2.07c"
                                                                                                                                                                                                                                                                                                                                                                                                  complement(4190. .4534)
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/note="Pfam match to ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7612. .7782)
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/transl_table=11
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/gene="SCP2.08"
7201. .7386
/gene="SCP2.08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Unknown/codon_start=1
                                                                                                                                           /codon_start=1
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gene CDS gene

gene

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GGRPPTRPDHYGGDRAYSSRRNRYLBRRRIHHTPEPKDQRANRRRRGREGGRPAGF
DRDHYRRRNEVERTINRLKNPRAVATRYDKRAYVFHGTVTAAAIRLWLRQ"
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LEKYGEPWYTYLKGYNEKERGRRYYRAADLSBRAALPPPWHIARPDGYRDVLTYAAA
EGRAPRLAPAEPKVAROAADERGARAYADSGABAIATHARPOGYRDVLTYAAA
DRYGGGTLAPAEPKVAROAADERGAEVAGYSODGVDEGABAIATLEAAVAQORQIY
DRYGGGTLAAALLYDPGRGDHLRRELIRQYAQRTAYRARDTSGEQVADDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSRRSLALPSTRSTEPDDADELEAAPEEKLAAARSAGVVASLTG
ADLSTPLTVAQLPTPYDVAETVTAPLNDQERGYLDVCEQALHGFRKSVVVAGKALEVI
                                                                                                                                                                                                 /note="Insertion element IS1648 bounded by 32bp imperfect inverted repeat. Copies of this IS element are also present in the Streptomyces coelicolor chromosome (EMBL:AL023861 and AL031035)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Identical to Streptomyces coellcolor putative IS1648 transposase SC3C8.16 or SC6A9.37 TR:O69928 (EMBL:ALO23861) (152 aa) fasta scores: E(): 0, 99.3% id 152 aa. Complete protein may be translated via a frameshift from the upstream CDS."
                                                                                                                                                                                                                                                                                                                                                                                             /jote="Identical to Streptomyces coellcolor putative IS1648 transposase SC3C8.15 or SC6A9.36 TR:069927 (EMBL:AL023861) (141 aa) fasta scores: E(;:0, 100.0% in 141 aa. Contains Pfam match to entry PF01511 Transposase_6, Transposase_Complete protein may be translated via a frameshift into the downstream CDS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="parA"
/note="Similar to Caulobacter crescentus chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF01511 Transposase_6,
Transposase, score 12.30, E-value 3.6e-05"
                                                                              coelicolor A3(2)"
/organism="Streptomyces coellcolor"
/db_xref="taxon:1902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                            /organism-"Streptomyces
                                                                                                                       /db_xref="taxon:100226"
/clone="plasmid SCP2"
425. .1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3033, .4010)
/gene="SCP2.04c"
complement(3033, .4010)
/gene="SCP2.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594. .839
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                                                                                                     /strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                914. .1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCP2.02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                       PAPTFALWRRWKLWAVATYAEAVELDKELRVYRVMLEREYGSYRKAPSDVRLPTTMER
YGLTIAEALALPRQAEERAQALREAEEDARLAEEARKOERAAAAEIARLKAAGAVQAA
RTEVNASTSRREVQAABEVAAAERAATAETEAVGSEAARAEADRAAAEHRAMEARRR
AAEADEAAAEARRAEAEALTAAEDEBATAAAEASTEEARARSQAGNDAAEAEQAAA
EARHRAEAERRAVAEDELTLSPRRKVRKVRRMILAEGAGHPENLPLESVWTACSV
SQTTASEYRSAAAQLLAEGYTPEAR"
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Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Burled, Submission
Submitted (14-NOV-2001) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinkron, Cambridge
CENO 1SA E-mail: barrell'seanger.ac.uk Plasmid supplied by Prof.
CENO 1SA E-mail: barrell'seanger.ac.uk Plasmid supplied by Prof.
Colney, Norwich, Norfolk NR4 7UH, UK
1. 31317
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Streptomyces coelicolor
Bacteria: Firmicutes; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; It (bases 1 to 31317)
Histeaer,T., Bibb,M.J., Buttner,M.J., Chater,K.F. and Hopwood,D.A. (in) Kieser,T., Bibb,M.J., Buttner,M.J., Chater,K.F. and Hopwood,D.A. (Eds.);
PRACTICAL STREPTOMYCES GENETICS: 1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 31317)
Haug, I., Brolle, D., Welssenborn, A., Kieser, T., Wohllebens, W. and
Altenbuchner, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL645771.1 GI:17026158
bldA regulation; GntR-family regulator; IS1648; partitioning
protein ParA; plasmid transfer; Tn5714; TraA; TraB; transposase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
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13
                           /function="putative membrane protein"
/note="ORF6"
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Conservative:
Mismatches:
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ISBN 0-7084-0623-8.
                                                                                                /transl_table-11
                                                                            /codon_start=1
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                                          J. Mol. Microbiol. Biotechnol. In press 2 (bases 1 to 7686)
Wilkinson, C.J.
Direct Submission
Submitted (28-SEP-2001) Wilkinson C.J., Department of Biochemistry, University of Cambridge, 80 Tennis Court Rd., Cambridge, CB2 1GA, UNITED KINGDOM
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    7686
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    /plasmid="2 SCP2*"

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/function="unknown"
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/function="unknown"
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ivrkekrotsarynasknceltaliplinese"
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Wilkinson,C.J., Hughes-Thomas,Z.A., Martin (nee Rowe),C.J.,
Bohm,I., Mironendor,T., Deacon,M., Wheatcroft,M., Wirtz,G.,
Staunton,J. and Leadlay, P.F.
Increasing the efficiency of heterologous promoters in
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Streptomyces coelicolor.
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
join(7165. .7303,8920. .9534,10965. .>11147)
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Mismatches:
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INSLELGATALFSNSDVDLDDVCLNEQVTNTNTSSAVGEVYQEQDLVRSQPDLMLLNN
SGDGVTSARAKKATGKREKERESEEPGRPSMVEKGGAAGIAGGNOTTQL"

JOIN (4128 4212, 4268 4485, 4610 4873)
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Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Aghaai, A., An, H.J., Basu, A., Bardex-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brocketch, P., Brocketch, C., Busan, D.A., Cawler, A., Chandra, I., Cherry, J.M., Cawler, A., Chandra, I., Dietz, S.M., Dogan, D.B., Delcher, A., Deng, Z., Davins, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferraz, Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrelli, J.H., Gu, Z., Gann, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Weil, M.H., Ibegwam, C., Jalali, M., Kalush, F., Korlen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Lidang, Y., Lin, X., Liush, F., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liush, F., Morlash, B., Murphy, B., Murphy, B., Moshrefi, A., Reise, R., Shen, M., Scheeler, F., Shen, M., Shue, B.C., Spradling, A., Stappeton, M., Scheeler, S., Shel, Y., Weinster, E., Wang, S., Pan, K., Woolsge, T., Worler, E., Wang, S., Wang, S
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SGQRLLSPREIDDLKGYIMMYTLIMLLVDTNRVYHIKSGSIIKLYIFYNNLEVGD
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TMKEFDWSITGFCVMLPDCFAVLFTEILIDWVKHAFITRFNELDESIYREYTTSLAYD
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TITLE
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FEATURES

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TITLE JOURNAL COMMENT

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                                          Direct Submission

Submitted (03-FBE-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
on Jan 31, 2000 this sequence version replaced gi:6587780.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgpefruitfly berkeley.edu. All contigs in this submission meet the following cutoffs: length >- 200 bases.

* NOTE: This is a "working draft' sequence record is a sont known and their order in this sequence record is a arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence * as soon as it is available and the accession number will

* be preserved.
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                          unknown length
of 121170 bp in length
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Truit fly.

Drosophila melanogaster

Burayota: Metazoa, Arthropoda; Tracheata: Hexapoda; Insecta;

Burayota: Meptera: Endopterygota: Diptera: Brachycera;

Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.

I (Bases I to 224896)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,

George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE003721 224896 bp DNA linear INV 05-OCT-2000 Drosophila melanogaster genomic scaffold 142000013386035 section 46 of 105, complete sequence. AE003721 AE002708
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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150241: gap of unknown length
150736: contig of 495 bp in length
150816: gap of unknown length
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154319: contig of 649 bp in length
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155422: contig of 599 bp in length
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of 390 bp in length
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152586: contig of 383 bp in le
152666: gap of unknown length
153590: contig of 924 bp in le
153670: gap of unknown length
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151239: gap of unknown length
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152203: gap of unknown length
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154743: contig of 344 bp in
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/db_xref="taxon:7227"
/chromosome="3"
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1. (bases 1 to 131610)

S. Celn Ker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Holt, R. A., Evans, C.A., Gocayne, J. D., Amanatides, P. G., Brandon, R. Gerlson, Y., An, H., Baldwin, D., Banzon, J., Beeson, K. Y., Busam, D. A., Champe, M., Davenport, L. B., Dietz, S. M., Dodson, K., Dorsett, V., Doup, L. E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R. F., Garg, N. S., George, R. A., Gonzalez, M., Houck, J., Hoskins, R. A., Hostin, D., Howland, T. J., McIncosh, T. C., Moy, M. Murphy, B., Nelson, C., Nelson, K. A., Nunoc, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouannenavong, S., Pitrana, G. S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Strikas, R., Tector, C., Williams, S. M., Zaveri, J. S., Smith, H.O., Rubin, G. M. and Venter, J. C. Sequencing of Drosophila chromosome 3R, region 90E-90E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC009462 151610 bp DNA linear INV 06-SEP-2001
Drosophila melanogaster, chromosome 3R, region 90E-90E, BAC clone
BACR37C04, complete sequence.
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For further information on this sequence e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. (bases 1 to 151610)
Celniker, S.E., Adbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Chew, M., Clesiolka, L., Dytle, C.M., Farfani, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequelra, A., Sethi, H., Shir, E., Sair, S., Sayiskas, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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/db_xref="taxon:7227"
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Requence Berkeley Notional Laboratory, NS 64.121
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FEATURES

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shows weak similarity to TR:AAF10061 (EMBL:AE001907), DR0482, Deinococcus radiodurans B-cell receptor associated protein related protein (328 aa), fasta scores; E(): 4.9e-07, 23.48 identity in 265 aa overlap. Highly similar to TR:CAB55231 (EMBL:AL17211), YPWT1.49C, Yersinia pestis CO-92 putative lipoprotein from plasmid pWT1 (276 aa), fasta scores: E(): 0, 97.58 identity in 280 aa overlap and TR:O68763 (EMBL:AF074611), Y1114, Yersinia pestis KIM5 hypothetical protein from plasmid pWT1 (276 aa), fasta scores; E(): 0, 97.58 identity in 280 aa overlap and protein protein sequence and an appropriately a positioned PSO0013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFQTYRKGVDDITDTDLRQKIADSLNRLASRMTTDTFTDGGKASLLDNALKDIQAEMS
PVGIEVISLSWVGKPDYPDTVIESINAKVTANQKTLQRQQEVEQRKAEANMLREQAEG
EADGEADAIRKRAQAEADAIKLRGEALRQNPNVMELEAINKHNGQLPQYMTEGANTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2493. .2693)
/gene="HCM2.0007c"
/note="HCM2.0007c, possible membrane protein, len: 66 aa;
/note="HCM2.0007c, possible membrane protein, len: 66 aa;
highly similar to TR:CAB62372 (EMBL:AL117211), YPMT1.49AC,
Yersinia pestis CO-92 hypothetical protein from plasmid
pMT1 (66 aa), fasta scores; E(): 3.5e-25, 97.0% identity
in 66 aa overlap. Contains hyrophobic, possible
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                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MKKGLLAVALTAICTMGLTGCDRVEPGYVGIKVNKLGEDKGIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                             VVGVGRQWTGLNTELYTFPTFKQMKTYDEPFTFQMSDGTAIGHKIGVAYLVNRDKVTT
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/gene="HCM2.0006c"
/note="PG0013 Prokaryotic membrane lipoprotein lipid
attachment site"
complement(2493. .2693)
/gene="HCM2.0007c"
complement(2493. .2693)
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Verbsky,J,W, and Turkewitz,A.P.
Proteolytic processing and Ca2+ binding activity of dense-core
vesicle polypeptides in Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp 25
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Burtrahymena thermophila
Eukaryota: Alveolata: Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
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                                                                                                                                                                                                                                                                                                                         /transl_table=11
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Db 39526 TCCGCG 39521
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/translation="MRVIAALLVIALVCQSAMAVTSKSQAKLMMEKINSKLEKSHLGR
ALGGWYTIATRLGYDYQDLYDAFAALKNQLLNULDBNSLEFTGYTASIDSAVAQFNAD
ISVANGQINDAQAQLADLNDSLNYTQQNLQDAQQALQDNYDALNAAERALARAEALYO
VATAEYSNADQVIGLAVEKLQPRQSHYDNADLGSFSFVQIKNTFVSFROKVTEATKGW
WARQLEVPRYVQAMAQVKNYTSQSSIQTAIKALQDLQAYFQYRTSDLTNEYYSFTQN
VQSTDGLNGIIDLLQNQVIPGYFRQISSLQAQIQQVEDALALAQQNLQDAQNALDAE
NAQWENVVARHQALVDRINSEYDLVTQADRIVNAQAQVNGSD"
2 (bases 1 to 1288)
Verbsky,J.W. and Turkewitz,A.P.
Direct Submission
Submitted (24-007-1997) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC014470 32270 bp DNA linear HTG 16-NOV-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                             /note="Ca2+ binding protein; translated as a proprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was identified as CDM:10212984 by the submitter.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 32270)
Adams,M. and Venter,J.C.
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Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=6
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314 c 202 g 355 t
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/strain="Bi686"
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24. .1157
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/note="Grl5p"
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AC014470.1 GI:6436865
HTG: HTGS_PHASE2.
fruit fly.
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complement(658. .663)
complement(719. .1129)
complement(719. .1129)
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complement(719. .1129)
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/note="HC
             /gene="HCM2.0003c"."/
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/note="HCM2.0003c, hypothetical protein, yowr1.46BC,
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Yersinia pestis CO-92 hypothetical protein from plasmid
pwT1 (91 aa), fasta scores; E(): 0, 94.5% identity in 91
aa overlap and TR:Q926X9 (EMBI.AF074611), Y1117, Yersinia
pestis KIM5 hypothetical protein from plasmid pwT1 (91
aa), fasta scores; E(): 0, 94.5% identity in 91 aa
overlap"
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/note="*...
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complement(1492, .1497)
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/note="repeat 1; 57 ]
complement(1647. .24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/gene="HRNZ.0002c", possible periplasmic protein, len: 101
aa: similar to TR:CAB5528 (EMBL:ALI17211), YPWT1.46C,
Yersinia pestis hypothetical protein from plasmid pWT1
(111 aa), fasta scores: E(): 2.88-26, 95.58 identity in 67
aa overlap. The N-terminal 37 aa are highly similar to
YPWT1.46Ac (EMBL:ALI17211) Yersinia pestis hypothetical
protein from plasmid pWT1 (59 aa) (86.8% identity in 38 aa
overlap) which lies immediately upstream of YPWT1.46C in
pWT1. Contains a possible N-terminal signal sequence"
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/protein_id-"CAD09869_1"
/brotein_id-"CAD09869_1"
/brotein_id-"CAD09869_1"
/branslation-"ktvl.DrillivsiafyldciffGairkalapvNGAMVVDSGEQ
FYVVRDDRYLSSPYLTKRNGKLSGVGEDKFVYNKSGDVYGVHAKNASYLFDDCKEVG"
                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-0CT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk Notes:
Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/S_typhi/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="FKM2.0001c"
/note="FKM2.0001c"
/note="FKM2.0001c, hypothetical protein, len: 68 aa;
/note="FKM2.0001c, hypothetical protein, len: 68 aa;
highly similar to TR: CABS5227 (EMBL:ALI17211), YPMI1.45c,
Yersinia pestis CO-92 hypothetical protein from plasmid
pMT1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity
Yersinia pestis KIM5 hypothetical protein from plasmid
pMT1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity
in 60 aa overlap. Spans the end of the sequence"
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/note="95.7% identical to Yersinia pestis CO-92 plasmid pmrl (EMBL:ALI17211) bases 48304. .48535"
/gene="HCM2.0002c"
Parry,C., Quail,M., Rutherford,K., Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
Nature 413 (6858), 848-852 (2001)
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Typhi"
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/protein_id="CAD09868.1"
/db_xref="GI:16505982"
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complement(1. .29)
/gene="HCM2.0001c"
complement(1. .29)
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224, .6722
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/gene="HCM2.0002c"
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Parkh111,J.
                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                         TITLE
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/db_xref-"GI:4155848"
/translation-"MKRLLLALALAFESLSCTNAQEIKETOETKKFKETKSOTRFNIS
YTKVIEKEFSQSRRYYALLEPNEALIFSOTLEFDGYVEKLYANKTYTPIKKGDRLLSY
YSPELAGVQSBLLSSLKHOQVGAIKEKLKLIGLENFSIEKTISSHKVONETTYSRF
NGVIFKKSPDLNEGSFIKKGOELFKIIDLSRLWALVKVNOEDLEFLKNTHOALLFVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGVG IDTALEYLKKSNAAIKOLDFVKOVFGKVGRANTSTDAAGLGMIETY IELKPQNE
WKEKLSYKEVRDKLEKTLOLKGLTNSWTYPIRGRTDMLLTGIRTPLGIKLYGNDTDKL
QELAILMEQQLKTLKESLSVFAERSNNGYYITLDLNDENLARYGINKNAVLDTIKFAL
                                                                                                                                                                                  VKGKQAITLENINPIINAQDÄMLEARFNVPNLKLLYYPNMFAQVEIFHKPQKMKILPK
EAVLIKGGKAIVFKKDDFGLSPLEIKAVRLSDGSYEILEGLKAGEEVANNALFVLDAD
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FKTLQYIVPVSVFIIFILIVFALKNLTNSLLCFFTLPFAFLGGLIFMNLMGFNMSVAA
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Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
Wain, J., Churcher, C., Muggall, K.L., Bentley, S.D., Holden, M.T. G.,
Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N.,
Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S.,
Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P.,
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO73 ATACAAGCCCTACAGGAGCAAATTGACGCTTTAGATTCTCAAGAAAAGTCGTTAGCAAA 5132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to H. pylori 26695 gene HP1329"
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                       7190. 10297
/gene="czcA_2"
/note="jhp1249"
7190. 10297
/gene="czcA_2"
/note="similar tc
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57.00
69.57%
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Best Local Similarity:
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IKNLENTLYQANHSSSPDLIAIAKLEILKSLLEIEKNDLEVALSSSHYSMGELTFKEN
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                                                                                                                                                 /note="similar to H. pylor1 26695 gene HP1324"
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Submitted (12-JAN-1999) Astra Research Center Boston, 128 Sidney Street, Cambridge, MA 02139, USA Address all correspondence to: hP@arcb.us.astra.com or Richard A. Alm. Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills, Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and Diane E. Taylor are with the University of Alberta Department of Medical Microbiology and Immunology, Edmonton, Alberta, Canada, 76G 2H7 and the Canadian Bacterial Diseases Network. All other authors are with Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Putative Identifications, sequence alignments, and name and sequence search capabiblity are available at ARCB's World Wide Web site. (URL:
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Location/Qualifiers
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2. (bases 1 to 12526)
King, B.L., Alm, R.A. and Trust, T.J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                               /translation="MRRILMILILEFSPLFANAQKTQEIKKTKEAKSQTRENISTTK
VIEKESSOSRRYYALEPNEALILEFGTLRFDGYVEKLYANKTYTPIKKGDRLLSVYSP
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IFKKSPDLNEGSFIKKGGELFQIIDLSOLMALVKVNQEDLEFLKNTHKAILEVEGIKG
PQEITLENINPIINKEDKMLEARFNVPNVKQIYYPNNFAQVEIFQKPOKMKILPKEAV
LIKGGKAIVFKKDDFGLSPLEIKAVRLSDGSYEILEGIKAGEEVANNALFVLDADAQN
NGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-wieth
AQVVQITPPNOSPRIVOEOVTYPLVSTFNSIANIDTVRGISSYEGGLIYIIFKDGVN
AQVVQITPPNOSPRIVOEOVTYPLVSTFNSIANIDTVRGISSYEGGLIYIIFKDGVN
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YRYALLGOVGCVSEVASVGGFVKDYEVTLONDSLIRVNLSLEOVANAIKNSNNDTGGGV
ILENGFEKIIRSHGYIQSLKDLEEIVVKKEGAIPLKIKDIASVRLTPKPRRGAANLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE001548 12526 bp DNA linear BCT 20-JAN-1999 Helicobacter pylori, strain J99 section 109 of 132 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alm, R. A., Ling, L. S., Moir, D. T., King, B. L., Brown, E. D., Dolg, P. C., Smith, D. R., Noonan, B., Guild, B. C., deJonge, B. L., Carmel, G., Tummino, P. J., Caruso, A., Uria-Nickelsen, M., Mills, D. M., Tves, C., Glbson, R., Merberg, D., Mills, S. D., Jiang, Q., Taylor, D. E., Genomic-sequence comparison of two unrelated isolates of the human quastric pathogen Helicobacter pylori agastric pathogen Helicobacter pylori Nature 397 (6715), 176-180 (1999)
/note="similar to GB:M26073 SP:P13510 PID:141927 percent
identity: 28.85; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note="similar to GB:W26073 SP:P13511 PID:141928 percent
dentity; 31.32; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
                                                                                                                                                                                                     /product-"cation efflux system protein (czcA)"
/protein_id="AAD08369.1"
/db_xref="GI:2314493"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="cation efflux system protein (czcA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-847-539A-6_COPY_S9_86 (1-28) x AE000634 (1-12496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAD08370.1"
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                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7149. .10256
/gene="HP1329"
7149. .10256
/gene="HP1329"
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Helicobacter pylori J99
                                                                                                                                             codon_start-1
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AE001548 AE001439
AE001548.1 GI:4155845
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1 (bases 1 to 12526)
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57.00
69.57%
52.17%
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 AlaAspAsn 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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KEYWORDS
SOURCE
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AE001548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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HLIIPSSPSDRKSVKNFEKELTEFIKRLRENRITHETCE"
complement(2949. .4340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EHLRELAIGGTAVGTĞLNAHKELSEKVAĒELSQFSGVKFVSAPNKFHALTSHĎAIAYA
HGAEKALANALMKIANDIRWLASGPRCGLGELNIPENEPGSSIMPGKVNPTQCEAMTM
VAQVWGNDTAIGIAASQGNPELNVFKPVIIYNFLQSLRLSDSMESFNIHCASGIEP
NREKIDYLHHSLMLVYTALNPHVGYENAAKIAKNAHKKGISLKESALELKLLSAEDFD
KFVVPEKMIGPKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mkklaalflusvlgvmginaweqtlkandlevkiksvgnpikgd
ntfilsptikgkalekaivrvqfmmpempgmpamkemaqvseknglyeaktnlsmngt
wqvrvdikskegqvyraktsldl"
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QKVDLNGKKLTQSQMIDLEKQKKILELKKTKQOLAISLMINGIENYKNQQEIELLKTA
IKNLENTLYQANHSSSPNLIAIAKLEILKSQLEIKKNNLEEALSASHYSMGELAFKEN
SKKLSLKKRFFLEYKIKTHGEVGFFVVKKSANEIDSLGLGACLKLAVQEILENGCSLV
BERLINGNFAGGLNKRYPHIQTIIKGDETIAQIAMASYLAKAFKDREMLELHALFKEY
GWDRINGGYGTKQHIBAIIKLGATPFHRHSFTLKNRILNPKLLEVEQRLI"
complement(2676...2927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MOFRIEHDTMGEIKVNDSOYWGAOTORSLENFKIGTEKMPKELI
GAFAKLKRSLAVVNHKLGKLSLEKSQAIIKACDCILKGELCGEFPLAIWOTGSGTQTN
MNLNEVIANKATEILGGNFREKKLIHPNDDVNMSQSSNDTFPTAMHIVSVLEITHRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLSFISAFDKRGVSIRLLTALLLESLGLAKDLEIQSFVAKYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELLSIAPKNFEFNREQELHNISATNYDIAIÄRLDEEKSQKDITLAKKSFLEDVNVTGV
YFREKQYYNYDMFSTALSIPLPIYGKQAKLVEQKKKEELVFKSEVENTKNKTHHLAL
KLLKKLETLQKNLESINKIIKQNEKIAQIYALDLKSNGDYNAYYNAFNDKITIQITQL
ETLSALNSTYLSLQUNKGLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLENLLKTFKEKSQQFKEIVKIGRTHLQDATPLTLGQEFSGYASMLEHSKQQILESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:U00096 percent identity: 63.68; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4897. .6135
/gene="HP1327"
/note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"hypothetical protein; identified by GeneMark;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2949. .4340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table-11
                                                                                                                                                                                                                                                      /codon_start*1
/transl_table*11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HP1326"
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6132. .7148
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/gene="HP1326"
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                                                                                                                                                                  /gene="HP1324"
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                                                                                                              /gene-"HP1324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HP1325"
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                                                                                                     E 2 (Dases 1 to 12496)
S Tomb.J.-F., White.O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Telschmann, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Dougherty, B.A., Nelson, K., Quackenbush, J., Zhou, L., Kirkness, E.F., Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khalak, H.G., Glodek, A., McKenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.E., Gozyne, J.D., Utterback, T.R., Peterson, J.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Bowman, C., Watthey, L., Wallin, E., Hayes, W.S., Borodovsky, M., Karp, P.D., Smith, H.O., Fraser, C.M. and Venter, J.C.
Direct Submission
L. Submitted (Ofe-NuG-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MRYDYLNPISFERKFMPLSCLHPFGPFETPKEPVLNNPLLKAPS
SDXTCLLGPRYGRYTFALKARVFKFWPYINYNDRLNQNITISSWILLKWHLEKKMDL
LIDDRIDREDPSLPFLDRIULPOCLSPITAPNFSCYALGLNFRFYTSFRFMDT TLFNRFLRDGNALDSLFTRENDGRILKKQENIQLIFQAYAPLMAKICSYQSKFVSAFY
TLFNRFLRDGNALDSLFTBNEGERILKKQENIQLIFQAYAPLMAKICSYQSKFVSAFY
LLNNFENMYPLELKKOPFWYELFALSKONTIFVRNFBNNKTKLYLDPRALPYSTTPSPS
LLNNFENMYPLELKKOPFWYELFSHDNGIFILRENGTNKLALIAHAFPTPHFLEKQLL
WCHKHGFLNIIVVSINAPISATNTPYKHLNFIDFSLDIQSILV"
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wleinffdeknppngyvgsasisgkrndfyanyipyddolppeqnaekiallrarina
ystlesilltkmhnrivkvlqvknnvishlfglydfltsksilakrfydtynhrvyvm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:L77117 PID:1592175 percent identity: 30.81; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-MAR-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="H. pylori predicted coding region HP1322"
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                                                       Erratum:[[published erratum appears in Nature 1997 Sep
25;389(6649):412]]
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    .12496
    /organism="Helicobacter pylori 26695"
/strain="26695"

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Nature 388 (6642), 539-547 (1997)
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DVKKTKDTKDYVKKEERQNVNTLPTTGEESNPFFTAAALAIMVSTGVLVVSSKCKEN"
COMPLEMENL(§939. .8198)
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Helicobacter pylori 26695 section 112 of 134 of the complete
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Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Fleischmann, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Fougherty, B.A., Nelson, K.A., Monckenbush, J., Zhou, L., Kirkness, E.F., Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khalak, H.G., Glodek, A., Mokenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.E., Gocayne, J.D., Utterback, T.R., Peterson, J.D., Kelley, J.M., Karp, P.D., Smith, H.O., Fraser, C.M. and Venter, J.C.
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Helicobacter pylori 26695
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
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UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE 2
(ENOYLPYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE
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WTRGIERAVIGNTKCDIGAAVQEYAGSFGGLADSCWAYAVGTPSDEIKQLMDVTKEA
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(AFV008220) ytoI [Bacillus subtilis]
>q112633392|emb|CAB14887.1| (299118) ytoI [Bacillus
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TROVREPVLODYKKVIGVVSKRDVVDOLPTTKLTKVMSKNPTTARPHTSLANISOKMI
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complement(2980. .3840)
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//note="Bast Blastp hit = sp|09Z9J4|AMPM_BACHD METHIONINE
AMINOPEPTIDASE (MAP) (PEPTIDASE M)
// 11.18) map {imported} - Bacillus halodurans
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complement(5148. .5690)
/gene="Spy1356"
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(AF124401) GRAB precursor [Streptococcus pyogenes]"
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/trans1_table=11
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/note="Best Blastp hit = spiP43905|AROA_LACLA
/note="Best Blastp hit = racarboxYVINVITANSFERASE
3-HOSPHOSHIKIMATE 1-CARBOXYVINVITANSFERASE
(5-ENOLPRIVIVISHIKIMATE-3-PHOSPHATE SYNTHASE)
SYNTHASE) (EPSPS) >qi|1075724|pir||552580
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
- Lactococcus lactis >qi|683583|emb|CAA55180.1| (X78413)
5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Lranslation="MKRWKLRPNAGPLOGTIOVPGDKSISHRAVILGAVAKGETRVKG
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ITYTLEISSAOWKSATLLAALGAKGTTOVVERITRHYTEEMIQOEGRLIVOGKRIT
LVGPQQLTAQEITVPGDISSAAFWLVAGLIIPRLDELPRLIDELPRILEVEKMG
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DAQELRYKETDRIQVYTDILLANGGANIKATAGGMIIKGPTVLYGANTSTYGDHRIGMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AaK34181_i"
/db_xref="G1:13622462"
/translation="MAEKKWFDKVLSKWQYEPIQVFWRHLQSAEMDLSAIAVAYYLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAFPLIVIAANIFPYLNIDIADLLRLMKQNLPKDIFRPASAIVENIFSKPSGSVLGVA
TLTGLWTMSRSLTSLQKAINKAYGASQHRDFFIGHLVGLLTSLIILFLLAFALIFSIF
SKAAIQVLDKHYHLSDNITTIFLLLIQPITVLIIFVGLMLLYFLLPNVKIKKIRYILP
                                                                                                                                                                                                                                                                                                                                                                       /note="Best Blastp hit = pir||D82693 shikimate kinase XF1335 [imported] - Xylella fastidiosa (strain 9a5c) >91|9106332|gb|AAF84144.1|AE003966_5 (AE003966) shikimate kinase [Xylella fastidiosa]"
Yuan,X., Clifton,S.W., RUE,L.... __.
Direct Submission

Submitted (10-APR-2001) Department of Microbiology and Immunology,
University of Oklahoma Health Sciences Center, 940 SL Young Blvd,
Oklahoma City, OK 73104, USA

Location/Qualifiers
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unknown conserved protein [Bacillus halodurans]"
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/product="conserved hypothetical protein"
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/transl_table=11
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1-carboxyvinyltransferase"
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/gene="SPy1353"
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                                                                                                                                                                                 /strain="SF370"
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/transl_table=11
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DVKKTKDTKPVVKKEERQNVNTLPTTGEESNPFFTAAALAINVSTGVLVVSSKCKEN"
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Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qlan,Y., Jlaf,H.G., Najar,F.Z., Ren,C., Zlu,H., Song,L., White,J., Vuan,X., Clifton,S.W., Roc,B.A. and McLaughlin,R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
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Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K.,
Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,
Olan,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J.,
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/product="GRAB"
100. .273
/note="Region: alpha2-macroglobulin-binding A domain"
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Matches:
      1. 832
/organism="Streptococcus
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                                              /strain="ATCC700294"
/db_xref="ATCC:700294"
                                                                                       /db_xref-"taxon:1314"
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AE006573 AE004092
AE006573.1 GI:13622
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Best Local Similarity:
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                                                                                                                                                                                                                                                          /product="GRAB precursor"
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/protein_id="AAD26341.1"
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/translation="VOSPIEOPRIIPNGGTLTNLLCNAPEKLALRNEERAIDELKKOA
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AAVVKADNAASDTLEALADQTDALQSEEAEVVQSDNAASDALEALADQTDALQSE
TKPVVKKEERONVNTLPTTGE"
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1 (Dases I to 804)

Rasmussen, M., Muller, H.P. and Bjorck, L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin

9269061 Chem. 274 (22), 15336-15344 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF124403 804 bp DNA linear BCT 14-AUG-2000 Streptococcus pyogenes strain AP49 GRAB precursor, gene, partial
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                         /product-"GRAB"
1. 174
/no.e- *region: alpha2-macroglobulin-binding A domain"
/no.e- "grab"
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Sweden
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163 g 157 t
            Rasmussen, M., Muller, H.P. and Bjorck, L. Direct Submission Submitted (28-JAN-1999) Cell and Molecular Pathogenesis, Scelvegatan 39, Lund 221 00, iLocation/Qualifiers
                                                                              1. 717
/organism="Streptococcus pyogenes"
/strain="KTL9"
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Conservative:
Mismatches:
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    (bases 1 to 804)
    Rasmussen, M., Muller, H.P. and Bjorck, L.
    Direct Submission

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/note="Region: repeat motif"
595. 777
/note="Region: cell-wall att.
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AF124403.1 GI:4589086
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Best Local Similarity:
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Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the Dacterial surface by binding alpha2-macroglobulin
J. Biol. Chem. 274 (22), 15336-15344 (1999)
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcacese;

    174
/note="Region: alpha2-macroglobulin-binding A domain"

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Streptococcus pyogenes strain ATCC700294 GRAB precursor, gene,
complete cds.
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Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular
Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden
Location/Qualifiers
  Biology, Molecular
Sweden
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Submitted (28-JAN-1999) Cell and Molecular Pathogenesis, Soelvegatan 39, Lund 221 00, Location/Qualiflers
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Matches:
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AF124402.1 GI:4589084
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AF124402
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ene, partial
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                  proteolysis at
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/note="Region: alpha2-macroglobulin-binding A domain"
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2 (bases 1 to 468)
2 (bases 1 to 468)
Rasmussen,M., Muller,H.P. and Bjorck,L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular
Submitted (28-JAN-1999) Cell and 221 00, Sweden
Location/Qualifiers
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Streptococcus pyogenes strain AP1 GRAB precursor, gene,
                                1 (bases 1 to 468)
Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates pacterial surface by binding alpha2-macroglobulin 99269061
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343. .468
/note="Region: cell-wall attachment"
91 c 100 g 99 t
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1 (bases 1 to 469)

Rasmussen,M., Muller,H.P. and Bjorck,L.
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Matches:
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Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin J. Biol. Chem. 274 (22), 15336-15344 (1999)
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Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin
J. Biol. Chem. 274 (22), 15336-15344 (1999)
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Streptococcus pyogenes strain KTL9 GRAB precursor, gene, partial
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                   2 (bases 1 to 469)
2 (bases 1 to 469)
Rasmussen, M., Muller, H.P. and Bjorck, L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden
Location/Qualifiers
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343. 469
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AF124401 468 bp DNA linear BCT 14-AUG-2000 Streptococcus pyogenes strain KTL3 GRAB precursor, gene, partial
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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AF096897 Drosophil
AF096896 Drosophil
AC011910 Drosophil
AC0711910 Drosophil
AE007416 Drosophil
AE003619 Drosophil
AL603646 Rhizobium
AY061146 Drosophil
MI01130 Plasdmodium
AF001155 Halobacte
                                                                                                                                                                                                                                                                                                                              AF031321 Tetrahyme AC014470 Drosophil AC006462 Drosophil AC006495 Drosophil AB416671 Streptomy AL645771 Streptomy AC067274 Homo sapi Y17920 Brosophila
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AL646065 Raistonia
AL596163 Listeria
AE003584 Drosophil
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AE000634 Helicobac
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                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AC037426
AC105899
AC092244
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AE000634
AE001548
STYPPHCM2
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AC006495
AE003721
SCO414671
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AE003619
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ALIGNMENTS

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Search completed: October 13, 2002, 04:45:47 Job time : 99.2834 secs

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US-09-847-539A-6_COPY_59_86 (1-28) x US-10-027-632-172755 (1-862)
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Sequence 172755, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: David G.
TITLE OF INVENTION: David G.
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PASS
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SECTION 172754
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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; ORGANISM: Human
US-10-027-632-172754
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Sequence 5807, Application US/10155881

GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Evaulc, Joyaid K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
TITLE OF INVENTION: WCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: WCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: WCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: WCLEIC ACID MOLECULES ASSOCIATED WITH
CURRENT APPLICATION WUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
SEQ ID NOS: 37595
LENGTH: 940
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                                                                         46 ACACAGACACTCCAGAGTCTCAGCAGTCAGACTCATTCTCTGCAGGAAARGCAGAGA 105
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1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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APPLICATION NUMBER: US/08/961,083
FILING DATE: 30-Oct-1997
CLASSIFICATION: <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u <u >cu <u <u <u <u <u <u >cu <u 
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; ORGANISM: 2ea mays
US-10-155-881-5807
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US-08-961-083-191
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SUBJECT OF THE CARDATION:

JULIA DE INVENTION:

JULIA DATE:

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Sequence 172754, Application US/10027632

Sequence 172754, Application US/10027632

Sequence 172754, Application US/10027632

SERBRAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129

CURRENT APPLICATION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR PAPLICATION NUMBER: US 60/190,676

PRIOR APPLICATION NUMBER: US 60/190,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483
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                                                             5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
                                                                                                                 120 GAGGCCGATGCCGACGCCACCGCCGCCGCGCAAGAAGATGGAGCGGCCGTGAATGCC
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US-09-847-539A-6_COPY_59_86 (1-28) x PCT-US02-27884-5555 (1-656)
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 172753, Application US/10027632
; GENERAL INFORMATION:
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Best Local Similarity:
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US-10-027-632-172753
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Sequence 4854, Application PC/TUS0227884
GENERAL INFORMATION:
APPLICANT: The Dow Chemical Company
APPLICANT: Dow Agro Sciences, LLC
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
FILE REFERENCE: DOW-07611
CURRENT APPLICATION NUMBER: PCT/US02/27884
CURRENT FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 7560
SOFTWARE: PATENTING PATE: 2002-08-30
SOFTWARE: PATENTING NOS: 7560
SEQ ID NO 4854
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Sequence 5555, Application PC/TUS0227884

Sequence 5555, Application PC/TUS0227884

GENERAL INFORMATION:
APPLICANT: The Dow Chemical Company
APPLICANT: The Dow Agro Sciences, LLC
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
FILE REPERENCE: Dow-07611
CURRENT APPLICATION NUMBER: PCT/US02/27884

CURRENT FILING DATE: 2002-08-30

NUMBER OF SEQ ID NOS: 7560

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 5555

LENGTH: 656
                                                                                                                                                  159 GCAGAAGCTCTGGCCCCTATGGCGGAGGAGGCCAATACTTTGCAAAACCACGAAACCAAG 218
                                                                                       1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
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                                                                                                                                                                                                               21 ValValLysAlaAspAsnAlaAla 28
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Best Local Similarity:
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COCATION: (1)...(546)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-23409
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81.25%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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US-10-027-632-13710
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Sequence 4262, Application US/10221279

GENERAL INFORMATION:

TITLE OF INVENTATION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-046

CURRENT APPLICATION NUMBER: US/10/221,279

CURRENT FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 12360

SEQ ID NO 4262

LENGTH: 489
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Matches:
Conservative:
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Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                            CATION: (398)
OTHER INFORMATION: n equals a,t,g, or
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44.00
61.548
38.468
34.118
NUMBER OF SEQ ID NOS: 350
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 137
LENGTH: 425
TYPE: DNA
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44.00
60.87%
43.48%
34.11%
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US-10-221-279-4262
                                                                     ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
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US-10-217-489-137
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 40/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-32
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-08
PRIOR PRICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-08
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-08
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
TITLE OF INVENTION:
FILE REFERENCE: 2041-75
CURRENT APPLICATION NOMBER: US/09/18, 995
CURRENT PILING DATE: 12041-75
FILE REFERENCE: 2041-75
CURRENT PILING DATE: 2001-07-30
FRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FESSISE OF WINGOWN VETSION 3.0
SEQ ID NO 23409
LENGTH: 546
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Matches:
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Mismatches:
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Gaps:
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US-09-918-995-37583
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US-10-217-489-137
                                       Alignment Scores:
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Pred. No.:
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Sequence 11911, Application US/09975254

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: NUMBER: US/09/975,254
CURRENT APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
SEQ ID NO 11911
LENGTH: 237
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                                                                                         US-09-847-539A-6_COPY_59_86 (1-28) x US-60-360-039-44171 (1-3435)
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CURRENT APPLICATION NUMBER: US/09/918,995
FRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEO FOR WINDOWS VEFSION 3.0
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; Sequence 37583, Application US/09918995
; GENERAL INFORMATION:
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52.38%
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ORGANISM: Homo saplens
Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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LENGTH: 370
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129 CAGGCATTAGAGCCCCAAACAGGTTTCCAAGGCCCAAGAGCAGCAGCAGTAATGATGAT 70
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                                                                                                                                                                                   Sequence 137, Application US/10217489
GENERAL INFORMATION:
APPLICANT: ROSEON et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM045C1N
CURRENT APPLICATION NUMBER: US/10/217,489
CURRENT APPLICATION NUMBER: 09/757,030
PRIOR APPLICATION NUMBER: 09/757,030
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                US-09-918-995-37603/c
; Sequence 37603, Application US/09918995
; GENREAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 1909-01-20
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FBASESQ for Windows Version 3.0
; SEQ ID NO 37603
                                                                                                                                            US-09-847-539A-6_COPY_59_86 (1-28) x US-09-918-995-37583 (1-370)
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Mismatches:
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Matches:
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29.8
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34.11%
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44.00
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; ORGANISM: Homo sapiens
US-09-918-995-37603
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Best Local Similarity:
Query Match:
                                      Percent Similarity:
Best Local Similarity:
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Sequence 4111, Application US/60360039

Sequence 4111, Application US/60360039

Sequence 4111, Application US/60360039

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Galdman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE 
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APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ. ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                           343 GTGGCCGATCAGACCGGCGCCGCGCGCGCGCGCCCAGTTCGAGGCAGT 287
                                                                                                                                                                                                                                                                                                                                    7 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp 25
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                                                                                                                                                                                                                                                                     US-09-847-539A-6_COPY_59_86 (1-28) x US-60-360-039-28506 (1-2688)
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                            Length:
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Sequence 31265, Application US/60360039
CBNERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Burkholderia cepacia
                            192
45.00
73.68%
52.63%
34.88%
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Best Local Similarity:
                                                                                               Percent Similarity:
Best Local Similarity:
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LENGTH: 2845
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   Alignment Scores:
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DB:
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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)A
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO S: 47374
                                                                                                                                                                                                                                            Sequence 262301, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-00-12
PRIOR FILING DATE: 2000-00-12
PRIOR FILING DATE: 2000-00-20
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 262301
LENGTH: 2243
1116 GATGCTATAACCAGCAGCAGGACAGCACCAACAGCAATCAGTCCGAAAGCGCCCAGCTG 1057
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Mismatches:
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; Sequence 28506, Application US/60360039
; GENERAL INFORMATION:
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US-60-360-039-28506
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Best Local Similarity:
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ORGANISM: Human
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Kovalic, David K.

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US-10-027-632-164208/C
Sequence 164208, Application US/10027632
Sequence 164208, Application US/10027632
Sequence 164208, Application US/10027632
Sequence 164208, David G
TITLE OF INVENTION: David G
TITLE OF INVENTION: POLYMorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR PRIOR APPLICATION NUMBER: US 60/185,218
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-03-28
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-08-08
FRIOR FIL
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 CCTATCAGAGTTTTAAAT 103
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                  Percent Similarity:
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Query Match:
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US-10-219-999-22677
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cac, Yongwel

APPLICANT: Cac, Yongwel

APPLICANT: Cac, Yongwel

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Stater, Steven C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS MITH IMPROVED PROPERTIES

TITLE REFERENCE: 38-10(52052)8 MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE REFERENCE: 28-10(52052)8 MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE REFERENCE: 28-10(52052)8 MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE REFERENCE: 38-10(52052)8 MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

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TITLE REFERENCE: 38-10(52052)8 MICROBIAL PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS IN PLANTS FOR PROTEINS FOR PROTEI
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APPLICANT: Stein, Joshua
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR PPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
NUMBER: OF SEQ ID NOS: 63520
SEQ ID NO 22677
LENGTH: 950
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Matches:
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US-60-360-039-27473
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63.64%
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45.00
66.67%
37.50%
34.88%
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; LOCATION: (200)...(538)
; OTHER INFORMATION:
US-10-219-999-22677
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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SEQ ID NO 164207
LENGTH: 825
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Pred. No.:
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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: HINKLe, Gregory J.
APPLICANT: HINKLe, Gregory C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT FILING NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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GENERAL INFORMATION:
APPLICANT: Wang, David
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108877.129
CURRENT APPLICATION NUMBER: US/10/027, 632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us-09-847-539A-6_COPY_59_86 (1-28) x us-60-360-039-44539 (1-1608)
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 44539
LENGTH: 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-360-039-42394
; Sequence 42394, Application US/60360039
; GENERAL INFORMATION:
                                                                                                                                                                                                   : TYPE: DNA
: ORGANISM: Rhodopseudomonas palustris
US-60-360-039-44539
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Sequence 164207, Application US/10027632
Sequence 164207, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PRILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-1-23
PRIOR APPLICATION NUMBER: US 60/186,218
PRIOR PILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEX ID NOS: 325720
SEQ ID NO 164206
LENGTH: 825
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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US-10-027-632-164207/c
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US-10-027-632-164206
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US-10-027-632-164207
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; LOCATION: (1)...(1410)
; OTHER INFORMATION:
US-10-219-999-6030
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Best Local Similarity:
Query Match:
Local Similarity:
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ORGANISM: Zea mays
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US-10-219-999-6030/c
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US-60-360-039-44539
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                      Query Match:
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Sequence 3217, Application US/10155881

GENERAL INFORMATION:

APPLICANT: Dotson, Stanton B.

APPLICANT: Lut, Jingdong

APPLICANT: Lut, Jingdong

APPLICANT: Lut, Jingdong

APPLICANT: Lut, Jingdong

TITLE OF: INVENTION: WUCLEIC AID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

TITLE OF: INVENTION: TRANSCRIPTION IN PLANTS

TITLE OF: INVENTION: TRANSCRIPTION IN PLANTS

FILE REFERENCE: 38-21(15300)J

CURRENT FILING DATE: 2002-05-22

WUMBER OF SEQ ID NOS: 37595

SEQ ID NO 3217

LENTH: 705
                                                                                                                                                                 Sequence 6, Application US/10161453
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: LIMES AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
TITLE OF INVENTION: LIMES AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
CURRENT FILLING DATE: 2002-06-03
CURRENT FILLING DATE: 2002-06-03
PRIOR FILLING DATE: 2001-06-05
PRIOR FILLING DATE: 2001-06-05
PRIOR FILLING DATE: 2001-01-00
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-02-15
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LEASTH: 128978
                                                                            Db 63278 GCTGAACAAACTGACTCCTTAGAACCAGCTGAGGCACAGGTCTTCAAAGGG 63328
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                  US-09-847-539A-6_COPY_59_86 (1-28) x PCT-US02-25766-4301 (1-128978)
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Matches:
Conservative:
Mismatches:
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CTHER INFORMATION: unsure at all n locations
US-10-155-881-3217
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Best Local Similarity:
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Percent Similarity:

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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6030, Application US/10219999
GENERAL INFORMATION:
APPLICANY: Gao, Yongwel
APPLICANY: Edgerton, Michael D
APPLICANY: Hinkle, Gregory J.
APPLICANY: Liu, Jingdong
APPLICANY: Liu, Jingdong
APPLICANY: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2001-08-15
FRIOR APPLICATION NUMBER: US 60/312,109
FRIOR APPLICATION NUMBER: US 60/312,544
FRIOR FILING DATE: 2010-08-15
FRIOR FILING DATE: 2010-08-15
FRIOR FILING DATE: 2010-08-15
FRIOR FILING DATE: 2010-08-15
FRIOR FILING DATE: 2010-08-15
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                                                                                                                                                                                                                                                US-09-847-539A-6_COPY_59_86 (1-28) x US-10-155-881-3217 (1-705)
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Matches:
Conservative:
Mismatches:
Indels:
      Mismatches:
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APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1254 GAGGCTGACAACGCCGCC 1237
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38.46%
35.66%
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RESULT 11

PCT-USO1-17423-6

Sequence 6, Application PC/TUSO117423

GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

TILLE OF INVENTION: LIMBA SA MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REFERENCE: EX02-064-PC

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US 60/296,076

PRIOR PILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-0-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Version 3.1

SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GENE LOGIC, INC.
APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNGER, William E
APPLICANT: SASAI, Hitoshi
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, Iwao
APPLICANT: WAGA, Iwao
APPLICANT: True OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
CURRENT PRILING DATE: 2002-08-14
PRIOR PLIING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
  Db 21239 GCTGAACAAACTGACTCCTTAGAACCAGCTGAGGCACAGGTCTTCAAAGCG 21189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 63278 GCTGAACAAACTGACTCCTTAGAACCAGCTGAGGCACAGGTCTTCAAAGCG 63328
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
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58.82%
36.43%
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4301
LENGTH: 128978
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Query Match:
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PCT-US02-25766-4301
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US-10-135-696-3/C

S Sequence 3. Application US/10135696

S GENERAL INFORMATION:

APPLICANT: YAN, Chunbua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01178DIV

CURRENT APPLICATION NUMBER: US/10/135,696

CURRENT FILING DATE: 2002-05-01

PRIOR FILING DATE: 2001-03-22

PRIOR FILING DATE: 2001-10-17

PRIOR FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 4

SOFTRARE: FESTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Indels:
                                                                                                                                                                APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR PILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 636
LENGTH: 6965
                                                                                                     US-09-440-302B-636; Sequence 636, Application US/09440302B; GENERAL INFORMATION:
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55.00%
36.43%
                         2235 CTGGCCGAGCATAAC 2221
22 ValLysAlaAspAsn 26
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
GORGANISM: Homo Sapiens
US-09-440-302B-636
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Best Local Similarity:
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Best Local Similarity:
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LENGTH: 59065
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Gaps:

Tue Oct 15 08:27:57 2002

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US-60-360-039-40814/c
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APPLICANT: Slater, Steven C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10/52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 40312
LENGTH: 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3446, Application US/10179131
GENERAL INFORMATION:
APPLICANT: HARE, ROBERTA S.
APPLICANT: SHAW, KAREN J.
APPLICANT: SHAW, KAREN J.
APPLICANT: SHAW, KARCO
APPLICANT: CESLER, MARCO
APPLICANT: CESLER, MARCO
APPLICANT: CESLER, MARCO
APPLICANT: CENC, OIANDONG
APPLICANT: CRENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: CANDIDA ALBICANS
FILE REPERENCE: 2976-4031
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 10194
SEQ ID NO 3446
LENGTH: 6093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-847-539A-6_COPY_59_86 (1-28) x US-60-360-039-40312 (1-1449)
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                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                          TYPE: DNA; ORGANISM: Bacillus thuringiensis US-60-360-039-40312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.00
70.83%
54.17%
37.21%
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; ORGANISM: Candida albicans
US-10-179-131-3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1285 ATTAAGGCA 1293
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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RESULT 8

US-60-360-039-27525/c

Sequence 27525, Application US/60360039

GENERAL INFORMATION:
APPLICANT: Cao, Yongweit

APPLICANT: Cao, Yanfeng

APPLICANT: Cao, Alanfeng

APPLICANT: Stater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: BYRESSION OF MICROBIAL PROPERTIES

FILE REFERENCE: 38-10(52052)A

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH: 4885
                                      APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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Mismatches:
Indels:
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Matches:
Conservative:
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Indels:
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Matches:
Sequence 40814, Application US/60360039 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  CORGANISM: Bacillus halodurans
US-60-360-039-40814
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47,00
63,64%
45,45%
36,43%
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; ORGANISM: Neurospora crassa
US-60-360-039-27525
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47.00
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Query Match:
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Best Local Similarity:
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us-09-847-539a-6_copy_59_86.rnpn

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TYPE: DNA
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Covalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
                                                                                             3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDMA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFRENCE: 38-10(52726)C;
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
PRIOR PILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NOS: 63520
                                                         US-09-847-539A-6_COPY_59_86 (1-28) x US-10-219-999-12394 (1-1679)
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Matches:
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                                                                                                                                                                                                  1195 GAGGCTGACAACGCCCC 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (3)..(1427)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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US-10-155-881-3337/c
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Query Match:
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Coo, Yongwei
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 30630
LENGTH: 3257
                                                                                                                                                                                                                                                                                                                                                                                                                  1915 TCAGATGCTATTCAAGAGCTTTCCGATCAAATCGAGCAACTTCAAAAGGAAAAGGGAAGA 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                           3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-847-539A-6_COPY_59_86 (1-28) x US-60-360-039-30630 (1-3257)
                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6_COPY_59_86 (1-28) x US-10-155-881-3337 (1-1783)
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Matches:
Conservative:
Mismatches:
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Mismatches:
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Matches:
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-60-360-039-30630
CURRENT FILING DATE: 2002-05-22 UNDBER OF SEQ ID NOS: 37595 SEQ ID NO 3337 LENGTH: 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1294 GAGGCTGACAACGCGCC 1277
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Best Local Similarity:
Query Match:
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US-60-360-039-30630
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                                                                                                           ; ORGANISM: Zea I
US-10-155-881-3337
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Sequence 4301, Ap Sequence 6, Appl1 Sequence 3217, Ap Sequence 6030, Ap Sequence 44539, A Sequence 14239, A Sequence 164206, Sequence 164206,

Sequence Sequence Sequence Sequence

Sequence 22677, A
Sequence 22677, A
Sequence 262301,
Sequence 24171, A
Sequence 41171, A
Sequence 1171, A
Sequence 1373, A
Sequence 137603, A
Sequence 137, App
Sequence 137, App
Sequence 1275, App
Sequence 1275, App
Sequence 1275, App
Sequence 12755, App
Sequence 172753, Sequence 172753, Sequence 172753, Sequence 172753, Sequence 172755, Sequen

Perfect score:

Run on:

Sedneuce:

Scoring table:

Minimum DB Maximum DB

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gao, Yongwel
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: How to all the gregory J.
APPLICANT: Hinkle, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITILE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 36-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-15
SEQ ID NOS: 63520
SEQ ID NOS: 63520
PCT-USO1-17423-6
US-10502-25766-4301
US-10-155-881-3217
US-10-219-999-6030
US-60-360-039-44539
US-60-360-039-42394
US-10-027-632-164206
US-10-027-632-164207
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US-10-027-632-164207
US-10-027-632-164207
US-00-999-22677
US-00-999-37583
US-09-918-995-37583
US-09-918-995-37583
US-10-217-489-137
US-10-027-632-172754
US-10-027-632-172754
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US-10-027-632-172754
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US-10-155-881-17609
US-10-1219-999-206942
US-10-1219-999-206942
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NAME/KEY: CDS
LOCATION: (2)..(1351)
OTHER INFORMATION:
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-Q=/Cgn2_1/USPTQ_spool/USO9847539/runat_10102002_092550_3509/app_query.fasta_1.526
-D=-Pending_Patents_N_N=w-vEYM=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE-LCCAL -OTTEMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-USO984539_eCGN 11_1186_erunat_10102002_092550_3509 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -KGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12394, A Sequence 8111, Ap Sequence 3337, Ap Sequence 30630, A Sequence 40312, A Sequence 27525, A Sequence 636, App Sequence 636, App Sequence 37, Appli
                                                                                                                                  October 13, 2002, 02:41:57; Search time 65.2834 Seconds (without alignments) 1453.830 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptcdata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptcdata/1/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

8: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
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US-10-219-999-8111
US-60-360-039-30337
US-60-360-039-40312
US-10-179-131-3446
US-60-360-039-40314
US-60-360-039-40814
US-60-360-039-27525
US-09-440-3028-636
US-10-135-696-3
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    129
1 SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                             2385415 seqs, 1694839300 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                  US-09-847-539A-6_COPY_59_86
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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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length: 2000000000
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Match Length
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1696
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337.2
336.2
336.2
336.4
36.4
36.4
44.5
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Sequence

Matches: Conservative: Mismatches:

12.8 50.00 73.08% 42.31%

Percent Similarity: Best Local Similarity:

Alignment Scores:

Score

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Result

Database

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US-09-595-129A-545/C
Sequence 545, Application US/09595329A
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLA!
APPLICANT: VYACHESLAV, Brover
ITILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
FILE REFERENCE: 2750-0948P
CURRENT APPLICATION NUMBER: US/09/595,329A
CURRENT FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3309
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValLys 23
: NAME/KEY: misc_feature
: LOCATION: (1)..(1230)
: OTHER INFORMATION: any n = a, g, c, t, unknown, or other
: NAME/KEY: misc_feature
: LOCATION: (1)..(1230)
: OTHER INFORMATION: 40182 : FINISHED (Clone Number : FINISHED)
US-09-565-309A-62025
                                                                                                                                                                                                                                                                               US-09-847-539A-6_COPY_59_86 (1-28) x US-09-565-309A-62025 (1-1230)
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LOCATION: (1)..(1230)
OTHER INFORMATION: Ceres Seq. ID no. 1013068
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: n is a, c, t, g, unknown, or other
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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50.00%
40.31%
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Best Local Similarity:
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458 GCGGAT 453
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LENGTH: 1230
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Sequence 67147, Application US/09565309A
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI
APPLICANT: BROVEN, Vyaccheslav
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TILLE COFINYENTION: THEREBY
FILE REFERENCE: 2750-08539
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
SEQ ID NO 67147
LENGTH: 999
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GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-0853P
FILE REPERENCE: 2750-0853P
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
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                                                                                     4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
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                                            US-09-847-539A-6_COPY_59_86 (1-28) x US-09-708-427-29368 (1-984)
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; OTHER INFORMATION: 40182 : CDS (Clone Number : CDS)
US-09-565-309A-67147
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Matches:
Conservative:
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ORGANISM: Arabidopsis thaliana
FEATURE:
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ORGANISM: Arabidopsis thaliana
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LOCATION: (1)..(999)
OTHER INFORMATION: any n = a,
NAME/KEY: misc_feature
LOCATION: (1)..(999)
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52.00
72.73%
50.00%
40.31%
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Best Local Similarity:
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382 GCGGAT 377
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NS-09-565-309A-67148/C
Sequence 67148, Application US/09565309A
Sequence 67148, Application US/09565309A
Sequence 67148, Application US/09565309A
Sequence 67148, Application US/09565309A
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT FILING DATE: 2750-09557309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
LENGTH: 939
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US-09-70868/C
US-09-70868/C
Sequence 29368, Application US/09708427
SEQUENCE 29368, Application US/09708427
GENERAL INFORMATION:
TILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNMER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 29368
LENGTH: 984
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LOCATION: (1)..(939)
COTHER INFORMATION: any n = a, g, c, t, unknown, or o
NAME/KEY: misc_feature
LOCATION: (1)..(939)
COTHER INFORMATION: 40182 : CDS (Clone Number : CDS)
US-09-565-309A-67148
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Mismatches:
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CCATION: 1.984
CTHER INFORMATION: Ceres Seq. ID 1825505
US-09-708-427-29368
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LOCATION: 1..984
OTHER INFORMATION: any
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Best Local Similarity:
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Best Local Similarity:
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GENERAL INFORMATION:
Sequence 32824, Application US/09565309A
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLa1
APPLICANT: ALEXANDROV, NICKOLa1
TAPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: THERBY
TITLE OF INVENTION: THERBY
FILE REFERENCE: 2750-0963P
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
SEQ ID NO 33824
LENGTH: 641
                      TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(594)
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc_feature
LOCATION: (1)..(544)
OTHER INFORMATION: 40182:107311 (Clone Number:Unique Sequence Identifier)
US-09-565-309A-32821
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VOHER INFORMATION: any n = a, g, c, t, unknown, or other

NAME.KEY: misc_feature

LOCATION: (1)...(641)

OTHER INFORMATION: 40182:957281 (Clone Number:Unique Sequence Identifier)
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Conservative:
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Mismatches:
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Matches:
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ORGANISM: Arabidopsis thallana
FEATURE:
NAME/KEY: misc_feature
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50.00%
40.31%
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Query Match:
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      LENGTH: 594
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERBNCE: 2750-0853P
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
APPLICANT: HEATH, JOE D.
APPLICANT: BROOKS, JACQUELINE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF PSEUDOMONAS AERUGINOSA
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 860
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GlualaLeuAlaAsp-----GluThrAspAlaLeuGlnSerGluGluAla 19
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                                                                                                                                                                                                                                                                                             COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPOPPY disk
COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: CERRONE, MICHAEL C.
RECISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0011-1 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-055
INFORMATION FOR SEQ ID NO: 513:
SEQUENCE CHARACTERISTICS:
LENGTH: 8830 base pairs
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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, NICKOlai
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MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
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52.50
71.43%
50.00%
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STRANDEDNESS: double
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: CALIFORNIA
RY: USA
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Best Local Similarity:
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Pred. No.:
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60/094,190

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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8951
LENGTH: 1239
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
TITLE OF INVENTION: Sequences and Uses Thereof
FILE REFERENCE: CLO00284
CURRENT APPLICATION NUMBER: US/09/528,237A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: FastSEQ for Windows Version 4.0
EDUCTH: 32275
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Matches:
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Mismatches:
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Indels:
  SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 1811, Application US/09528237A
; GENERAL INFORMATION:
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; Sequence 8951, Application US/09252991A
; GENERAL INFORMATION:
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                                                                                    ORGANISM: Drosophila
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Best Local Similarity:
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Best Local Similarity:
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                   SEQ ID NO 17589
LENGTH: 7206
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                                                                  TYPE: DNA
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Sequence 8732, Application US/09252991A

Sequence 8732, Application US/09252991A

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGIN SEQ ID NOS: 33142

LENGIN SEQ ID NOS: 33142
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US-60-082-302-513/c
; Sequence 513, Application US/60082302
; GENERAL INFORMATION:
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-8951
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; SEQ ID NO 13896
; LENGTH: 6398
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-681-13896
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US-60-173-464-14400
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LENGTH: 7203
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Pred. No.:
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Sequence 13896, Application US/60191681
Sequence 13896, Application US/60191681
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF:
FILE REFERENCE: c1000390
TITLE OF INVENTION: US/60/191,681
CURRENT APPLICATION NUMBER: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                              US-60-191-637-17580/c
Sequence 17580, Application US/60191637
Sequence 17580, Application US/60191637
GENERAL INFORMATION:
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000392
CURRENT APPLICATION UNMERE: US/60/191,637
CURRENT FILICATION UNMERE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SEQ ID NO 17580
LENGTH: 6398
                                                                                                                                                                                                                                                                        2298 GAGGAGGAAGCTGACGAGGAGGACGCCCCCGAGGAGAGGATGCCGCAGCGCTGCCGC 2239
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                               ; ORGANISM: DROSOPHILA US-09-614-150-17530
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                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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 LENGTH: 6398
               TYPE: DNA
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Sequence 14400, Application US/60173464
GENERAL INFORMATION:
APPLICANT: Li, Peter W.
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLO00173
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: PASELSEQ for Windows Version 4.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: L1, PETCH W. D.
17TILE OF INVENTION: ISOLAYED DROSOPHILA PROTEINS, NUCLEIC
17TILE OF INVENTION: THEREOF
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
DB:
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Sequence 13897, Application US/60191681
GENERAL INFORMATION:
TAPLICAMT: Li, Peter, W.D.
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND TITLE OF INVENTION: USES THEREOF.
FILE REFERENCE: c1000390
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANI: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLO00728

CURRENT APPLICATION NUMBER: 60/15/,832

PRIOR FILING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 2000-02-44

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FASTSEQ for Windows Version 4.0
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Mismatches:
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Matches:
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LENGTH: 3349
TYPE.
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Sequence 17530, Application US/09614150

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig
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66.67%
50.00%
41.86%
58
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                                                                           1062 GATGCTGCGGCG 1051
                                   25 AspAsnAlaAla 28
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US-60-191-681-13897
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Best Local Similarity:
Query Match:
                                                                                                                     RESULT 24
US-60-191-681-13897/c
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US-60-191-637-17581/C
Sequence 17581, Application US/60191637
Sequence 17581, Application US/60191637
GENERAL INFORMATION:
TATLE OF INVENTION: UCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNBER: US/60/191,637
CURRENT APPLICATION UNBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1122 GAGGAGGAAGCTGACGAGGACGAGCCGAGGCAGGAGGCAGCGGCTGCCGCC 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GlualaLeualaaspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR PLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 2000-01-12
PRIOR PRICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-23
NUMBER OF SED ID NOS: 43008
SEQ ID NO 17531
LENGTH: 3349
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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Length:

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954 GATGCTGCGGCG 943
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   ; LENGTH: 3046
; TYPE: DNA
; ORGANISM: Drosophila
US-60-173-464-14401
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US-60-167-217-17590
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Best Local Similarity:
Query Match:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-614-150-17531/c
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Sequence 143, Application US/60145134

Sequence 143, Application US/60145134

Sequence 143, Application US/60145134

Sequence 143, Application

Sequence 143, Application

THERORMATION:

APPLICANT: BONAZZI, VIVIEN

TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE

TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE

CURRENT APPLICATION NUMBER: US/60/145,134

CURRENT PILING DATE: 1999-07-22

NUMBER OF SEQ ID NOS: 342

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 143

LENGTH: 1785
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US-60-173-464-14401/C
US-60-173-464-14401/C
Sequence 14401, Application US/60173464
Sequence 14401, Application US/60173464
TITLE OF INVENTION: SOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00173
CURRENT APPLICANTON NUMBER: US/60/173,464
CURRENT APPLICANTON NUMBER: US/60/173,464
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 14401
                                                                                                                                                                                                                                                  5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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Mismatches:
Indels:
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Matches:
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CORGANISM: Drosophila
US-60-145-134-143
                                ; ORGANISM: Drosophila
US-60-142-845-289
                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Pred. No.:
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LENGTH: 1783
                 TYPE: DNA ORGANISM: [
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US-560-167-217-17590/c
Sequence 17590, Application US/60167217
Sequence 17590, Application US/60167217
GENERAL INFORMATION:
APPLICANT: Li, Peter W. D.
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: THEROF
FILE REPERENCE: CLO00152
CURRENT PALLICATION NUMBER: US/60/167,217
CURRENT PALLICATION NUMBER: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 17590
LENGTH: 3049
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
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Mismatches:
Indels:
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Conservative:
Mismatches:
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Matches:
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COUNTRY:
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GENERAL INFORMATION:
APPLICANT: DOUGLAS Smith
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 495
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS NUMBER OF SEQUENCES: 10031
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Matches:
Conservative:
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Indels:
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
FILING DATE:
PRIOR PAPLICATION NUMBER:
PRIOR PAPLICATION NUMBER:
FILING DATE:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617)742-4214
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STREET: 60 State Street, Suite 510
                                                      ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street CITY: Boston STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO
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                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                      02109-1875
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Query Match:
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                                                                                                                                   USA
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Sequence 289, Application US/60142845

GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ADDED TO THEREOF
CURRENT APPLICATION NUMBER: US/60/142,845
CURRENT FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 704
SEQ ID NO 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LeuGlualaLeualaaspGlnThraspalaLeuGlnSerGluGlualaalaValValIys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6_COPY_59_86 (1-28) x US-08-621-425-49 (1-3497)
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                    SOFTWARE: tar

CURRENT APPLICATION DATA:

PELING DATE: 25-MARCH-1996

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08487,032

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

RAME: MANDER MANDER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION PROMATION:

TELECOMMUNICATION PROMATION                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

REDIUM TYPE: 8mm cartridge tape

COMPUTER: SPARC station LX

OPERATING SYSTEM: sunOS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
57.00
69.57
52.17
44.19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
Massachusetts
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Best Local Similarity:
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4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
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US-08-993-002A-4235
; Sequence 4215, Application US/08993002A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
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Mismatches:
Indels:
Gaps:
                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,742
FILING DATE: 01-APRIL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,742
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/736,791
FILING DATE: 20-CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/739,150
FILING DATE: 20-CT-1996
PRIOR APPLICATION NUMBER: US 08/739,150
FILING DATE: 20-CT-1996
ATTORNEY, AGENT INFORMATION:
NAME: MANDARGOURAS, AMY E.
REFERENCE, DOCKET NUMBER: GTN-001CP8
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
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Matches:
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ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUPOLOGY: CITCULAR MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1...1239
                                                                                                                          CURRENT APPLICATION DATA:
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STRANDEDNESS: double
                                                           OPERATING SYSTEM:
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205 TGGGATAAC 213
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Query Match:
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Sequence 250, Application US/08759739
Sequence 250, Application US/08759739
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH ET AL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI VACCINE COMPOSITIONS THERE
COMPRESSONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                   PETLING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/739,150
FILING DATE: 28-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/759,739
FILING DATE: 06-DEC-1996
FILING DATE: 06-DEC-1996
FILING DATE: 14-JULY-1997
APPLICATION NUMBER: US 08/891,928
FILING DATE: 14-JULY-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANGRAGOULAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
INFORMATION FOR SEQ 1D NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: NOA (GENOMIC)
HANDLECTLE TYPE: NOA (GENOMIC)
ANDLECTLE TYPE: NOA (GENOMIC)
ANDLECTLE TYPE: NOA (GENOMIC)
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                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19575
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1...1239
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STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
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Best Local Similarity:
Query Match:
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                                                                                         SOFTWARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4234, Application US/08993002A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI
FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-847-539A-6_COPY_59_86 (1-28) x US-08-759-739-92 (1-666)
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
RELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
LENGTH: 666 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-010-1995
PRIOR APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-00'-1995
PRIOR APPLICATION NUMBER: US 08/561,469
FILING DATE: 01-APRIL-1996
FILING DATE: 01-APRIL-1996
FILING DATE: 06-010-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,742
FILING DATE: 25-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/736,791
FILING DATE: 25-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/736,791
FILING DATE: 28-0CT-1996
ATTORREY AGENT INFORMATION:
AMARE: MANGINER AND FAREST AND FAILOR DATE: 28-0CT-1996
ATTORREY AGENT INFORMATION:
APPLICATION NUMBER: US/08/759,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.00
69.57%
52.17%
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LOCATION: 1...666
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Best Local Similarity:
Query Match:
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US-08-993-002A-4234
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229 ATACAAGCCTACAGGAGCAAATTGACGCTTTAGATTCTCAAGAAAAGTCGTTAGCAAA 288
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
TITLE OF INVENTION: VACCINE COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE 6 COCKFIELD
STREET: 28 State Street
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12
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Mismatches:
Indels:
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Matches:
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
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                                                                                                                                                                                                                                           FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-(TELECOMMUNICATION INFORMATION:
TELEPRAX: (61)727-7400
INFORMATION FOR SEQ ID NO: 4234:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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57.00
69.57%
52.17%
44.19%
: Massachusetts
RY: USA
02109-1875
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COUNTRY: USA
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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 STATE: M. COUNTRY:
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CURRENT APPLICATION DATA:
        COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSE: LABITUR & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-847-539A-6_COPY_59_86 (1-28) x US-08-759-739-43 (1-576)
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Matches:
Conservative:
Mismatches:
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PAPLICATION NUMBER: US 08/660,742

FILING DATE: 06-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 25-007-1996

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/739,150

FILING DATE: 28-007-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-001CPB

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 576 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,405
FILING DATE: 01-APRIL-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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57.00
69.57%
52.17%
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LOCATION: 1...576
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02109-1875
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Best Local Similarity:
Query Match:
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US-08-759-739-43
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Sequence 92, Application US/08759739
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TILLE OF INVENTION: RELATING TO HELICOBACTER PYLORI VACCINE COMPOSITIONS THERE
NUMBER OF SEQUENCES: 608
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVylLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6_COPY_59_86 (1-28) x US-08-993-002A-4232 (1-576)
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Mismatches:
Indels:
                                                                                                                                                                                                                              NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELEPONNINICATION INPORMATION:
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4232:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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57.00
69.57%
52.17%
44.19%
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OPERATING SYSTEM:
SOFTWARE:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE
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                                                                                                                                                                                            FILING DATE:
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MEDIUM TYPE: Floppy disk
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Sequence 282, Application US/08561469A

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 994
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-847-539A-6_COPY_59_86 (1-28) x US-08-487-032A-282 (1-576)
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS NUMBER OF SOUTBNCES: 880
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston
                                                                                                                                                                                                          STATE: Mac.
CUNTRY: USA
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: MANDER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/CDCKET NUMBER: GIN-001
TELECHONE: (617)227-7400
TELECHONE: (617)227-7401
TELECHONE: (617)227-5941
STELERA: (617)227-5941
SOURCE CHARACTERISTICS:
LENGTH: 3/6 base pairs
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"NUCLE CALL ADDI
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Mismatches:
Indels:
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Matches:
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STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity:
Query Match:
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Sequence 43, Application US/08759739
GENERAL INFORMATION:
APPLICANT: DOUGLAS SHITH ET AL
APPLICANT: DOUGLAS SHITH ET AL
ATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI VACCINE COMPOSITIONS THERE NUMBER OF SEQUENCES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1874
COUNTY: USA
ZIP: CLORABBBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-847-539A-6_COPY_59_86 (1-28) x US-08-561-469A-282 (1-576)
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,469A
FILING DATE: 17 NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-740
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: NOULDER CALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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APPLICATION NUMBER: US/08/759,739
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APPLICATION NUMBER: US 08/487,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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52.17%
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ORIGINAL SOURCE:
ORGANISM: Heli
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TOPOLOGY: cir
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Pred. No.:
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1 SerAspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
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US-09-847-5394-13
US-09-847-5394-13
Sequence 13, Application US/09847539A
GENERAL INFORMATION:
APPLICANT: RASSMUSSEN, Magnus
APPLICANT: RASSMUSSEN, Magnus
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084-415US / N.75312B
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 777
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APPLICANT: Rassmussen, Magnus
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084.415018 / N.75312B
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 764
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Conservative:
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18-09-147-539A-15
Sequence 15, Application US/09847539A
; GENERAL INFORMATION:
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CORGANISM: Streptococcus pyogenes
US-09-847-539a-27
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ORGANISM: Streptococcus pyogenes
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APPLICANT: Rassmussen, Magnus
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
FILLE REFERENCE: 2709.2004001
FILLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILLIG DATE: 2000-01-27
PRIOR PAPLICATION NUMBER: US/09/489,039A
PRIOR FILLIG DATE: 1909-01-29
PRIOR FILLIG DATE: 1909-01-29
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Sequence 282, Application US/08487032A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-847-539A-6_COPY_59_86 (1-28) x US-09-489-039A-318 (1-828)
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FITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN FILE REFERENCE: 100064.4150S / N.75312B CURRENT APPLICATION NUMBER: US/09/847,539A CURRENT FILLING DATE: 2001-05-01 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 15 LENGTH: 853
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US-09-847-539A-15
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US-09-489-039A-318
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SEQ ID NO 318
LENGTH: 828
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Best Local Similarity:
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Query Match:
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1443, App
17590, A
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17581, A
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1811, Ap
8732, App
513, App
52851, A
62025, A
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26605, A
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Sequence 14, Application US/09847539A

GENERAL INPORMATION:

APPLICANT: Bassmussen, Magnus

TITLE OF INVENTION: STREPTCCCCAL ALPHA ZM BINDING PROTEIN

FILE REFERENCE: 100084.415US / N.75312B

CURRENT APPLICATION NUMBER: US/09/847,539A

CURRENT FILING DATE: 2001-05-01

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

LENGTH: 469
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US-60-145-134-143

US-60-147-1460-14401

US-60-111-637-17531

US-60-191-631-13897

US-60-191-631-13896

US-60-191-631-13896

US-60-191-64-14400

US-60-191-64-14400

US-60-191-681-13896

US-60-187-464-14400

US-60-187-464-14400

US-60-187-464-14400

US-60-187-464-14400

US-60-187-464-14400

US-60-187-464-14400

US-09-555-309A-57148

US-09-555-309A-67148

US-09-555-309A-67148

US-09-555-309A-67148

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US-09-555-309A-52256

US-09-555-309A-52256
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Conservative:
Mismatches:
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US-60-171-627-1946
US-60-173-464-26803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Streptococcus pyogenes
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129.00
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Best Local Similarity:
Query Match:
US-09-847-539A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bjorck, Lars H
APPLICANT: Rassmussen, Magnus
APPLICANT: Rassmussen, Magnus
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REPERENCE: 100084.415US / N.75312B
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT APPLICATION NUMBER: US/09/847,539A
NUMBER OF SEQ ID NOS: 30
SCFTWARE: Patentin Ver: 2.1
SEQ ID NO.
APPLICANT: Bjorck, Lars H
APPLICANT: Rassmussen, Magnus
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084.4150S / N.75312B
CURRENT APPLICATION NUMBER: 05/09/847,539A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 16
LENGTH: 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 GTTGTTAAAGCGGATAACGCTGCT 291
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                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptococcus pyogenes US-09-847-539A-12
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October 13, 2002, 04:57:28 ; Search time 558.053 Seconds (without alignments) 1085.518 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Perfect score:
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                                                                                                                                                                                                                                                                              Searched:
                                                                                  Run on:
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Pending_Patents_NA_Main:*

Database: | G9n2_6/ptodata/2/pna_VPCTUS_COMB.seq:*
| G9n2_6/ptodata/2/pna_VDSO_COMB.seq:*
| G9n2_6/ptodata/2/pna_VDSO_COMB.seq:*
| G9n2_6/ptodata/2/pna_VDSO_COMB.seq:*
| G9n2_6/ptodata/2/pna_VDSOB_COMB.seq:*
| G9n2_6/pt
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29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq: 30: /cgn2_6/ptodata/2/pna/US097B_COMB.seq: 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq: 32: /cgn2_6/ptodata/2/pna/US098A_COMB.seq: 33: /cgn2_6/ptodata/2/pna/US099B_COMB.seq: 34: /cgn2_6/ptodata/2/pna/US099B_COMB.seq: 35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq: 36: /cgn2_6/ptodata/2/pna/US099B_COMB.seq: 36: /cgn2_6/ptodata/2/pna/US099B_COMB.seq: 36: /cgn2_6/ptodata/2/pna/US6001_COMB.seq: 40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq: 40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq: 40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq: 40: /cgn2_6/ptodata/2/pna/US6002_COMB.seq: 60: /cgn2_6/ptodata/2/pna/US6002_COMB.seq: 60: /cgn2_6/ptodata/2/pna/US6012_COMB.seq: 60: /cgn2_6/ptodata/2/pna
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	t Query Match Length DB	DB	ΙD	Description
	129	100.0		32	IIS-09-847-539A-14	Sequence 14. Apr
8	129	100.0	504	3.5	US-09-847-539A-16	Sequence 16, Ap
m	129	100.0		32	US-09-847-539A-12	12,
4	129	100.0		32	US-09-847-539A-27	Sequence 27, Apr
ß	129	100.0		32	US-09-847-539A-13	13,
9	129	100.0		32	US-09-847-539A-15	Sequence 15, Api
7	58	45.0		18	US-09-489-039A-318	Sequence 318, A
œ	57	44.2	576	8	US-08-487-032A-282	Sequence 282, Ap
6	57	44.2		Ф	US-08-561-469A-282	Sequence 282, Ap
10	57	44.2	576	11	US-08-759-739-43	Sequence 43, Ap
11	57	44.2	576	13	US-08-993-002A-4232,	Sequence 4232,
12	57	44.2	999	11	US-08-759-739-92	Sequence 92, App
13	57	44.2	999	13	US-08-993-002A-4234	Sequence 4234,
14	57	44.2	1239	П	PCT-US97-19575-51	Sequence 51, App.
15	57	44.2	1239	11	US-08-759-739-250	Sequence 250, Ap
16	57	44.2	1239	13	US-08-993-002A-4235	Sequence 4235, 7

Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply Apply

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Db 1594 GAGCAGAAACTTCAAGGACAAAGGATGCTTCGAAAAGCACCAG 1653

Qy 107 ValValGinSerAspAsnAlaalaSerAspAlaTrpGluLysAlaAlaThrProIleAla 126

ii:

Db 1654 ATCACTGCACAGAACAAGACCTGGAGGCTGCTCCAAGCTGACAGGTGCC 1713

Qy 127 LeuAspValLysLysThrLysAspThrLys 136

Db 1714 AAGCTGTCAAAAGAACAAGTGCCAAG 1743

Search completed: October 13, 2002, 03:34:51

Job time: 82.8663 secs
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linear
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-899-595-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                          STREET: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALTERN.
                                                                                       APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1714 AAGCTGTCAAAAGAACTAGAAGATGCCAAG 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILLIG DATE:
ATTORNEY/AGET INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REBERNEMCE/DOCKET NUMBER: UW97-001
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4378 base pairs
TYPE: nucleic acid
cmp.Numbnugger: Adminib
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
FILING DATE:
King, Mary-Claire
                                   Lee, Ming
Morrow, Jan E.
Welcsh, Piri L.
                   Eric D.
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62.00
40.00%
22.22%
7.98%
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ADDRESSEE: SCIENCE &
STREET: 75 DENISE DRI
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Best Local Similarity:
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                                   APPLICANT:
APPLICANT:
APPLICANT:
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1474 GATAAAACAAGGTGGAAAAATCTGAGGCCAAAGCTACAGAGCTGGAAAAAAGTTGGAT 1533
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                                                                         APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4399
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                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION NUMBER: JP 8-242701
FILING DATE: 36-Aug-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-AAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION NUMBER: 29,768
TELECOMMUNICATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Sequence 2, Application US/08899595
Patent No. 6111072
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)672-5300
(202)672-5399
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 4399 base palrs
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40.00%
22.22%
7.98%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2463 GTTGTTCAAGCACAAATTGATCAAGCACCTTTAAATCCTGATACAACAAATGAAGAAGTA 2522
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                                                      COMPUTER READABLE FURM.
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/678,614
FILING DATE: 10-JUL-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/POCKET NUMBER: 600-1-139
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 1:
TELECOMMUNICATION OF 1:
SEQUENCE CHARACTERISTICS:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus
STRAIN: RUSA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Sequence 3, Application US/09080897
; Patent No. 5985574
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: King, Mary-Claire APPLICANT: Lynch, Eric D.
                                                                                                                                                                                                                                                                                                                                                LENGTH: 4248 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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62.00
41.56%
23.38%
7.98%
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1497..3500
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154..1410
             New Jersey
USA
Hackensack
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Best Local Similarity:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-080-897-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-678-614-1
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DB:
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1474 GATAAAACAAGGTGGAAAAATCTGAGGCCAAAGCTACAGAGCTGGAAAAAAGTTGGAT 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1594 GAGCAGAAACTICAGGATCTTCAAGGAGAAAAGGATGCCTTGGATTCTGAAAAGCAGCAG 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1654 ATCACTGCACAGAAACAAGACCTGGAGGCAGAGGTGTCCAAGCTGACAGGAGAGGTTGCC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGlu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 ValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAla 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 AspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 AspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAla
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20
16
54
0
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentul Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-847-539A-6 (1-159) x US-09-080-897-3 (1-4378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STARE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 LeuAspValLysLysThrLysAspThrLys 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHEAD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-434
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4378 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-323-735-3
; Sequence 3, Application US/09323735
; Patent No. 6197932
; GENERAL INFORMATION:
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62.00
40.00%
22.22%
7.98%
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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ZIP: 22040-0747

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                               US-09-847-539A-6 (1-159) x US-08-770-301A-4 (1-3252)
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Sequence 4, Application US/09175581

Sequence 4, Application US/09175581

GENERAL INFORMATION:

APPLICANT: IKEDA, JUN

APPLICANT: KANEDA, SUMIKO

APPLICANT: YANAGI, HIDEKI

APPLICANT: YANAGI, HIDEKI

APPLICANT: YURA, TAKASHI

TITLE OF INVENTION: NOVEL STRESS PROTEINS
                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                   Gaps:
TELEFAX: (703)-205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                             26.6
62.00
38.83
21.36
7.98%
                                                                                                                                                                         IDENTIFICATION METHOD:
                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity:
                                                                                                                                                         NAME/KEY: CDS
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Sequence 1, Application US/08678614
Patent No. 6013507
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF NUMBER OF SEQUENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 2
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2018 GAGAGCCTGCTGAGGGGAGCAAGGATGAGCCTGCAGAACAGGGGGAACTCAAGGAGGAA 2077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 :::::::::||| ::: 2138 GCCGTGAGGAGAAACATGAGAAAAGAAAGTGGGGACAAGTCTGAGGCCCAGAAG 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 LysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AspSerProIleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeuLeu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLyS
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22
22
18
63
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
              FILING DATE:

CLASSIFICATION WIBER: 05/07/17/501

PRIOR APPLICATION:

APPLICATION NUMBER: US 08/770,301

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1422-287

REFERENCE/DOCKET NUMBER: 1422-287

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)-205-6000

TELEPHONE: (703)-205-6000

TELEPHONE: (703)-205-6050

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 3252 base pairs

TYPE: nucleic acid
APPLICATION NUMBER: US/09/175,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.6
62.00
38.83
21.36
7.98%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; IDENTIFICATION METHOD:
US-09-175-581-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2198 CCCAATGAG 2206
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09253691
Sequence 3, Application US/09253691
Fatent No. 6124100
GENERAL INFORMATION:
FAPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
TITLE OF INVENTION: UNBER: US/09/253,691
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-26
SEALIER PILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
SEQ ID NOS: 3
SEQ ID NO 3
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
                                                                                                                                                                                                             70 AspalaLeuGlnSerGluGluAlaAlaValVysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGLnThr 69
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                                                                                                                                 10 ATAGAAGAGGTGGTGGAAGAGTACGAGGAGGAGGAGCAGGAAGAAGCAGCTGTTGAAGAG
                                                                                                                                                                                                                                                       102 SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla
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25
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 867
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Conservative:
Mismatches:
Indels:
Gaps:
                             Conservative:
Mismatches:
Indels:
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                                                                                                      US-09-847-539A-6 (1-159) x US-08-950-925-3 (1-867)
 Length:
Matches:
                                                                             Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.58
62.00
43.04%
31.65%
7.98%
3.2
63.00
51.67%
25.00%
8.11%
                     Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: human
US-09-253-691-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-346-408-7
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DB:
   Pred. No.:
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3 SerProlleGluGlnProArgllelleProAsnGlyGlyThrLeuThrAsnLeuLeuGly 22
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APPLICANT: Allen, Steve
APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER PLILNG DATE: 1999-07-01
BARLIER PLILNG DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 GlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSer 59
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
SOTWARN APPLICATION DATA:
APPLICATION NUMBER: US/08/770,301A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-847-539A-6 (1-159) x US-09-346-408-7 (1-1890)
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Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IKEDA, JUN
APPLICANT: KANEDA, SUMIKO
APPLICANT: YANAGI, HIDEKI
APPLICANT: YANAGI, HIDEKI
APPLICANT: WIRA, TAKASHI
APPLICANT: WURA, TAKASHI
TITLE OF INVENTION: NOVEL STRESS PROTEINS
WUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1422-287
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; Patent No. 5948637
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NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 142
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                              12.8
62.00
49.12$
29.82$
7.98$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                        LENGTH: 1890
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US-08-770-301A-4
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DB:
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Alignment Scores:
                      Pred. No.:
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                                                                                                                                                                                                                                                       62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVys 81
                                                                                                                                                                                                                                                                                                                                                                                                    102 SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-089-593-4

Sequence 4, Application US/09089593

Sequence 4. Application US/09089593

Sequence 6. Application US/09089593

Patent No. 660078

Patent No. 660078

Patent No. 600078

APPLICANT: Liu, Shigui

APPLICANT: Liu, Shigui

APPLICANT: Shi, Qinwei

TITLE OF INVENTION:

WUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                           867
15
16
29
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,593
                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                     US-09-847-539A-6 (1-159) x US-09-089-593-2 (1-867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
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APPLICATION NUMBER: 08/961,858
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-1-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFRAX: 201-343-1684
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
DESCRIPTION: native form
                                                                                                                         51.678
25.00%
8.11%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
MOLECULE TYPE:
               ; HYPOTHETICAL:
US-09-089-593-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                      Alignment Scores:
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70 CAGGAGGAGGCAGCGGAAGATGCTGAAGCAGGGTGAGACCGAGGAGACCAGGCCA 129
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                                                                                                                                                                                                                                                                                                                                                                                 102 SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla 121
                                                                                                                                                                                                                                                                                                                                                                                                                             130 GAAGAAGATGAAGAAGAAGAAGCAAAGGAGGCTGAAGATGGCCCAATGGAGTCC 189
                                                                                                                                                                                                                                             10 ATAGAAGAGGTGGTGGAAGAGTACGAGGAGGAGGAGCAGGAAGAAGAAGACAGCTGTTGAAGAG
                                                                                                                                                                                                     62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08950925
Patent No. 6072040
GENERAL INFORMATION:
APPLICANT: Dave, Kirti I.
APPLICANT: Botyanszki, Janos
APPLICANT: Botyanszki, Janos
TITLE OF INVENTION: Stabilized Conjugates of Uncomplexed
TITLE OF INVENTION: Submits of Multimeric Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
867
15
16
29
0
                                              Conservative:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,925
FILING DATE:
                                                                   Mismatches:
                                                                                                                                                           US-09-847-539A-6 (1-159) x US-09-089-593-4 (1-867)
  Length:
Matches:
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                                                                                          Indels:
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TELECOMMUNICATION INFORMATION:
TELEPAONE: 650-813-5600
TELEPAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence
LOCATION: 1...864
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
- APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                            51.67%
25.00%
8.11%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 CAGGAGGAGGCAGCGGAAGAGGATGCTGAAGCAGAGGCTGAGACCGAGGAGACCAGGGCA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValLys 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ATAGAAGAGGTGGTGGAAGAGTACGAGGAGGAGGAGCAGGAAGAAGCAGCTGTTGAAGAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liu, Shigui
APPLICANT: Liu, Shigui
APPLICANT: Shi, Oinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OS SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: All Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                             867
15
16
29
0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201333-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-847-539A-6 (1-159) x US-08-961-858-2 (1-867)
                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-961-858-4
; Sequence 4, Application US/08961858
: Patent No. 583410
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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51.67%
25.00%
8.11%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201-343-1684
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                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133521
                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                          HYPOTHETICAL:
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TELEFAX: 2
                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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70 CAGGAGGAGGCAGCGGAAGAGGATGCTGAAGCAGAGGCTGAGACCGAGGAGACCAGGGCA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                     62 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09089593
Patent No. 6060278
GENERAL INFORMATION:
APPLICANT: Liu, Shigui
APPLICANT: Liu, Shigui
APPLICANT: Liu, Cliwel
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                       867
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ZIP: 07601

MODIUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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FILLING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: JACKSON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742-
REFERENCE, POCKET NUMBER: 1112-1-044 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
FELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                   US-09-847-539A-6 (1-159) x US-08-961-858-4 (1-867)
                                                                                                                                                                                                                                                                                          Indels:
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APPLICATION NUMBER: 08/961,858
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: native form
                                                                                                     native form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEO ID NO: 2
SEQUENCE CHARACTERISTICS:
LRNCTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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51.67%
25.00%
8.11%
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STREET: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                         ; HYPOTHETICAL:
US-08-961-858-4
                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                 30 LeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08800593
; Sequence 12, Application US/08800593
; Patent No. 6143505
; GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Kallunki, Pekka
APPLICANT: AAllunki, Pekka
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

ZIP: 66066
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,593
FILING DATE: 18-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
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NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778-B
TELECHOUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,450
FILING DATE: 04-0CT-1994
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO: 12:
                 NAME/KEY: polyA_site

LOCATION: 4433

FEATURE:

NAME/KEY: polyA_site

LOCATION: 5195

US-08-317-450B-12
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STATE: Illinois
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Best Local Similarity:
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FEATURE:
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3100 AGAGCCCTGGGAGCGCTGCTGCTGATGCACAGAGGGCAAAGAATGGGGCCGGGAGGCC 3159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 LeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu 49
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| Patent No. 5834210
| GENERAL INFORMATION:
| APPLICANT: Liu, Shigui
| TITLE OF INVENTION:
| NUMBER OF SEQUENCES: 6
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Klauber & Jackson | STREET: 411 Hackensack | STREET: 411 Hackensack | STREET: New Jersey | CITY: Hackensack | STREET: New Jersey | CONTRY: USA | STREET: USA | ST
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE CHARACTERISTICS:
LENGTH: 5200 base pairs
TYPE: nucledc acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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64.00
45.16%
32.26%
8.24%
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4433
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5195
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118..3699
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Query Match:
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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; LOCATION:
US-08-800-593-12
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US-08-961-858-2
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NAME/KEY:
LOCATION:
FEATURE:
  Alignment Scores:
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                                         3100 AGAGCCCTGGGGAGCGCTGCTGCTGCACAGAGGGCAAAGAATGGGGCCGGGGAGGCC 3159
50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69
                                                                                  70 AspAlaLeuGinSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

LIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,593
FILING DATE: 18-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/317,450
FILING DATE: 04-OCT-1994
FILING DATE: 04-OCT-1994
CLASSIFICATION: A35
ATTORNEY/AGNT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 37,293
TELECOMMUNICATION INFORMATION:
TELEPRAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 14:
SECUENCE CHRACTERISTICS:
CENGTH: 4316 base pairs
TTREEDOMES: SIQ10
TTREEDOMES: SIQ10
TTREEDOMES: SIG10
TTREEDOMES: SIG10
TTREEDOMES: SIG10
TTREEDOMES: SIG10
TTREEDOMES: SIG10
                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08800593
Patent No. 6143505
Patent No. 6143505
BAPPLICANT: Tryggvason, Karl
APPLICANT: Tryggvason, Karl
APPLICANT: FABIUNE, Pekka
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: repeat_unit
LOCATION: 4021..4316
OTHER INFORMATION: /rpt_family="HUMAN ALU"
OTHER INFORMATION: /rpt_family="HUMAN ALU"
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LOCATION: 118..183
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4296
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118..3453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                          3160 CTGGAA 3165
                                                                                                                                                                 90 LeuGlu 91
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LOCATION:
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; LOCATION;
US-08-800-593-14
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US-08-800-593-14
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3100 AGAGCCCTGGGGGGGCGCTGCTGATGCACACAGGGCAAAGAATGGGGCCGGGGGGGCC 3159
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                                                                                                                                                                                                                                                                                                                     70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Trygqvason, Karl
APPLICANT: Pyke, Charles

TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSE: BANNER & ALLEGRETI, LTD.

STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: 0506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                   Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                  US-09-847-539A-6 (1-159) x US-08-800-593-14 (1-4316)
   Length:
                                                                                              Gaps:
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US-08-317-450B-12
; Sequence 12, Application US/08317450B
; Patent No. 5660982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Chao, Mark
REGISTATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,7'
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5200 base pairs
19.6
64.00
45.16%
32.26%
8.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
118..3699
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                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                      3160 CTGGAA 3165
                                                                                                                                                                                                                                                                                                                                                                                                90 LeuGlu 91
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LOCATION:
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1339 GAAGCCACGAAGGTTGCCGAAGCGGAGAAGCAGAAGGCAGCT 1380
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                                                     RESULT 24
US-08-317-450B-14
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                                                   GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: OLSU, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
                                                                                                                                                                                                                                                                                    ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,672-5300
TELEFRAX: (202)672-5399
                                                                                                                                                                                                        3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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Sequence 7, Application US/09115746
Patent No. 6228601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904/36
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1932 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                     Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 1.,1929
US-09-115-746-7
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                        ADDRESSEE:
STREET: 3(
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Pred. No.:
                                                                                                                                                                                                                                                                       COUNTRY:
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2980 CICAGAGAGTITGACCTGCAGGTGGACAACAGAAAAGCAGAAAGCTGAAGAAGCCATGAAG 3039
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATENTING SYSTEM: DC-DCS/MS-DOS
APPLICATION NUMBER: US/08/317,450B
FILING DATE: 04-OCT-1994
CLASSIFFCATION: 435
ATTORNEY/AGENT INPERMATION:
NAME: Chao, Mark
RESISTATION NUMBER: 94,778
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Sequence 14, Application US/08317450B
Patent No. 5660982
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Kallunki, Pekka
APPLICANT: Kallunki, Pekka
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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LOCATION: 4021..4316
OTHER INFORMATION: /rpt_type="other"
OTHER INFORMATION: /rpt_family="HUMAN ALU"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & ALLEGRETTI, LTD.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4316 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LOCATION: 118..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: polyA_site
LOCATION: 4296
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NAME/KEY: CDS
LOCATION: 118..3453
FEATURE:
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Best Local Similarity:
Query Match:
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US-09-115-746-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1279 GAGAAGCAGAAGGCAGCTGAGGCCACGAAGGTTGCCGAAGCGGAGAAGCAGAAGGCAGCT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 GluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGln
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 POLYPEPTIDES FOR DIAGNOSING INFECTION WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1695
19
20
55
0
                                                                                                                      ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPA: (202)672-5309
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches:
                                                                                     3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
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US-08-216-894-7
: Sequence 7, Application US/08216894
                                                                     Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.49%
20.21%
8.24%
                                                                   ADDRESSEE: Foley & Larc
STREET: 3000 K Street,
CITY: Washington, D.C.
COUNTRY: USA
TITLE OF INVENTION: POI
TITLE OF INVENTION: WI'
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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US-09-115-746-1
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Best Local Similarity:
Query Match:
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1159 CAGAAGGCAGCTGAGGCCGCCAAGGCCGTGGAGAAGGAAAGCAGAGGGCAGCTGAAGCC 1218
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: O'EU, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1932
19
20
55
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                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                  ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURERNY APPLICATION NUMBER: US/08/216,894
ATTORNEY AGENT: 10FORMATION:
NAME: BENT: 24-MAR-1994
ATTORNEY AGENT: INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107028672-5309
TELERS 304136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1932 base pairs
TYPE: nucleic acid
STRANDEDBESS: double
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Matches:
                                                                                                                                                                           3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.498
20.218
8.248
                                                                                                                                                                                                  STREET: 3000 K Street, CITY: Washington, D.C.
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Best Local Similarity:
                                                                                                                                                                                                                                                       USA
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; LOCATION:
US-08-216-894-7
                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                COUNTRY:
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NAME/KEY:
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                                                                                                                                                                                                   GENERAL INCORNATION:
APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bobencky, Roy A
APPLICANT: Russo, Jasidore S
APPLICANT: Edelman, Isidore S
APPLICANT: Bornick S
APPLICANT: Moore, Patrick S
APPLICANT: Woore, Patrick S
APPLICANT: Woore, Patrick S
APPLICANT: Woore, Patrick S
APPLICANT: Woore, Patrick S
CURRENT APPLICATION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: 1999-11-17
PRIOR APPLICATION NUMBER: POTYUS97/13346
PRIOR FILING DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19431 CAGGAGCAGGAAGAGCAGGAATTAGAGGAGGTGGAGGAGCAAGAGCAGGAGGAGGAGGAG 19372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19431 CAGGAGCAGGAAGAGCAGGAATTAGAGGAGGTGGAGGAGCAAGAGCAGGAGCAGGAGGAG 19372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AspalaLeuGlnSerGluGluAlaAlaValVysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08216894
Patent No. 5876734
GENERAL INFORMATION:
APPLICANT: Otsu, Kelko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
                                        130 LysLysThrLysAspThrLysProValValLysLysGluGluArgGln 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LystysThrLysAspThrLysProValValLysLysGluGluArgGln 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6 (1-159) x US-09-230-371A-20 (1-32207)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Kaposi's sarcoma-associated herpesvirus US-09-230-371A-20
                                                                                                                                             US-09-230-371A-20/c
; Sequence 20, Application US/09230371A
; Patent No. 6348586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Ver. 2.0
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45.69%
15.52%
8.37%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Paten
SEQ ID NO 20
LENGTH: 32207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-216-894-1
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1099 GCCGTGGAGACGGAGAAGCAGAGGCAGCTGAAGCCACGAAGGTTGCCGAAGCGGAGAAG 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1279 GAGAAGCAGAAGGCAGCTGAGGCCACGAAGGTTGCCGAAGCGGAGAAGCAGAAGGCAGCT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValVal 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLys 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ThrAspAlaLeuGlnSerGluGLuAlaAlaValValLysAlaAspAsnAlaAlaSerAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-847-539A-6 (1-159) x US-08-216-894-1 (1-1695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
  WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                         CURRENT AFFLICATION NUMBER: US/08/216,894
ATTORNEY AGENT: 24-MAR-1994
ATTORNEY AGENT: NFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
RECISTRATION FOR SEQ ID NO: 1:
SEQUENCE CHARATERISTICS:
LENGTH: 1695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-LEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
                                                                                                3000 K Štreet, N.W.,
                                                                           Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                         ADDRESSEE: Foley & Lard
STREET: 3000 K Street, 1
CITY: Washington, D.C.
COUNTRY: USA
21P: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.58
64.00
41.49%
20.21%
8.24%
                       NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"

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FEATURE:
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NAME/KEY: misc_feature
LOCATION: 2034..2747
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NAME/KEY: misc_feature
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OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 3444.3728
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OTHER INFORMATION: frame"
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LOCATION: 2747.3109
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382..5747
CHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5837..6307
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 222.425
OCCARTION: /tunction- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109..3444
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3731..4855
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 4855..5376
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OTHER INFORMATION: sequence"
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                            P-3283
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-32.
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: 6403..7770
                                                                                                                                                                             linear
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FOTHER INFORMATION: Itame
FOTHER INFORMATION: Itame
LOCATION: 11917...12741
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NAME/KEY: misc_feature
LOCATION: 12748..1449
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OTHER INFORMATION: frame"
FEATURE:
NAME/KEY: misc_feature
LOCATION: frame"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15164...15426
OTHER INFORMATION: frame"
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LOCATION: 15429..15664
CTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
US-08-402-282-3
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7770..8006
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OTHER INFORMATION: frame"
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OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 10371..10586
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OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 11115..11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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Matches:
Conservative:
Mismatches:
Indels:
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63.64%
36.36%
32.56%
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Best Local Similarity:
Query Match:
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Sequence 19, Application US/09521668B Patent No. 6303383
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73.68%
47.37%
32.56%
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US-09-521-6688-19
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Query Match:
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US-09-521-668B-19
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-05-51-668B-17
US-05-521-668B-17
Sequence 17, Application US/09521668B
Fatent No. 6303383
GENERAL INFORMATION
APPLICANT: NAKAMURA, JUN
APPLICANT: KANNO, SOHEI
APPLICANT: KAUNKA, EICHIRO
APPLICANT: MAKAMATSU, TSUYOSHI
TITLE OF INVENITON: TEMBERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
FILE REFRENCE: 010-1093-0
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT PLILNG DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: J999-03-16
SEQUENCE: 1999-03-16
NUMBER OF SEQUENCE: 1999-03-16
NUMBER OF SEQUENCE: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 17
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                           LOCATION: 1-2248
IDENTIFICATION METHOD: experiment
                                                                                                                                                              ORGANISM: Brevibacterium flavum
STRAIN: MJ-233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin version 3.0
             INFORMATION FOR SEQ ID NO: 16:
                              SEQUENCE CHARACTERISTICS:
LENGTH: 2248 base pairs
                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1318)..(2598)
US-09-521-668B-17
                                                                                                                                                                                                                        NAME/KEY: promoter
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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SEQ ID NO 17
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GENERAL INFORMATION:
APPLICANT: NARAMURA, JUN
APPLICANT: KANNO, SOHEI
APPLICANT: KANNO, SOHEI
APPLICANT: MATSUI, KAUHIKO
APPLICANT: MATSUI, KAUHIKO
APPLICANT: MATANI, KAUHIKO
APPLICANT: MATANI, KAUHIKO
APPLICANT: NARAMATSU, TSUYOSHI
TITLE OF INVENTION: TEMPERAUDE SENSITIVE PLASMID FOR CORYNEFORM, BACTERIA
FILE REPERENCE: 0010-1093-0
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT FILING DATE: 2000-033-08
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2083 TIGGATATGTTGGCCGATCAAAGCGACGCCGGCGAGGATATGGACGCTGTTTTGGTG 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-847-539A-6_COPY_59_86 (1-28) x US-09-521-668B-19 (1-4447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Hamilton, Paul T.
APPLICANT: Beyer Jr., Wayne F.
APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
STATE: US
2IP: 07417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/402,282
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
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FILING DATE: 1-AUGUST-1994
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918 GAAATACTGGAAGCCGTAGGGGCACGCTCCAGGTCTGGTGGAGGAAGCCGCGGAGCTT 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08285641
Patent No. 5726299
GENERAL INFORMATION:
APPLICANT: Zubancic, Thomas J.
APPLICANT: Yukawa, Hiddaki
TITLE OF INVENTION: PROMOTER DNA FRAGMENT FROM CORNYNEFORM BACTERIA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.#1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FLING DATE: 29-DEC-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
RESTSTRATION NUMBER: 3543
REFERENCE/DOCKET NUMBER: 3730
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (312) 616-5700
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1903 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
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Indels:
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APPLICATION NUMBER: US/08/285,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 ATAGAAGCTGACAGT 844
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ValLysAlaAspAsn 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                           COUNTRY: US
ZIP: 60601-6780
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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Sequence 16, Application US/08285641
Sequence 16, Application US/08285641
Setent No. 5726299
GENERAL INFORMATION:
APPLICANT: Zupancic, Thomas J.
APPLICANT: Zupancic, Thomas J.
TITLE OF INVENTION: PROMOTER DNA FRAGMENT FROM CORNYNEFORM BACTERIA VINERRO PS EXQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-847-539A-6_COPY_59_86 (1-28) x US-08-285-641-20 (1-2213)
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Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/285,641
FILING DATE: 1-AUGUST-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,091
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: US 07/709,151
FILING DATE: 29-MAY-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 080776,091
FILING DATE: 15-UNN-1993
APPLICATION NUMBER: US 07/709,151
FILING DATE: 29-MAY-1991
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: promoter
LOCATION: 1-2213
IDENTIFICATION METHOD: experiment
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium flavum
STRAIN: MJ-233
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 2213 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE:
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Best Local Similarity:
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US-08-943-915-4/C
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                                                                                                                                            2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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                                                                              US-09-847-539A-6_COPY_59_86 (1-28) x US-09-238-557-1 (1-1254)
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Peery, Robert B
APPLICANT: Skatrud, Paul L
APPLICANT: Thornewell, Susan J
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: CYPTOCOCCUS NEOFORMANS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 46285

COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,521
FILING DATE:
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Mismatches:
Indels:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                      % Sequence 1, Application US/08612521; Patent No. 5786463; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hemilton, Amy.
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-96;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3169
TELEFAX: 317-276-3169
                                                                                                                                                                                                                    559 TTCAAGGCTGGTAAGAAGGCA 579
                                                                                                                                                                                              22 ValLysAlaAspAsnAlaAla 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4224 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    33,33%
33,33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
    Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-612-521-1
                        Query Match:
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GENERAL INFORMATION:
APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Hansen, Joel D.
APPLICANT: Aix, Xiaojie
APPLICANT: Xu, Xiaojie
APPLICANT: Xu, Xiaojie
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6_COPY_59_86 (1-28) x US-08-943-915-4 (1-621)
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                                                                                                                                                                                                                                                                                                                                                     COMPOTER READ-LIFE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                APPLICANT: Itch, No. 5998170uyuki
APPLICANT: Martin, Frank
APPLICANT: Martin, Frank
APPLICANT: Danilenko, Dimitry
ITILE OF INVENTION: A FIBROBLAST GROWTH FACTOR
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Leydig, Voit & Mayer, Ltd. STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
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US-08-581-148C-15/c
Sequence 15, Application US/08581148C
; Patent No. 6060644
                                                                                                                                                                                                               ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
Sequence 4, Application US/08943915
Patent No. 5998170
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/POCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 805.447.4112
TELEPAX: 805.447.1090
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Percent Similarity:
                                                                                                                                                   Pred. No.:
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                                                                                                                                                                       Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-847-539A-6_COPY_59_86 (1-28) x US-09-238-557-3 (1-1221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastESC for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                             ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET WUMBER: GM10088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08934846
Patent No. 5893898
GENERAL INFORMATION:
APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folc
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GM10088
APPLICATION NUMBER: 08/934,846
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ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ValLysAlaAspAsnAlaAla 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-238-557-3
                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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US-08-934-846-1
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2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL FOIC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOSTWARE: FSSESSO FOR Windows Version 2.0
CUSCHWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,846
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-238-557-1
; Sequence 1, Application US/09238557
: Patent No. 6165472
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    22 ValLysAlaAspAsnAlaAla 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
43.00
51.85%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-09-238-557-1
                                                                            TOPOLOGY: linear
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: CLASSIFICATION:
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COUNTRY: US
ZIP: 19103
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APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Multice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BNCODING THEM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-847-539A-6_COPY_59_86 (1-28) x US-08-960-022-13 (1-1772)
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Patent No. 5812898
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Streets Try:
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [ndels:
                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
ATTORREY FAGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
; INFORMATION FOR EGO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1772 base pairs
; TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855 GAAAGTAACAACGCA 869
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                                                                                                                                                                                                                                   CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-960-022-13
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                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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Patent No. 6165470.

GENERAL INFORMATION: Stewart C.

APPLICANT: Pearson, Stewart C.

TITLE OF INVENTION: NOVEL FOIC

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: Dechert Price & Rhoads

STREET: 4000 Bell Aliantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/934,846
FILING DATE:
APPLICATION NUMBER: US/08/934,846
FILING DATE:
APPLICATION NUMBER: US/08/934,846
FILING DATE:
APPRICATION NUMBER: 28,354
REGISTRATION NUMBER: 28,354
REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: CM10088
TELEDHONE: 215-994-2252
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1221 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 TTCAAGGCTGGTAAGAAGGCA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ValLysAlaAspAsnAlaAla 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.5
43.00
51.85%
33.33%
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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COUNTRY: US
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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US-09-847-539A-6_COPY_59_86 (1-28) x US-09-103-840A-1 (1-4411529)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                               Db 4044125 GGTGCT 4044120
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Best Local Similarity:
Query Match:
                                                                                                                          27 AlaAla 28
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US-08-961-083-191
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                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCHLOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
             PATENT NO. 6294328
GENERAL INFORMATION:
APPLICANT FLEISCHMAN, ROBERT D.
APPLICANT FLEISCHMAN, ROBERT D.
APPLICANT FRASER, Claire M.
APPLICANT FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: TRASER, Claire M.
APPLICANT: TRASER, Claire M.
APPLICANT: TRASER, Claire M.
APPLICANT: TURE CLOIN TOWNER JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn 26
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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
COTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
Sequence 2, Application US/09103840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.94e + 05
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54.55%
40.91%
36.43%
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54.55%
40.91%
36.43%
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 4036196 GGTGCT 4036191
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                               LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Db 4044185 TTGATGGACGCCGCCGACCTGCTGGAAGGCGAACAGGTAACCATCGTCGATATCGACAAC 4044126
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                                                                                                                                                                                                            Sequence 191, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-847-539A-6_COPY_59_86 (1-28) x US-08-961-083-191 (1-1033)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP VECTEA 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CAURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08960022; Patent No. 5976837; GENERL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEYAGEWT INFORMATION:
NAME: BLOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REGISTROCAFORET UNBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.2
44.00
65.00%
55.00%
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

October 13, 2002, 02:17:36 ; Search time 9.13369 Seconds (without alignments) 753.008 Million cell updates/sec Run on:

Title:

US-09-847-539A-6_COPY_59_86 129 1 SDALEALADQTDALQSEEAAVVKADNAA 28 Perfect score:

Sequence:

**BLOSUM62** Scoring table:

Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

383533 seqs, 122816752 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

Database :

/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:* Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 3. Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 191, App	Sequence 13, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 4. Appli	Sequence 15. Appl
	QI	59065 4 US-09-813-817-3	US-09-103-840A-2	US-09-103-840A-1	US-08-961-083-191	US-08-960-022-13	US-08-934-846-3	US-09-238-557-3	US-08-934-846-1	US-09-238-557-1	US-08-612-521-1	US-08-943-915-4	US-08-581-148C-15
	DB	4	4	4	m	~	~	4	N	4	-	N	.ന
	Query Match Length DB ID	59065	4403765	4411529	1033	1772	1221	1221	1254	1254	4224	621	1903
op.	Query	36.4	36.4	36.4	34.1	34.1	33.3	33.3	33.3	33.3	33,3	32.6	32.6
	Score	47	47	47	44	44	43	43	43	43	43	42	42
	ult No.	-	7	m	4	S	o	7	8	6	10	11	12
	Result No.	ပ	ပ	ပ							U	U	ပ

RESULT 2 US-09-103-840A-2/c

Sequence 20, Appl Sequence 16, Appl Sequence 17, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 17, Appl Sequence 1, Appl Sequence 2, Appl Sequence 3, Appl Se	PROTEINS, AND USES	5) 
US-08-285-641-20 US-09-285-641-16 US-09-521-6688-17 US-09-521-6688-19 US-08-402-282-3 US-08-402-066-3 US-08-402-066-3 US-09-354-409-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-568-480-1 US-09-104-294-9 US-09-104-294-9 US-08-16-666-2 US-08-16-666-2 US-08-16-666-2 US-08-16-666-2 US-08-16-661-2 US-08-16-661-2 US-09-104-291-2 US-09-104-291-2 US-09-104-291-2 US-09-104-291-2	ALTGUMENTS  13817  1.  HUMAN KINASE PROTEINS, NUCLEIC LECULES ENCODING HUMAN KINASE P 15/09/613,817  3.24  3.24  3.24  3.24	Scores:  1.77e+03 Length: 59065 47.00 Matches: 10 Matches: 10 X6.478 Conservative: 3 X6.438 Mismatches: 4 Indels: 0 Gaps: 0 S39A-6_COPY_59_86 (1-28) x US-09-813-817-3 (1-59065 AlaaspGlnThragpalaLeuGlnSerGluGluAlaalaValValLysala III:::     ::     :::       :::   GCTGAACAAACTGACTCCTTAGAACCAGCTCAAGGCGCACAGGCTCTTCAAAGCG
c 14 42 32.6 2213 1 15 42 32.6 2248 1 1	AESULT 1  US-09-813-817-3/C Sequence 3, Application US/09813817 Parent No. 6340583 GENERAL INFORMATION: APPLICANT: YAN, Chunhua et al. TITLE OF INVENTION: ACID MOLECULES TITLE OF INVENTION: THEREOF FILE REPERENCE: CLOO1178 CURRENT APPLICATION NUMBER: US/09-68 CURRENT FILIAD DATE: 2001-03-24 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FEALSEQ for WIndows Versic SEC ID NO 3 LENGTH: 59065 TYPE: DNA ORGANISM: Human US-09-813-817-3	Alignment Scores:  1.77e+03 Score:  8 47.00 Percent Similarity: 76.47% Best Local Similarity: 58.82% Ouery Match: 4 US-09-847-539A-6_COPY_S9_86 (1-28)  Oy 8 AlaAspGinThrAgpAlaLeuGin Db 21239 GCTGAACAACTGACTTAGAA

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Sequence 6, Application US/09089593
Patent No. 6060278
GENERAL INFORMATION:
APPLICANT: Liu, Shigui
APPLICANT: Shi, Qinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 3; Leny...
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 13, 2002, 02:12:51 Job time : 6.34225 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,858
                  4 LEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 111: TELECOMMUNICATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.2%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-089-593-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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TOPOLOGY: 11n
                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                        US-09-089-593-6
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                                                                                      RESULT 40
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APPLICANT: Shi, Oinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.2%; Score 39; DB 2; Length 288; 32.0%; Pred. No. 1.9e+02; Live 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                        Length 58
                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,858
                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                        Score 39;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICALL...
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
                                                                                     P50164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-961-858-6; Sequence 6, Application US/08961858; Patent No. 5834210; GENERAL INFORMATION:
       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SULFON, JEFFERY A.
REFERENCE/DOCKET NUMBER: 34028
REFERENCE/DOCKET NUMBER: P501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5030
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ACCURACY: Circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 288 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                       30.2%;
                                                                                                                                                                                                                                                                                                   Query Match 30.2
Best Local Similarity 56.2
Matches 9; Conservative
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39 ALNQEVDALQEEVAAL 54
                                                                                                                                                                                                                                                                                                                                                                             6 ALADQTDALQSEEAAV 21
                                                                                                                                                                                                                ; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
PCT-US94-06655-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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Best Local Similarity
Matches 8; Conserv
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Length 1261;

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APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG, ALAN R.; NICHOLS, EVERETT J.
FITTLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS FOR ENHANCED CYTOTOXICITY AND IMAGING NUMBER OF SEQUENCES: 45
CURRENT APPLICATION NUMBER: US/07/390,241
FILING DATE: 07-NUG-1989
PRIOR APPLICATION DATA:
                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: translation of msina9 cDNA; see Figure 29A,
uvpnmHFTICAL: YES
                                                                                                                                                                                                                                                      ; DB 1; Le..
7.6e+02;
7.7.6e+03; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application PC/TUS9406655
GENERAL INFORMATION:
APPLICANT: Chalken, Irwin
APPLICANT: Graddis, Thomas
APPLICANT: Myszka, David
TITLE OF INVENTION: Colled-Coll Stem Loop Templates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: Corporate Patents / P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                          Pred. No. 7.6e
4; Mismatches
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Pred, No. 10;
                                                                                                                                                                                                                                                                          Score 40;
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                                                                                                                                                                                                                                                                                                                                                    4 LEALADQTDALQSEEAAVVKADN 26
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FILING DATE: 15-AUG-1988
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55.6%;
                                                                                                                                                                                                                                                                        31.0%;
39.1%;
                                                           1261 amino acids
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                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.13
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.2
Best Local Similarity 55.6
Matches 10; Conservative
   TELEFAX: (206) 224-077
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                   single
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COMPUTER READABLE FORM:
                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                  ORGANISM:
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                                                             LENGTH:
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;Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Elsenman, Robert N.
APPLICANT: Hurlin, Peter J.
APPLICANT: Hurlin, Peter J.
APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Requistory Proteins that Dimerize with
TITLE OF INVENTION: Mad or Max
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
 10; Indels
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MOORE, K.
APPLICANT: MOORE, K.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAW
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OI
FILE REFERENCE: 7853-136
CURRENT FOLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER PLING DATE: 1998-10-20
SARVIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6e+02;
es 8;
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Pred. No. 7.6e+02
6; Mismatches
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REGISTRATION NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: FHCR17694
TELECOMMUNICATION:
TELEPHONE: (206) 682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08252966B Patent No. 5624818 GENERAL INFORMATION:
                                                                           920 EAYVDRSDVCRHDHASAYKAHTAS 943
                                       5 EALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                         Sequence 2, Application US/09245041 Patent No. 6274339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 SDVLVFTSEQCDAHRSEAACV 489
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 8; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
US-09-245-041-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
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                                                                                                                                 RESULT 35
US-09-245-041-2
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 Matches
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Length 25; Indels

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Score 40; DB 4; Length 1253;
Pred. No. 7.6e+02;
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US-08-466-277-3
US-08-466-277-3
Sequence 3, Application US/08466277
Patent No. 619666
GENERAL INFORMATION:
Liliestrom, Peter
Liliestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1; Pred. No. 7.6e+02; 6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u >cu <u <u >cu <u >cu <u <u <u>cu <u <u >cu <u <u <u>cu <u <u >cu <u <u <u>cu <u <u <u>cu <u <u <u>cu <u <u <u>cu <u>cu <u <u>cu <u>cu <u <u>cu <u <u>cu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-466-277-3
                                                  NAME: MUTPHY JI., Gerald M.
REGISSTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELERAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1253 amino acids
TYPE: amino acid
TOPOLOGY: linear
GC-07-920-281C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920 EAYVDRSDVCRHDHASAYKAHTAS 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1253 amino acids
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.3%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
STREET: 1420 Fifth Ave., Suite 2800 CITY: Seattle STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.0%; Score 40; DB 1; Length 125
39.1%; Pred. No. 7.6e+02;
tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
DESCRIPTION: translation of msina cDNA; see Figure 23
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/07920281C
PRICAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION:
TITLE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/920,281C
FILING DATE: 13-AUG-1992
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997.
REFERENCE/POCKET NUMBER: FHCR17694
TELECOMMUNICATION INFORMATION:
TELECHONE: (206, 682-8100
TELECAX: (206, 224-0779
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 LEAIOKKLSRLSAEEQAKFRLDN 674
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                                                                                                                                                                                                                                                                                                                               Floppy disk
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Best Local Similarity 39.1:
Matches 9; Conservative
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                                                                                                                                                                                                                                                                ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-252-966B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-920-281C-3
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GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-960
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
LENGTH: 1094
TYPE: PRT
TYPE: PRT
ORGANISM: Haemophilus influenzae
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Patent No. 5624818
Patent No FORMATION:
APPLICANT: Eisenman, Robert N.
APPLICANT: Hurlin, Peter J.
APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.0%; Score 40; DB 4; Length 1094; Best Local Similarity 37.5%; Pred. No. 6.5e+02; Matches 9; Conservative 5; Mismatches 10; Indels
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40.0%; Pred. No. 5.1e+02;
tive 5; Mismatches 7; Indels
                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,069
                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,822
FILING DATE: 11-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REPERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-268-347-32; Sequence 32, Application US/09268347; Patent No. 6335182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 ETMOGLQTQRDALQQEVASL 555
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Best Local Similarity 40.0
Matches 8; Conservative
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MOLECULE TYPE: protein

US-09-005-069-62
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US-08-252-966B-12
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Patent No. 5932470

GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: WALLENFELS, LYNDA

ITTLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        Sequence 62, Application US/08630822A
Patent No. 5840695
GENERAL INFORMATION:
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.0%; Score 40; DB 2; Length 900; 40.0%; Pred. No. 5.1e+02; Live 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Deriver STATE: Colorado COUNTR: U.S.A.

ZIP: 80203
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OFFER: Ploppy disk COMPUTER: IBM PC COMPATIBLE OFFER: PC DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,822A FILING DATE: 11-APR-1996 CLASSIFICATION: WAME: CONNELL, GARY J. REGISTATION NUMBER: 22.020 REFERENCE/DOCKET NUMBER: 26.18-17-C3 TELEPOMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPAST (303) 863-023 INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUENCE CHRARCTERISTICS: LENTH OFFER SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                      469 SDVLVFTSEQCDAHRSEAACV 489
1 SDALEALADQTDALQSEEAAV 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 900 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-822A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 40.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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US-09-005-069-62
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT APPLICATION NUMBER: 60/093,630
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER PILING DATE: 1998-07-21
EARLIER PILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.0%; Score 40; DB 4; Length 549; 47.6%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 287
Pred. No. 1.3e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                         COUNTRY: US

ZIP: 94105-1493

COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Guy W.
REGISTRATION NUMBER: 30,617
REFERENCE/DOCKET NUMBER: 15280-216000
TELECOMMUNICATION INFORMATION:
TELEBRAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: all Xaa positions
COTHER INFORMATION: Xaa-unknown amino acid
US-09-245-041-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/09245041; Patent No. 6274339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: MACE protein US-08-457-245-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.0%;
Best Local Similarity 61.1%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SDALEALADQTDALQSEE 18
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moore, K. APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 9
LENGTH: 549
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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Patent No. 5573915
GENERAL INFORMATION:
APPLICANT: BARRY III, Clifton E.
APPLICANT: YIAN, Ying
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA INVOLVED
TITLE OF INVENTION: IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS IN TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELTE COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TOWN COMPATIBLE
COMPUTER: TOWN COMPATIBLE
COMPUTER: TOWN COMPATIBLE
COMPATION NUMBER: US/08/858,207A
FILING DATE: US/08/858,207A
FILING DATE: US/08/858,207A
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1997
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATORNEY/AGENT INFORMATION:
NAME: GIMMI, Edward R
REGESTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 38,891
TELEPHONE: 610-270-4478
TELEPHONE: 610-270-4778
                                                                                                                                                                                                                                                     APPLICANT: Hodgson, John
APPLICANT: Hodgson, John
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                 Sequence 334, Application US/08858207A Patent No. 6348328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::|| || | ::|::: |
8 DKVDALLDQLSANSKDKTALLESTKA 33
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                                               INFORMATION FOR SEQ ID NO: 394:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                      5 EALADQTDALQSEEAAVVKADN 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: No. 6348328e
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Best Local Similarity
Matches 8; Conserv
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US-08-457-245-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schnepf, Harry E. APPLICANT: Schneb, George E. APPLICANT: Payne, Jewel M. APPLICANT: Payne, Jewel M. APPLICANT: Payne, Jewel M. APPLICANT: Proncerrada, Luis APPLICANT: Foncerrada, Luis TITLE OF INVENTION: NOVel Nematode-Active Toxins and Genes TITLE OF INVENTION: Which Code Therefor NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS: ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                     ;
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                                                                                                                                                        Query Match 31.8%; Score 41; DB 4; Length 395; Best Local Similarity 40.9%; Pred. No. 1.4e+02; Matches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US92/03624
FILING DATE: 19920501
        IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC2317) NRRL B-18816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS69D1
INMEDIATE SOURCE:
CLONE: E. COLI NM522(PMYC2317) NRRL B-18816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEO ID NO: 10 (PS69D1):
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application PC/TUS9203624 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REPERING/DOCKET NUMBER: MA20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                       231 EELLKKVDDLKKELEAAIKAEN 252
                                                                                                                                                                                                                                            5 EALADQTDALQSEEAAVVKADN 26
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.8
Best Local Similarity 40.9
Matches 9; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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LOCATION: 1..395
                                                                      NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
PCT-US92-03624-10
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US-09-222-594-10
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                                                  FEATURE
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TITLE OF INVENTION: No. 6166195el Nematode-Active Toxins and Genes Which Code TITLE OF INVENTION: Therefor FILE REFERENCE: M-20CCCD2 CURRENT APPLICATION NUMBER: US/09/076,137B CURRENT FILING DATE: 1998-05-12 EARLIER PILING DATE: 1998-05-12 BARLIER FILING DATE: 1994-09-30 NUMBER OF SEQ ID NOS: 42 SOFTWARE: PAtentin Ver. 2.1 SEQ ID NO 10 LENGTH: 395
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thompson, Mark
APPLICANT: Thuth, Mark
APPLICANT: Knuth, Mark
APPLICANT: Cardineau, Guy
TITLE OF INVENTION: Bacillus thuringiensis Toxins With Improved
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                              Length 395;
                                                                                                                                                                                                                                                                                                        Score 41; DB 4; Length 37-2.
Pred. No. 1.46+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Galnesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/222,594
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ORIGIANL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS69D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION UNBER: 39,355
REFERENCE/DOCKET NUMBER: MA-702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/904,278
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09222594 Patent No. 6303364
                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bacillus thuringlensis
US-09-076-137-10
                                                                                                                                                                                                                                                                                                                                                                                                                                        231 EELLKKVDDLKKELEAAIKAEN 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                            31.8%;
40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.9%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES
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CLASSIFICATION:
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US-09-222-594-10
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NAME/KEY: Protein
LOCATION: 1..395
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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US-08-904-278-10
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      No. 5753492el Nematode-Active Toxins and Genes Which Code Therefor
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                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DUS
SOCTAME: Patentin Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,301A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/693,018
FILING DATE: 23-APR-1992
CLASSIFICATION NUMBER: US/693,018
FILING APPLICATION DATA:
APPLICATION NUMBER: US/693,018
FILING DATE: 10-AUG-1991
CLASSIFICATION NUMBER: US/55,544
FILING DATE: 10-AUG-1990
CLASSIFICATION NUMBER: US/655,544
FILING DATE: 12-AUG-1987
CLASSIFICATION NUMBER: US/655,544
FILING DATE: 12-AUG-1987
CLASSIFICATION NUMBER: US/655,544
FILING DATE: 13-AUG-1987
CLASSIFICATION NUMBER: US/655,544
FILING DATE: 12-AUG-1987
CLASSIFICATION NUMBER: US/655,544
FILING DATE: 
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INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC2317) NRRL B-18816
TITLE OF INVENTION: NO. 5753492el Nematode-TITLE OF INVENTION: Which Code Therefor NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
LOCATION: 1..395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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231 EELLKKVDDLKKELEAAIKAEN 252

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5 EALADOTDALQSEEAAVVKADN 26

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SERIERAL INFORMATION:

APPLICANT: Thompson, Mark
APPLICANT: Thompson, Mark
APPLICANT: Thompson, Mark
APPLICANT: Thompson, Mark
APPLICANT: Thompson, Mark
APPLICANT: Canture, Mark
APPLICANT: Canture, Mark
APPLICANT: Canture, Mark
MUMBER OF SERIERTOR SELILIUS THAT APPLICANT
CANTERTOR SERIER CANDESSES:
ADDRESSES: Saliwanchik & Saliwanchik You's Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mark Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture, Mumber Canture,
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TOPOLOGY: linear

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No. 5439881el Nematode-Active from Bacillus thuringiensis Isolates
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MEDLUM TYPE: Floppy disk
COMPUTER: I END PY disk
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COMPUTER: PEN PY COMPATIBLE
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                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Narva, Kenneth E
APPLICANT: Schwab, George E
APPLICANT: Schwab, George E
APPLICANT: Payre, Javel M
TITLE OF INVENTION: Gene Encoding No.
TITLE OF INVENTION: Toxins Cloned fro
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeff Lloyd
STREET: 2421 N.W. 41st Street
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 73206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08316301A
Fatent No. 5753492
GENERAL INFORMATION:
APPLICANT: Schwab, George E.
APPLICANT: Schwab, George E.
APPLICANT: Narva, Kenneth E.
APPLICANT: Narva, Kenneth E.
APPLICANT: Poncerrada, Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM(TM)-11 LIBRARY
                                                                                            Sequence 6, Application US/08049783 Patent No. 5439881
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Best Local Similarity 40.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
1..395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-049-783-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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US-08-316-301A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for ITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length sy. Pred. No. 1.4e+02;
                                                                                            Query Match 31.8%; Score 41; DB 5; Length 370 Best Local Similarity 43.5%; Pred. No. 1.3e+02; Matches 10; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALIF: 3.2000
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: M/S 104
REFERENCE/DOCKET NUMBER: M/S 104
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-810
TELEPHONE: SEO ID NO: 9: SEOUENCE CHARACTERISTICS:
LENGTH: 395 anning acids
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC2317) NRRL B-18816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEB: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                  343 ADSLMQLARQVSRLESGQAALPK 365
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Best Local Similarity 40.9%;
Matches 9; Conservative 4
MOLECULE TYPE: protein
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; LOCATION: 1..395
US-07-876-280-9
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                             PCT-US93-01676A-4
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US-07-876-280-9
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COUNTRY: US
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PCT-US93-01676A-4
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                   US-09-568-472-6
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Gretach, Soss
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERENCE: 4.30582A
CURRENT FILING DATE: 2000-05-10
FRIOR PLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Girkle, Ross
APPLICANT: Grant Ross
APPLICANT: Cyr, Devon
APPLICANT: Gorlach, Joen
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3798;
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                   3434 DALRSMAEAGAEVQIVEADVARRDDVA 3460
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2 DALEALADQTDALQSEEAAVVKADNAA 28
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; Sequence 6, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
                                                                                                                                         Sequence 6, Application US/09568480 Patent No. 6355458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Sorangium cellulosum
US-09-568-486-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Sorangium cellulosum
US-09-568-480-6
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Matches 10; Conserv
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                                                                                                    RESULT 15
US-09-568-480-6
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Gaps
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TITLE OF INVENTION: MUTAGENICITY TESTING USING REPORTER
TITLE OF INVENTION: GENES WITH MODIFIED METHYLATION FREQUENCIES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
Sequence 6, Application US/09568472;
Patent NO. 6358719
GENERAL INFORMATION:
PAPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Gyr, Devon
APPLICANT: Gyr, Devon
APPLICANT: Gyr, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERBRUE: 4.30582A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elab PC COMPUTER:
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01676A
FILING DATE: 19930226
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/842,644
FILING DATE: 02-FEB-1992
ATTOREY/AGENT IRFORMATION:
ANALY AND ATTOR THEORMATION:
AND ATTOREY/AGENT IRFORMATION:
AND ATTOREY/AGENT IRFORMATION:
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.6%; Score 42; DB 4; Best Local Similarity 37.0%; Pred. No. 1.4e+03 Matches 10; Conservative 6; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application PC/TUS9301676A GENERAL INFORMATION:
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REGISTRATION NUMBER: 28,005
REFRENCE/DOCKET NUMBER: STAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CRGANISM: Sorangium cellulosum US-09-568-472-6
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: AMINO ACID
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3434 DALRSMAEAGAEVQIVEADVARRDDVA 3460
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Patent No. 6355457
                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/09568102
; Patent No. 6346404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Soranglum cellulosum
US-09-568-102-6
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                    32.6%;
illarity 37.0%;
Conservative (
                         Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                   RESULT 13
US-09-568-102-6
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US-09-567-969-6
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APPLICANT: Gesellscheft fuer Biotechnologische Forschung mbH
APPLICANT: Beyer, Stefan
APPLICANT: Beyer, Stefan
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Coldberg, Steven L
APPLICANT: Mofle, Gerhard
APPLICANT: Mofle, Gerhard
APPLICANT: Mofle, Gerhard
APPLICANT: Motler, Joachim
APPLICANT: Meller, Joachim
APPLICANT: Meller, Joachim
APPLICANT: Meller, Steven L
APPLICANT: Mofle, Gerhard
APPLICANT: Mofle, Gerhard
APPLICANT: Mofle, Gerhard
APPLICANT: Mofle, Gerhard
APPLICANT: Mofle, Gerhard
APPLICANT: Woller, Joachim
APPLICANT: Woller, Joachim
APPLICANT: Woller, Joachim
APPLICANT: Woller, Succession
APPLICANT: PETRERERERE
APPLICANTION: MUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
ERALIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
COFFWARE: Patentin Ver. 2.1
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US-09-335-409-6

Sequence 6, Application US/09335409

Patent No. 6121029

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Schupp, Thomas

APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REPERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/335,409

CURRENT FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0
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                                              Length 427;
                                              Query Match 32.6%; Score 42; DB 4; Le
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/09413814
Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Soranglum cellulosum US-09-413-814-67
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                                                                                                                                                                           |: ||||:|| : | :| :| 256 LDMLADQSDAGEDMDAVLV 274
                                                                                                                                                 4 LEALADQTDALQSEEAAVV 22
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LENGTH: 3798
TYPE: PRT
US-09-521-668B-20
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LENGTH: 2890
                                                                                                                                                                                                                                                                                                     US-09-413-814-67
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                                                     Gaps
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APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon Genes
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Goellach
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR PRILING DATE: 2000-05-10
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Cyr, Devon
TILE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
TILE REFERENCE: 4.30582A
FILE REFERENCE: 2000-05-10
CURRENT APPLICATION NUMBER: US/09/568,102
FRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
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Length 3798;
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Score 42; DB 3; I
Pred. No. 1.4e+03;
6; Mismatches 11;
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Sequence 20, Application US/09521668B

Sequence 20, Application US/09521668B

Patent No. 6303383

SEQUENCE 20, SECURIARY ON:
APPLICANT: NARAMURA, JUN
APPLICANT: NARAMURA, JUN
APPLICANT: MARAMURA, SOHEI
APPLICANT: MARAMATSU, KOHEI
APPLICANT: MARAMATSU, TSUYOSHI
TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORVNEFORM BACTERIA
FILE REPEREBREE: 0010-11093-0
CURRENT FILING DATE: 2000-03-08
PRIOR PLICATION NUMBER: JP 11-69896
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 20
SECTION NUMBER: PALENTIN NUMBER: SECTION NUMBER: SECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAWINA, JUN
APPLICANT: KANNO, SOHEI
APPLICANT: KANNO, SOHEI
APPLICANT: KANNO, SOHEI
APPLICANT: MATSUI, KAUHKO
APPLICANT: MATSUI, KAUHKO
APPLICANT: NAKAMATSU, TSOYOSHI
TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORVNEFORM BACTERIA
FILE REFERENCE: 0010-1033-0
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATCHIN VETSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2; Length 102;
Pred. No. 20;
4; Mismatches 8; Indels
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ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-521-668B-18; Sequence 18, Application US/09521668B; Patent No. 6303383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%;
milarity 45.5%;
Conservative
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256 LDMLADQSDAGEDMDAVLV 274
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: amino acid US-08-710-749-8
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Best Local Similarity 47.4%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserva'
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LENGTH: 427
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| Sequence 8, Application US/08710749
| Patent No. 5955089
| GENERAL INFORMATION:
| APPLICANT: Briles, David E. |
| APPLICANT: Briles, David E. |
| TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE |
| TITLE OF INVENTION: PROPERINS |
| TITLE OF INVENTION: PROPERINS |
| TORRESPONDENCE ADDRESS: |
| ADDRESSEE: Curtis, Morris & Safford |
| STREET: 530 Fifth Avenue |
| CITY: New York |
| STATE: New Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
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LOUNDING TYPE: RIOPY disk
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATENING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REFERENCE/POCKET NUMBER: 25.666
REFERENCE/POCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,5e+02;
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                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
FILING DATE: 17-MR-1993
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MR-1993
APPLICATION NUMBER: US 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700715, Allen E.
REGISTRATION NUMBER: 34,490
REGISTRATION NUMBER: 34,490
REGISTRATION NUMBER: 34,490
RECISTRATION NUMBER: 34,490
RECIS
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(212) 840-0712
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; MOLECULE TYPE: protein
US-08-764-100-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: un
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Sequence 2, Application US/09238557
Patent No. 6165472
                                     GENERAL INFORMATION:
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US-08-764-100-25
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                                                                                                                                                                      Ouery Match
33.3%; Score 43; DB 4; Length 407;
Best Local Similarity 33.3%; Pred. No. 72;
Matches 9; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.3%; Score 43; DB 2; Length 418; Best Local Similarity 33.3%; Pred. No. 74; Matches 9; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pearson, Stewart C.
APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folC.
WUMBER OF SEQUENCES: 4
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
                                                                                                                                                                                                                                                                     2 DALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DALEALADQTDALQSEEAAVVKADNAA 28
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Sequence 2, Application US/08934846

Patent No. 5882898

GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
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TELEFAX: 215-994-2222
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TOPOLOGY: linear
US-08-934-846-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                              ; TOPOLOGY: linear
US-09-238-557-4
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COUNTRY:
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US-09-238-557-2

RESULT 6

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Gaps
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Fatent No. 5773700
GENERAL INFORMATION:
APPLICANT: Van Grinsven J., Martinus Q.
APPLICANT: Oberland, Petrus T.
APPLICANT: Gelen L., Johannes J.
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
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APPLICANT: Pearson, Stewart C.
APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                     SUFTWARE: FRAESEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/238,557 FILING DATA: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 DHQETLGDSLEAIAEQKAGIFKAGKKA 193
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APPLICATION NUMBER: 08/934,846
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: DICKINSON, TOCK OR
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-994-2252
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                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
LPPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
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TELEX:
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stree
CITY: Philadelphia
STATE: PA
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: DOSSERATIONS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
FILING DATE:
FILING DATE:
FILING DATE:
                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,846
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NAME: Dicknison, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10088
TELEPHONE: 215-994-2252
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                               28,354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folc
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-238-557-4
Sequence 4, Application US/09238557
Patent No. 6165472
GENERAL INFORMATION:
                                                                                                                                           PILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-994-2252
                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 407 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 33.3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-934-846-4
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                                                                                                                                           APPLICANT: GACODS, Neumerin
APPLICANT: LaVallie, Edward R.
APPLICANT: LaVallie, Edward R.
APPLICANT: Macle, Lisa A.
APPLICANT: Machel David
APPLICANT: Spallding, Vikki
APPLICANT: Spallding, Vikki
APPLICANT: Spallding, Vikki
APPLICANT: Spallding, Vikki
APPLICANT: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ESCRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STRRET: 87 CambridgePark Drive
CITY: CambridgePark Drive
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.1%; Score 44; DB 2; Length 514; Best Local Similarity 36.0%; Pred. No. 67; Matches 9; Conservative 8; Mismatches 8; Indels
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APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folc
NUMBER OF SEQUENCES: 4
CORRESPONDER ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                           Sequence 14, Application US/08960022
Patent No. 5976837
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ALEALADQTDALQSEEAAVVKADNA 27
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; Sequence 4, Application US/08934846
; Patent No. 5882898
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41.323
TELECOMMUNICATION INFORMATION:
TELEPHOR: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 514 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-960-022-14
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                                      US-08-960-022-14
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Gaps

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TYPE: amino a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 2, Apsendence 2, Apsendence 3, Apsendence 18, Apsendence 20, Apsendence 6, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Al
Sequence 4, Al
Sequence 9, Al
Sequence 6, Al
Sequence 10, Sequence 10,
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Sequence 10,
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/ cgn2_6/ptodata/2/laa/5A_COMB.pep:*

// cgn2_6/ptodata/2/laa/5B_COMB.pep:*

// cgn2_6/ptodata/2/laa/6A_COMB.pep:*

// cgn2_6/ptodata/2/laa/6A_COMB.pep:*

// cgn2_6/ptodata/2/laa/PGTUS_COMB.pep:*

// cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

// cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
              5.1.3
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             1 SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                   231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
              GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          US-09-847-539A-6_COPY_59_86
129
                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length
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                                                                                    OM protein
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                                  Sequence 32, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 25, Appl
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 192, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HE DISKette, 3.50 inch, 1.4Mb storage
COMPUTER: HE MSDG Version 6.2
OPERATING SYSTEM: MSDGS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING PAGENT INFORMATION:
NAME: BYGOOKES, A. ANGERS
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US-08-630-822A-62

US-09-005-069-62

US-09-005-069-62

US-09-2812-32

US-08-252-966B-12

US-08-466-277-3

US-09-245-966B-18

S16993-42

PCT-US94-0655-12

US-09-089-593-6

US-08-950-955-4

US-08-950-955-4

US-08-950-925-4

US-08-928-213B-8

US-08-928-213B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 192:
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LENGTH: 344 amino acids
TYPE: amino acid
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Best Local Similarity 55.0
Matches 11; Conservative
                  TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-192
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                     27 KLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                    26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 ASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEER 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 KKQAEEEVKKQAAADAKKKAEEEAKTKAAAAEAKKKAEEEAKAKAAAADAKQKAEEEAK 225
                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=556;
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26.0%; Pred. No. 14;
Live 17; Mismatches 40; Indels
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                                      Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, L2
01-DEC-2001 (TrEMBLrel. 19, L4
ES/130 (FRAGMENT).
ES/130.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                   87 SDALEALADQTDALQSE 103
                                                                                                                                                                                              316 REQMDRLQKVHNAGQED 332
                                                                                                                                     20; Conservative
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                                                                                                                             Local Similarity
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Best Local Similarity
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SEQUENCE FROM N.A.
STRAIN-3937;
                                SEQUENCE FROM N.A.
                NCBI_TaxID-6239;
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TISSUE-HEART;
MEDLINE-93300839; PubMed-7686155;
Rezace M., Isokawa K., Halligan N.L.N., Markwald R.R., Krug E.L.;
"Identification of an extracellular 130-kDa protein involved in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 EKEAEEQRAAAVEREREVEEQRAAAAAAAAAAAAAAAABEKREREEEGRAAAAAAAAA 378
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 KLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAA
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MEDLINE=21342572; PubMed=11448154;
Wan Hulten M.C.W., Mitteveldt J., Peters S., Kloosterboer N.,
Van Hulten M.C.W., Sandbrink H., Lankhorst R.K., Vlak J.M.;
Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.;
"The white spot syndrome virus DNA genome sequence.";
Virology 286:7-22(2001).
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                                                                                                                                                                                                                                                                                                   cardiac morphogenesis.";
J. Biol. Chem. 268:14404-14411(1993).
EMBL: L13973; AAA48557.1:
1 1
SEQUENCE 725 AA; 81051 MW; 24DB5A88670AE900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 76; DB 13;
29.8%; Pred. No. 11;
tive 17; Mismatches 42;
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Matches 25; Conservative
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   Eukaryota; Metazoa;
Archosauria; Aves;
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SEQUENCE FROM N.A.
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                          86 ASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQ 145
                                                                                                                     of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmid K.J., Nigro L., Aquadro C.F., Tautz D.;
"Large number of replacement polymorphisms in rapidly evolving genes
of Drosophila. Implications for genome-wide surveys of DNA
EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DLI;
Takahashi Y., Konishi K., Yoshikawa M.;
Takahashi Y., Konishi K., Yoshikawa M.;
"Cloning and characterization of the gene encoding a hemagglutinin of Streptococcus gordonii Dli.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO29393; BAA97453.1;
InterPro; IPR004089; Chemotaxis.transducer.
InterPro; IPR001899; Chemotaxis.transducer.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 2178 AA; 203507 MW; 75CC27E27F41DA8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus gordonii.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%; Score 78; DB 2; Length 2178; 21.4%; Pred. No. 22; tive 27; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
STREPTOCOCCAL HEMAGGLUTININ.
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
ANONIA3 (FRAGMENT).
CG1910 OR ANONIA3.
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                                                                                                                                                                              146 NVNTLPTTGEESN 158
                                                                                                                                                                                                               347 STSTESSTTTEES 359
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56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petromyzon marinus (Sea lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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MEDLINE-95287814; PubMed-7770000;
Jacobs A.J., Kamholz J., Selzer M.E.;
Jacobs A.J., Kamholz J., Selzer M.E.;
The single lamprey neurofilament subunit (NF-180) lacks
multiphosphorylation repeats and is expressed selectively in
projection neurons.";
Brain Res. Mol. Brain Res. 29:43-52(1995).
Brain Res. Mol. Brain Res. 29:43-52(1995).
InterPro; IPR001664; IF.
InterPro; IRR000333; Tropomyosin.
                                                                                                                                                                                                       9.9%; Score 77; DB 5; Length 310; 22.2%; Pred. No. 3.4; cive 19; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKK 131
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PRIMTS; PR00194; TR0POMYOSIN.
PR051E; PS00226; IF; UNKNOWN. I.
SEQUENCE 1110 AA; 123818 MW; 6558DA73DAF6974C CRC64;
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310
310 AA; 32336 WW; 10CF3F4A40A1E13A CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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23.1%; Pred. No. 13;
Live 24; Mismatches
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polymorphism.";
Genetics 153:1717-1729(1999).
EMBL: AF161729; AAD45733.1; --
Flybase; FBgn0022349; CG1910.
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01-NOV-1996 (TrEMBLrel. 01, Cx
01-MAY-1999 (TrEMBLrel. 10, La
01-JUN-22001 (TrEMBLrel. 17, La
F59A2.6 PROTEIN.
F59A2.6.
Caenorhabditis elegans.
                                                                                                                                                                                                                              Best Local Similarity 22.23
Matches 24; Conservative
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 21; 0
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ilarity 20.5%; Pred. No. 19; Conservative 27; Mismatches
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Matches 19; Conservative
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Best Local Similarity
Matches 23; Conserv
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Q08245;
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                                                                                                                                                                                                                                                                       Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.; "The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 EERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEA 92
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MEDLINE-9642202; PubMed-8824639;
Redriguez-1
Rodriguez-1
Rodrigue
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"An accessory sec locus of Streptococcus gordonii is required for export of GspB and for platelet binding.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY028381; AAL13053.1; -.

SEQUENCE 3072 AA; 285770 MW; 0B148372697CF7F2 CRC64;
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                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                  cell envelope.";
J. Bacteriol. 178:1699-1706(1996).
                                                                                                                                                                                                                                        MEDLINE-96198174; PubMed-8626299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MT-2;
Ramos-Gonzalez I.;
Submitted (JUN-1995)
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                               Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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DB 2; Length 3072;

10.3%; Score 80;

Query Match

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                                                                                            1031 ESASTSASVSASESASTSASVSASTSASTSASVSASESASTSASVSASESASTSASSSAST
                                               47 DKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAE 106
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi, Ascomycota; Saccharomycotaes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                                                                                                                                                                          1091 ESASTSASVSASESASTSASVSASESSSTSASVSASESSSTSASVSASESAS 1142
                                                                                                                                           107 VVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEESN 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 78; DB 3; Length 113; 37.3%; Pred. No. 0.9;
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Indels
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Durand P., Hilger F., Portetelle D., Vandenbol M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases EMBL; 274831; 27489128.1; -. SGD, SO05469; ZEO1. SEQUENCE 113 Aa; 12589 WW; 1EA3634565D517FA CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHROMOSOME XV READING FRAME ORF YOL109W.
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Last sequence update)
Last annotation update)
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62;
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XX SUCHENCE TROWN N.A.

XX SUCHENCE TROWN N.A.

XX STRAIN-C57BL/G3; TISSUB-TESTIS;

XX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XX Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

XX Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XX Alzawa T., Hara A., Fukunishi Y., Bono H., Kasukawa T., Saito R.,

XX Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XX Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XX Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XX Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XX Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

XX Schriml L.M., Marchiona N., Home D.A., Kamiya M., Lee N.H.,

XX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

XX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

XX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

XX Brownstein M.J., Bult C., Fletcher C., Saya T., Shibata Y., Storch K.-F.,

XX Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

XX Sazuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

XX Hayashizaki Y.,

XX Hayashizaki Y.,

XX Hayashizaki Y.,

XX Fletciional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
38 DELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.3%; Score 80; DB 11; Length 274; 29.2%; Pred. No. 1.4; Live 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32075 MW; C810F3986D46B5C2 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                PRT;
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EMBL; AR014981; BABA2656.1; -.
EMBL; AR0149816; BABA4271.1; -.
MGD; MGI:1913982; 4921530L21R1k.
                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, TOLA PROTEIN.
                                                                                                                                      866 DIEGAGATEGAGATEGA 882
                                                                                              98 DALQSEEAEVVQSDNAA 114
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                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Sampei G., Motomura K., Masuda S., Yamaguchi T., Ando K., Oishi T.,
Furuya N., Komano T., Mizobuchi K.;
"Organization and diversification of plasmid genomes: complete
nucleotide sequence of the RV19 genome ";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-11437603; PubMed-11553540;
Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
Song X.M. Perez-Casal J., Bolton A., Potter A.A.;
"Surface-Expressed Mig Protein Protects Streptococcus dysgalactiae
against Phagocytosis by Bovine Neutrophils.";
Infect. Immun. 69:6030-6037(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 81; DB 2; Length 669; ilarity 53.1%; Pred. No. 2.9; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1272 AA; 145804 MW; 30A4839C42519BA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5C8982B952029B03 CRC64;
                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of the R721 shufflon.";
J. Bacteriol. 174:7053-7058(1992).
EMBL; AP002527; BAB12624.1;
                                                                        669 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                     PRT;
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STRAIN-K-12; TRANSPOSON-TN7;
MEDLINE-93015772; Pubmed-1400257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      669 AA; 72682 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                   Streptococcus dysgalactiae.
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 43078;
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                                                                                                                                                                                                                                                                                    NCBI_TaxID-1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1040
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                                                                                                                                                                                        MIG PRECURSOR.
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Best Local S
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Q9F553;
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                        RESULT 27
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Streptococcus.
NCBI_TaxID=1314;
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         STIPPE REPRESSION SOCCES
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                         44 AIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSE 103
                                                                                                                                                                                                                                                     Gaps
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"Large number of replacement polymorphisms in rapidly evolving genes
of Drosophila. Implications for genome-wide surveys of DNA
polymorphism.";
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                                                                                                                                Ouery Match 10.8%; Score 84; DB 9; Length 540; Best Local Similarity 31.9%; Pred. No. 1.1; Matches 23; Conservative 10; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 83; DB 5; Length 310; 23.1%; Pred. No. 0.78; tive 19; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
                                                                                         540 AA; 51936 MW; 450329FFA7A9B09D CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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InterPro; IPR004089; Chemotaxis_transducer.
InterPro; IPR001778; POA_allergen.
PRINTS; PR00308; ANTIFREEZI.
PRINTS; PR00833; POAALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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EMBL; AF16743; AAD45747.1; --
EMBL; AF161725; AAD45729.1; --
EMBL; AF161735; AAD45739.1; --
EMBL; AF161736; AAD45740.1; --
Flybase; FBgn0022349; CG1910.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
ANONIAS (FRAGMENT).
CG1910 OR ANONIAS.
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SEQUENCE
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ZIMBABWE 33;
MEDLINE=Z065669; PubMed=10581279;
Schmid K.J., Nigro L., Aquadro C.F., Tautz D.;
Large number of replacement polymorphisms in rapidly evolving genes of Drosophila. Implications for genome-wide surveys of DNA
polymorphism.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.4%; Score 81; DB 2; Length 558; 1. Similarity 23.5%; Pred. No. 2.4; 23; Conservative 24; Mismatches 51; Indels
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STRAIN-TYPE 19;
Dale J.B., Simmons M., Chiang E., Chiang E.;
Toctavolent group A streptococcal M protein vaccine, ";
Vaccine 0:0-0(1996).
EMBL; U39838; AAA96959:1; -.
InterPro; IPR001899; Gram.pos_anchor.
InterPro; IPR001845; M.repeat.
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310 AA; 32378 MW; FDB7ED985EBCF62F CRC64;
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Last sequence update)
Last annotation update)
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Pfam: PF02370; M; 12.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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EMBL; AF161748; AAD45752.1; -.
FlyBase; FBgn0022349; CG1910.
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Bacteria; Firmicutes; E
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Best Local Similarity
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Gerge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfelifer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berkova D., Botchan M.R., Bouck J., Broktela P., Bolshakov S.,
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R.,
RA Harris N.L., Harvey D., Heinan T.J., Weil M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heinan T.J., Weil M.-H., Ibegwam C.,
A Jalali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Matherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Matrphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mopper P., Pacieb J.M.,
RA Nelson D.R., Naxon K., Nasskern D.R., Pacieb J.M.,
RA Palazolo M., Pittman G.S., Paul B.W., Pollard J., Pull V., Paese M.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                             STRAIN-PADUA/ITALY 15, AND PADUA/ITALY 14;
MEDLINE-20050669 PubMed-10581279;
Schmid K.J. Nigro L., Aquadro C.F., Tautz D.;
Large number of replacement polymorphisms in rapidly evolving genes of Drosophila. Implications for genome-wide surveys of DNA
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                                                                                                                                                                                                                              5; Length 310;
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Matches 25; Conservative 20; Mismatches 63; Indels
                                                                                                                                                                                  310 310
310 AA; 32392 MW; F7657E8CCDA2F81E CRC64;
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01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAR-2001 (TEMBLrel. 16, Last annotation update)
ANON-EST:FELA3 PROTEIN (ANONIA3).
CG1910 OR ANON-EST:FELA3 OR ANONIA3.
                                                                                                                                                                                                                            10.8%; Score 84; DB 5; 23.1%; Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 AA.
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                                                                                               POLYMOLPHISM.
Genetics 153:1717-1729(1999).
EMBL; AF161739; AAD45743:1; -.
EMBL; AF161788; AAD45742:1; -.
FlyBase; FBGn0022349; CG1910.
NON TER.
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinsty K.C., Mu, Weissenbach J., Williams S.M., Woodege T., Worley K.C., Mu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong Y.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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"Large number of replacement polymorphisms in rapidly evolving genes
of Drosophila. Implications for genome-wide surveys of DNA
polymorphism.";
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Viruses; dSDNA viruses, no RNA stage; Caudovirales; Podoviridae;
T77-like phages.
NCBL_TaxID-136084;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL, ARG02590.1; -
INTERPRO'S IPRO00104; Antifreeze_1.
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EMBL, AF161745; AAD45746.1; -.
EMBL, AF161745; AAD45780.1; -.
EMBL, AF161746; AAD45750.1; -.
Flybase; FEGNO022349; CG1910.
SEQUENCE 489 AA; 51587 MW; 85BBFA05060A9FD2 CRC64;
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MEDLINE-20050669; PubMed-10581279;
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EMBL, AE003779; AAF57190.1; EMBL, AF161747; AAD457731.1; EMBL, AF161723; AAD457731.1; EMBL, AF161727; AAD45731.1; EMBL, AF161732; AAD45741.1; EMBL, AF161740; AAD45744.1; EMBL, AF161741; AAD45744.1;
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Best Local Similarity 23.1%;
Matches 25; Conservative 2
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CG1910 OR ANONIA3.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa Arthropoda; Tracheata; Hexapoda; Insecta;
Ephygrota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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CG1910 OR ANONIA3.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
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"Large number of replacement polymorphisms in rapidly evolving genes of Drosophila. Implications for genome-wide surveys of DNA polymorphism.";
Genetics 153:1717-1729(1999).
EMBL. AFIGITA3; AAD45738.1; -.
Flybase; FBgn0022349; CG1910.
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"Large number of replacement polymorphisms in rapidly evolv
of Drosophila. Implications for genome-wide surveys of DNA
polymorphism.";
Genetics 153:1717-1729(1999).
EMBL; AF161733; AAD45737.1;
MOM MEDE.
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             84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKK 131
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01-WAY-2000 (TrEMBLrel. 13, Last sequ
01-WAR-2001 (TrEMBLrel. 16, Last anno
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MEDLINE-20050669; Pubmed-10581279;
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MEDLINE-20050669; Pubmed-10581279;
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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pteryyota: Neoteera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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"Large number of replacement polymorphisms in rapidly evolving genes of Drosophila. Implications for genome-wide surveys of DNA polymorphism.";
polymorphism.";
EMBL; AF161744; AAD45748.1;
Flybase, FBgn0022349; CG1910.
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                                                                                DB 5; Length 310;
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310 310
310 AA; 32408 MW; 0BC43895EAABEE94 CRC64;
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310 AA; 32394 MW; 31C93E6BE9D9059D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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CG1910 OR ANON1A3.
Drosophila melanogaster (Fruit fly).
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MEDLINE-20050669; Pubmed-10581279;
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Best Local Similarity
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nes 25; Conserv
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CG1910 OR ANONIA3.
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Q9U4R0
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STRAIN-AUSTRALIA 5;
MEDLINE-20050669; PubMed-10581279;
MEDLINE-20050669; PubMed-10581279;
MEDLINE-20050669; PubMed-10581279;
"Large number of replacement polymorphisms in rapidly evolving genes of Drosophila. Implications for genome-wide surveys of DNA polymorphism.";
Genetics 153:177-1729(1999).
EMBL; AF161726; AAD45730.1;
FlyBase; FBgn0022349; CG1910.
                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
         Schmid K.J., Nigro L., Aquadro C.F., Tautz D.;
"Large number of replacement polymorphisms in rapidly evolving genes of Drosophila. Implications for genome-wide surveys of DNA polymorphism."; polymorphism."; EMBL: 71729(1999).
EMBL: AF161724; AAD45728.1; FlyBase: FBgn0022349; CG1910.
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                                                                                                                                                                 Gaps
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Last annotation update)
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Best Local Similarity 23.1%;
Matches 25; Conservative 2
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                               Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;

Pteryyota, Neoptera, Endopterygota, Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

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"Large number of replacement polymorphisms in rapidly evolving genes of prosophila. Implications for genome-wide surveys of DNA polymorphisms.";
Genetics 153:1717-1729(1999).
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ANONIA3 (FRAGMENT).
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Flybase; FBgn0022349; CG1910.
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NON_TER 310 310
SEQUENCE 310 AA; 32306 MW;
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MEDLINE-99081771; PubMed-9864244;
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"Identification and molecular analysis of pcsb, a protein required for cell wall separation of group B streptococcus.";
J. Bacteriol. 183:1175-1183(2001).
EMBL: AJ277292; CAC28144.1: -.
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MEDLINE-94192673; PubMed-8143736;
Jonsson H., Mueller H.-P.;
"The type-III Fc receptor from Streptococcus dysgalactiae is also an
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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01-JUN-2001 (TTEMBLEEL. 17, Last annotation update)
IMMUNOGLOBIN G BINDING PROTEIN MIG PRECURSOR (IGG BINDING PROTEIN
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Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
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                                                                                                              90 LEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKD 134
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PCSB PROTEIN.
F4DB14B0A5F962C8 CRC64;
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Eur. J. Biochem. 220:819-826(1994).
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01-JUN-2001 (
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FUNCTION.
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SIGNAL
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SIMILARITY:

SIMILARITY:

THE REGION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER

THE REGION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER

STREPTCCCCCAL TYPE-III FC RECEPTORS.

REMBL, 229666; CAA82764; 1:

RISP: P06654; 1PGX.

RICEPTO: IPRO00748; 1gG_bind_B.

RICEPTO: IPRO00751; TonB_boxC.

DR Pfam: PP00746; Gram_pos_anchor: 1.

Pfam: PP00746; Gram_pos_anchor: 1.

PRM: PROSITE; PS00343; GPOSANCHOR.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

BR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

RESIDENT RECETAL SIGNAL STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD
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2-5.
6 X 5 AA REPEATS OF [DEVP]-[DE]-|AT]-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Vasi J., Svensson J., Frick I.-M., Mueller H.-P.;
"Five homologous repeats of the protein G-related protein MIG cooperate in binding to goat immunoglobulin G.";
Infect. Immun. 67:413-416(1999).
-1- FUNCTION: BINDS TO THE CONSTANT FC REGION OF IGG WITH HIGH AFFINITY. N-TERMINUS MEDIATES BINDING TO PLASMA PROTEINASE INHIBITOR ALPHA 2-MACROGLOBULIN AFTER COMPLEX FORMATION WITH
                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBIN G BINDING PROTEIN MIG
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MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
Z X 24 AA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-2.
5 X 70 AA TANDEM REPEATS
(IGG CONSTANT REGION-BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA 2-MACROGLOBULIN-BINDING
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Last annotation update)
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Q1 MAX-2000 (TrEMBLrel. 13, Created)
Q1-MAX-2000 (TrEMBLrel. 13, Last sequen
Q1-MAR-2001 (TrEMBLrel. 16, Last annott
ANOMIA3 (FRAGMENY)
CG1910 OR ANOMIA3.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638
659
664
1110
1189
558
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488
558
621
635
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Best Local Similarity
Matches 18; Conserv
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STRAIN-AUSTRALIA 2;
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                                                                                                                                                                                                                                                                                      PROTEASES
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN-NG1;

Nyitray L., Farkas L., Nagy A., Kovacs M., Nakamura A., Kohama K.;

"Cloning of the major plasmodial myosin II of Physarum polycephalum.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF335500; AAK17202.1; -.

REMBL; AF335500; AAK17202.1; -.

RISSP; P08799; LMMD.

RICEPPO: JPR001069; Myosin_head.

RICEPPO: JPR001609; Myosin_head.

RICEPPO: JPR001609; Myosin_head; 1.

Remm: PF00736; Myosin_head; 1.

Remm: PF00736; Myosin_head; 1.

Remm: PR00136; Myosin_head; 1.

Remm: PR00136; Myosin_head; 1.
                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
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                                                                                                                                                                                                                                                                   STRAIN-Y, CN BW SP,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewisis S.E., Rubin G.M., Celniker S.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY060997; AAL28545.1; --
SEQUENCE 619 AA; 68641 MW; 7DDCB26ADIAB9CEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Physarum polycephalum (Slime mold).
Eukaryota, Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 90; DB 5; Length 619; 29.4%; Pred. No. 0.3; ative 16; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00015; 1Q; 2.
SMART; SM00242; MYSC; 1.
SEQUENCE 2148 AA; 246972 MW; F12D4DD67F5ECA0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR PLASMODIAL MYOSIN HEAVY CHAIN.
                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 ASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AAQKVAEEAAQKAAEEARLAEEAAAQKAAEEAAQKAAEEAAL
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Best Local Similarity 29.4%
Matches 30; Conservative
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Best Local Similarity 24.88
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5791;
                                                                                             HL01392P.
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Q9BJD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                169 EALNSKOAAAGSEANAKASENAAAASQQAAATSESNARASKEAAAASQTAALQSEQVAAA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N. Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Hollroyd S., Jagels K., Chrogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica servora Typhi (TTH8."; Mature 413:848-852(2001).
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                                                                                                                                                                                                                                                                                        Query Match 13.4%; Score 104; DB 2; Length 850; Best Local Similarity 34.6%; Pred. No. 0.014; Matches 28; Conservative 12; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-94259307; PubMed-7515368;
Jonsson H., Frykberg L., Rantamaeki L., Guss B.;
Jonsson H., Frykberg L., Rantamaeki L., Guss B.;
"MAG, a novel plasma protein receptor from Streptococcus dysgalactiae.";
Gene 143:85-89(1994).
EMBL: 127798; AAA26921.1; -.
HSSP: P06654; 1PGX.
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                                                                                                                                                                                                                                                     850 AA; 90917 MW; 21271493A07A6563 CRC64;
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Last annotation update)
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InterPro: IPR001899; Gram_pos_anchor.
InterPro: IPR001899; Gram_pos_anchor.
InterPro: IPR00184; IgG_bind_B.
Pfam; PF01468; GA; I.
Pfam; PF01378; IgG_binding_B; I.
PR01378; IgG_binding_B; I.
PR0157FE; PS00313; GFOSANCHOR.
Signal; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 HADSAKSEAEKAKKFADLLDV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 OSDNAASDAWEKAATPIALDV 129
                                                                                                                                                                                                  EMBL; AL513384; CAD09918.1; -. Plasmid.
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Matches 19; Conservative
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STRAIN-CT18;
MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungail K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKA 121
                             Gaps
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                                                                                                                                                                                                                                                                                                                                                "Isolation and molecular characterization of a novel albumin-binding
                                                                                                                                                                                                                              Streptococcus canis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
NCBL_TaxID=90370;
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0
                                                       1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAA
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     Length 103;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE PHAGE TAIL PROTEIN.
PUTATION DISC.
Salmonella enterica subsp. enterica serovar Typhi.
Plasmid pHCM2.
                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALBUMIN-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                         protein from group G streptococci.";
Infect. Immun, 60:3601-3608(1992).
BMBL; M95520, M9542847.1;
INTERPO: IPRO02988; GA.
InterPro: IPRO01999; Gram_pos_anchor.
Pfam; PF01468; GA; 2.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
  18.3%; Score 142; DB 2; 57.9%; Pred. No. 1.3e-07; ive 3; Mismatches 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.2%; Score 126; DB 2; 42.6%; Pred. No. 2.2e-05; iive 14; Mismatches 21
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MEDLINE-92363555; PubMed-1500168;
Sjobring U.;
                             33; Conservative
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              Best_Local Similarity
Matches 33; Conserv
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"Expression and purification of a truncated recombinant streptococcal
                                                                                                                                                                                                                                                                          **Resmussen M., Muller H.P., Bjorck L.;
**Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2 macroglobulin.";
J. Biol. Chem. 274.15336-15344(1999).
EMBL. AF144402; AAD26341.1; --
InterPro; IPR001899; Gram_pos_anchor.
PR051TE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 239;
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Blochem. J. 267:171-177(1990),
EMBL: X53224; CAA37409.1; -,
SEQUENCE 103 AA; 10828 MW; E7AEE8DIC073423C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                24846 MW; 61AC4F6F863AF0F5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                 Last sequence update)
Last annotation update)
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Pred. No. 6.2e-49;
4; Mismatches 6;
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MEDLINE-99269061; PubMed-10336419;
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MEDLINE-90226312; Pubmed-2183792;
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91.8%;
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Matches 112; Conservative
                                                                                            PRELIMINARY;
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Q9X5C5;
01-NOV-1999 (TrEMBLrel.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                  Streptococcus.
NCBI_TaxID=1314;
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NCBI_TaxID=1320;
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121 AA 122
                         LA 122
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Q54180;
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61 ALEALADQTDALQSEBAAVVKADNAASDALEALADQTDALQSEBAEVVQSDNAASDAWEK 120
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Rasmussen M., Muller H.P., Bjorck L.;
"Protein GRAB of Streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin.";
J. Biol. Chem. 274:15336-15344(1999).
EMBL. ARI244403; AAD26342.1;
InterPro: IPR001899; Gram.pos.anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNRNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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. 4.3e-49; Indels
                                                                                                                                                                                                                                                                                                         Score 754; DB 2; Length 15
Pred. No. 1.5e-72;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                         16587 MW; 19FAA98D0599D866 CRC64;
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27744 MW; 1C59239260CDC7E7 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                 Rasmussen M., Muller H.P., Blorck L.;
"Protein GRAB of streptococcus pyogenes regulates bacterial surface by binding alpha2-macroglobulin. J. Biol. Chem. 274:15336-15344(1999).
EMBL; AF12440. AAD26339.1; --
InterPro; IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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2; Mismatches
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                                                                                                    MEDLINE=99269061; PubMed=10336419;
                                                                                                                                                                                                                                                                                                         Query Match 97.0%;
Best Local Similarity 99.4%;
Matches 155; Conservative
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Matches 113; Conservative
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156 AA;
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                                                                 SEQUENCE FROM N.A.
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                                 NCBI_TaxID=1314;
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SEQUENCE
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MEDLINE-99569061; PubMed-10336419;
Rasmussen M., Muller H.P., Bjorck L.;
Rasmussen M., Muller H.P., Bjorck L.;
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin.";
J. Blol. Chem. 274-15336-1534(1999).
EMBL: AF124401; AAD26340.1; -
InterPro; IPR001899; Gram_pos_anchor.
PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                    Gaps
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                                                                                                                    VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                    ;
                                                   Length 217;
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                                                                                    Indels
GRAB.
: 79AA8C4FF5F3FA06 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GRAB (FRAGMENT).
                                                 ; Score 777; DB 16;
; Pred. No. 7.9e-75;
0; Mismatches 0;
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Pred. No. 3.6e-73;
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                                                                                                                                                                                                                                                                                                                                                                                  156 AA
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Matches 156; Conservative 0; Mismatches
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                                               Query Match
Best Local Similarity 100.0
Matches 159; Conservative
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34 :
217 AA;
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SEQUENCE FROM N.A.
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CHAIN
SEQUENCE
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Q9S6G4;
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Length 268;

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October 13, 2002, 01:14:06; Search time 70.5722 Seconds (without alignments) 389.760 Million cell updates/sec
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777
1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
                                                                                        OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                  Scoring table:
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sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_human:*
sp_manmal:*
sp_mor:*
sp_organelle:* sp_vertebrate:* sp_unclassified:* sp_rvirus:*
sp_bacteriap:* sp_archeap: sp_rodent:* sp_plant: * sp_virus:* SPTREMBL_19:* Database

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

098694 streptococc 098693 streptococc 0985c6 streptococc 054180 streptococc 053900 streptococc 0935b1 salmonella 053974 streptococc 095818 drosophila 09b445 drosophila 09u445 drosophila 09u445 drosophila Q9x5c4 streptococc Description SUMMARIES 09563 098566 098566 098180 093390 093581 095394 095518 053975 0904R5 0904R4 0904R3 Query Match Length DB 100.0 97.8 697.0 687.0 688.7 118.3 111.6 111.6 111.5 111.5 111.5 111.5 110.8 Score Result . 02

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09u4r0 drosophila 09u4q9 drosophila 09u4q9 drosophila 09u4q7 drosophila	0979u3 drosophila 09g0h8 roscophago 09tw87 drosophila 09u4q6 drosophila	7	0939n5 streptococc 008245 saccharomyc 09Kj3 enterococcu 09Kwr3 streptococc 09U4r2 drosophila	091255 petromyzon 021022 caenorhabdi 0937k4 erwinia chr 007718 gallus gall 0911f6 white spot	
5 Q9U4R0 5 Q9U4Q9 5 Q9U4Q8 5 Q9U4Q7 5 Q9T4G2		2 093EM8 2 09F553 11 09C047 2 09WWX1	2 0939N5 3 008245 2 09KJJ3 2 09KWR3 5 09U4R2	13 091255 5 021022 2 0937K4 13 007718 12 091LF6	11 099JX1 10 09C8J7 13 09DGL1 5 09NDI9 2 09LCH2
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ALIGNMENTS

RESULT 1

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TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                          COMPUTRY: U.C.

COMPUTRY: U.C.

COMPUTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTRY: IBM PC compatible

CLASSIFTCATION: S14

PRIOR APPLICATION NUMBER: 29,768

FILING DATE: 28-5EP-1993

ATTORNEY AGENT INFORMATION:

NAME: BENT, Stephen A.

RESISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 51916/104/INBI

TELEPHONE: (202)672-5399

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Lawrence Rajendra
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Best Local Similarity 24.2%
Matches 37; Conservative
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US-08-482-847-23
SHARMA,
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                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08127499A
Patent No. 5510264
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CORRESPONDENCE SEQUENCES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.6%; Score 90; DB 1; Length 695; Best Local Similarity 24.2%; Pred. No. 0.89; Matches 37; Conservative 23; Mismatches 61; Indels
                                                ----VKADNAASDALEALADQTDALQSEEAEVVQSDNAA-
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTONREY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAN: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                           115 -- SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
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332 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 364
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
LIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/08482847 Patent No. 5556757 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEO ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown US-08-127-499A-23
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APPLICANT: WI, Hong-Yin
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION OF
TITLE OF INVENTION: PMUNOCCCAL SURFACE PROTEIN A (PSPA)
TITLE OF INVENTION: PNEUMOCCCAL SURFACE PROTEIN A (PSPA)
FILE REFRENCE: 454312-2018
CURRENT APPLICATION NUMBER: 08/312,949
EARLIER PILING DATE: 1994-05-30
EARLIER PILING DATE: 1994-06-30
EARLIER PILING DATE: 1994-06-20
EARLIER PILING DATE: 1994-06-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-02-15
EARLIER FILING DATE: 1991-02-15
EARLIER FILING DATE: 1991-02-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%; Score 90; DB 3; Length 648; 24.2%; Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%; Score 90; DB 2; 24.2%; Pred. No. 0.81; iive 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 32,147
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
23-JUN-1994
23-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08446201B Patent No. 6042838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptococcus pneumoniae US-08-446-201-3
                                                                                                                                                                                                                                                                                                                               LENGTH: 648 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 24.29
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                      APPLICATION NUMBER:
FILING DATE: 23-JUN
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TY
US-08-247-491A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-446-201-3
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LENGTH: 648
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Suite 1203, 2001 Jefferson Davis Highway
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,068
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08247491A Patent No. 5965400 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-468-718-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                           Virginia
                                                             COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                        FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
                                                                          Sequence 2, Application US/08467852A
Patent No. 5856170
GENERAL INFORMATION:
APPLICANT: BRILES, David E.
APPLICANT: WOTHER, Janet L.
APPLICANT: WORNIEL, LAIRY S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Indels
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER RELABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/467,852A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Shoemaker and Mattare, Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.6%; Score 90; DB 2; Best Local Similarity 24.2%; Pred. No. 0.81; Matches 37; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : !! : !: 1: 322 320 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
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; Sequence 2. Application US/08468718
: Patent No. 5871943
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 648 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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STATE: N'
                                                        US-08-467-852A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
TITLE OF INDUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: FROMMER LAWRENCE & HAUG LLP
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.6%; Score 90; DB 2; Best Local Similarity 24.2%; Pred. No. 0.81; Matches 37; Conservative 23; Mismatches
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DB 1; Length 648;

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Query Match
Best Local Similarity
Matches 37; Conserv
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CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                    24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
                                                                                                                                                                                                                                     32;
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                                                                                                                                                                                       Query Match 11.6%; Score 90; DB 1; Length 648; Best Local Similarity 24.2%; Pred. No. 0.81; Matches 37; Conservative 23; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08469434
Patent No. 5753463
GNEBAL INFORMATION:
GNEBAL INFORMATION:
GNEBAL INFORMATION:
GNEBAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Briles, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,434
                                                                                                                                                                                                                                                                                                                                                                                                                                              115 --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,065
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SD ID NO: 2:
SEQUENCE CHARACTERISTICS:
TELEX: LUKPAT WASHINGTON INFORMATION FOR SEQ ID NO: 2:
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 648 amino acids TYPE: amino acid
                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-072-070-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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US-08-469-434-2
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                                                                                                  24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
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                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%; Score 90; DB 1; Length 648; illarity 24.2%; Pred. No. 0.81; Conservative 23; Mismatches 61; Indels
                                                                                                                                                                                                    --VKADNAASDALEALADQTDALQSEEAEVVQSDNAA-
                                                   61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Briles, David E
APPLICANT: YOTHER, Janet L
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1,25
11.6%; Score 90; DB 1; 24.2%; Pred. No. 0.81; iive 23; Mismatches
                                                                                                                                                                                                                                                                                                 115 --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
                                                                                                                                                                                                                                                                                                                                290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,222
FILING DATE: 17-MAR-1994
CLASSIFFCATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08214222
Patent No. 5804193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 415-0810
TELERAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
                                                   37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-08-214-222-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 37; Conserval
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230 ESEDYAKEGFRAPLOSKLDAKKAKLSKLEELSDKIDELDAEIAKLEDQLKAAEENNNVED 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,070
FILING DATE: 19930603
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDanlel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.6%; Score 90; DB 3; Best Local Similarity 24.2%; Pred. No. 0.76; Matches 37; Conservative 23; Mismatches
                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2049
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 840-3333
TELEFAN: (212) 840-312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 619 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : || : |: || : |: | 322
                         APPLICATION NUMBER: US/08/312,949
FILING DATE: 30-SEP-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08072070 Patent No. 5476929 GENERAL INFORMATION:
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TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 521-0378
          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-312-949-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-072-070-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 ESEDYAKEGFRAPLOSKLDAKKAKLSKLEELSDKIDELDAEIAKLEDQLKAAEENNNVED 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08312949 .

Patent No. 6027734 .

GENERAL INFORMATION:

APPLICANT: Bulles, David E.

APPLICANT: Wu, Hong-Yin

TITLE OF INVENTION: PNEUMOCOCCAL ANTIGENS

TOWNERS OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 11.6%; Score 90; DB 2; Best Local Similarity 24.2%; Pred. No. 0.76; Matches 37; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Curtis, Morris & Safford, P.C.
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : || : |: || 290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
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                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US 08/246,636
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,896
FILING DATE: 20-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTER: SEGUES:
TEMPORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTER: SEGUES:
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 619 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-468-985-2
                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-312-949-2
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24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
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Patent No. 5997882
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Yother. Janet. L.
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: Epitopic Regions of Pneumococcal Surface
TITLE OF INVENTION: Protein A
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.6%; Score 90; DB 2; Length 619;
Best Local Similarity 24.2%; Pred. No. 0.76;
Matches 37; Conservative 23; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sheomaker and Mattare, Ltd.
STREET: 1203 Crystal Plaza Bldg. 1, 2001 Jefferson
STREET: Davis Highway
                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
                                                                                                                                                                                                                                           PILING DATE:
CLASSFEICATION ATE:
CLASSFEICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,636
FILING DATE: 20-MAY-1994
PRIOR APPLICATION UNMBER: US 08/048,896
FILING DATE: 20-APR-1993
PRIOR APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US 07/656,773
APPLICATION NUMBER: US 07/656,773
                                                                                                                                                                                               SOFIWARE: FACEULIN RELEASE #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/319,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 619 amino acids
                                     STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-319-795-2
                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                     Arlington
                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
US-08-468-985-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VKADNAASDALEALADQTDALQSEEAEVVQSDNAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Yother, Janet L.
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: Epitopic Regions of Pneumococcal Surface
TITLE OF INVENTION: Protein A
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheomaker and Mattare, Ltd.
STREET: 1203 Crystal Plaza Bldg. 1, 2001 Jefferson
                                                                                                                   APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
UNMER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 619;
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/247,491A

FILING DATE: 23-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 90; DB 2; ilarity 24.2%; Pred. No. 0.76; Conservative 23; Mismatches
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                                                                                                                                                                                                                       ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STRET: 745 Fifth Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454312-2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08247491A Patent No. 5965400 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08319795
Patent No. 5980909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: amino acid
US-08-247-491A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                              USA
                                  US-08-247-491A-3
                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-319-795-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                       APPLICANT: McDaniel, Larry S
APPLICANT: Wu, Hong-Tin
TITLE OF INVENTION: EPITOPIC REGIONS OF PNEUMOCOCCAL SURFACE
TITLE OF INVENTION: PROTEIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              S: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.6%; Score 90; DB 3
Best Local Similarity 24.2%; Pred. No. 0.76,
Matches 37; Conservative 23; Mismatches
                                                                                     290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
                                                            115 -- SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/656,773
FILING DATE: 15-FEB-1991
PRIOR APPLICATION NUMBER: 05 07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 08/048,896
FILING DATE: 20-APR-1993
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/246,636 FILING DATE: 20-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    Sequence 2, Application US/08246636
Patent No. 5965141
                                                                                                                                                                                                                     atent No. Syour.
GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: LUKPAT WASHINGTON INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-246-636-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite 12
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                                                                                      80 ------VKADNAASDALEALADQTDALQSEEAEVVQSDNAA----- 114
                                                                                                                                                                                                                                                                                      ------VKADNAASDALEALADQTDALQSEEAEVVQSDNAA----- 114
                                                                                                                                                                               24 APEKLALRNEERA-IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAV--- 79
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                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
APPLICANT: WCDANIEL, Larry S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 11.6%; Score 90; DB 2; Length 619; I Similarity 24.2%; Pred. No. 0.76; 37; Conservative 23; Mismatches 61; Indels
                                                                                                                                          61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/467,852A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                       Pred. No. 0.76;
                                                                                                                                        23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
                                                                                                                                                                                                                                                                                                                                            115 --SDAWEKAATPIALDVKKTK-DTKPVVKKEER 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2064
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                    Score 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08467852A Patent No. 5856170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                  11.6%;
24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 745 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 619 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: amino acid
                                                                                                                     Best_Local Similarity 24.29
Matches 37; Conservative
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                                   ; MOLECULE TYPE: protein US-08-214-164-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TYPE: amino acid
TOPOLOGY: linear
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Matches 37; Conserv
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                                                                                                  Query Match
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80 .....VKADNAASDALEALADQTDALQSEEAEVVQSDNAA----- 114
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Patent No. 5728387
GENERAL INFORMATION:
APPLICANT: BRILES, DAVID E.
APPLICANT: YOTHER, JANET L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCCOCCAL PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.6%; Score 90; DB 1; Length 619; Best Local Similarity 24.2%; Pred. No. 0.76; Matches 37; Conservative 23; Mismatches 61; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,164
FILING DATE: 17-MAR-1994
CLASSIFICATION: A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W.
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 22,651
TELECOMMUNICATION NUMBER: 6102-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 YFKEGLEKTIAAKKAELEKTEADLKKAVNEPEK 322
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                                                              US 07/835,698
                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/835,
FILING DATE: 12-FEB-1992

TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 415-0810

TELEPAX: (703) 415-0810

TELEPAX: (703) 521-0378

TELEPX: LUKPAT WASHINGTON:
SEQUENCE CHARACTERISTICS:
LENGTH: 619 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
TYPE: amino acids
TYPE: protecin
US-08-465-746-2
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TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 amino acids
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CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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US-08-214-164-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08465746

Patent No. 5679768

GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: WCDAniel, Larry S
TITLE OF INVENTION: EPITOPIC REGIONS OF PNEUMOCOCCAL SURFACE
TITLE OF INVENTION: PROTEIN A
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shite 1203, 2001 Jefferson Davis Highway
CITY: ARIINGIAN
STREET: Suite 1203, 2001 Jefferson Davis Highway
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ---AIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.6%; Score 90; DB 1; Length 190;
Best Local Similarity 31.0%; Pred. No. 0.16;
Matches 36; Conservative 15; Mismatches 45; Indels
                                                                 COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,981
FILING DATE: 16-AUG-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 163-23
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 2202-0286

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Protein
ORIGINAL SOURCE: Triticum Aestivum L.
US-08-106-981-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/048,896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
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                                      3Y: U.S.A.
22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-465-746-2
                               COUNTRY:
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369 VLRELKPAVASADAVEAAAAELTA-QAEEAANAKWEADKAEAAEKARAEA-EAAAEGOKA 426
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                                                                                                                                                                                                                                                  57 -----ADNAASDALEALADQTDALQSEEAAVVK-----ADNAASDALEALADQTDA 99
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                                                                                                                                                                                                                                                                                                                                          100 LQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPV-VKKEERQNVNTLP 151
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                                                                       DB 4; Length 527;
                                                                                                                 Indels
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APPLICANT: SARHAN, Fathey
APPLICANT: HOUDE, Mario
APPLICANT: HOUDE, Mario
TITLE OF INVENTION: TOLERANCE PROTEINS IN GRAMINEAE
ITILE OF INVENTION: TOLERANCE PROTEINS IN GRAMINEAE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08745404B
Patent No. 6096717
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts And Proteins
FILE REFERENCE: 2087-961422
CURRENT APPLICATION NUMBER: US/08/745,404B
CURRENT FILING DATE: 1996-11-08
EARLIER APPLICATION NUMBER: 08/000,619
EARLIER FILING DATE: 1993-01-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 90.5; DB 27.2%; Pred. No. 0.59; tive 22; Mismatches
                                                                   Query Match 11.6%; Score 90.5; DB Best Local Similarity 27.2%; Pred. No. 0.55; Matches 47; Conservative 22; Mismatches
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Patent No. 5731419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.2%
Matches 47; Conservative
  FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Chlamydomonas
US-08-745-404-3
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LENGTH: 552
TYPE: PRT
         , FRAGMENI I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 LLEELAA----TAAAEAEERGEEPPAEPPSLPDGVEPVDVEAEVAKAVEAVP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 RAIDELKKQA-----IEDKEATTA--------IEA----
                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 90.5; DB 2; Length 527; 27.2%; Pred. No. 0.55; tive 22; Mismatches 41; Indels 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-320-774-9

Sequence 9, Application US/09320774

Patent No. 6265545

GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/320,774
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Harris Brotman
STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla
STATE: Callfornia
APPLICATION NUMBER: US/08/762,106
FILING DATE: 09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
FILING DATE:
                                                       ATTORNEY AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 9;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  LENGTH: 527 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 527 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                               47; Conservative
                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-762-106-9
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| :| :| :| :| 298 RVVDKLVEDAAAALAANRSTIADKAASTAATVDAWAERQAKMEAELQGKELEAVRRRPTF 357
                                                                                                                                                                                                                                                                                                                                              298 RVVDKLVEDAAAALAANRSTLADKAASTAATVDAWAERQAKMEAELQGKELEAVRRRPTF 357
                                                                                                                                                                                                                                                                                                                                                                                      57 ------ASSDALEALADQTDALQSEEAAVVK------ADNAASDALEALADQTDA 99
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                                                                                                                                                                                                                                                             41; Indels 63;
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                                                                                                                                                                                                                  Query Match 11.6%; Score 90.5; DB 2; Length 516; Best Local Similarity 27.2%; Pred. No. 0.54; Matches 47; Conservative 22; Mismatches 41; Indels 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 90.5; DB 3; Length 516; 27.2%; Pred. No. 0.54; tive 22; Mismatches 41; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08745404B
Patent No. 6096717
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts And Proteins
FILE REFERENCE: 2087-961122
CURRENT APPLICATION NUMBER: US/08/745,404B
CURRENT FILING DATE: 1996-11-08
EARLIER APPLICATION NUMBER: 08/000,619
EARLIER FILING DATE: 1993-01-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-320-774-8

Sequence B, Application US/09320774

Patent No. 626545

GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE

TITLE OF INVENTION: TAGGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 RAIDELKKQA-----IEDKEATTA----
                                                                                                                                                                                                                                                                                                      35 RAIDELKKQA------IEDKEATTA----
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Conservative
                                                                                                                         ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-762-106-8
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CORGANISM: Chlamydomonas
US-08-745-404-2
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Best Local Similarity
                                                                                                             linear
                                                                                                         TOPOLOGY:
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LENGTH: 516
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358 VLRELKPAVASADAVEAAAAELTA-QAEEAANAKWEADKAEAAEKARAEA-EAAAEEQKA 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 LQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPV-VKKEERQNVNTLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 90.5; DB 4; Length 516; 27.2%; Pred. No. 0.54; Live 22; Mismatches 41; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEORGE 9. Application US/08762106
Sequence 9. Application US/08762106
GENERAL INCORAGITON:
APPLICANT: Jarvik, Jonathan W.
TILLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: La Jolla
STREET: California
STREET: California
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                               Suite 111
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/320,774
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brotman, Harris F. REGISTRATION NUMBER: 35,461 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
TYPE: amino acids
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harris Brotman
STREET: 202 COAST Blvd., 5
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                        STREET: 202 COASE CITY: LA JOLIA STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOC ACCURRENT PROCESSOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 TDATVKAGTDAKAKAEKADNILT 228
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NAME: Brotlman, Harris F.
REGISTRATION NUMBER: 35.461
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-762-106-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 GTLTNLLGNA----PEKLALRNEERAIDELKKQAIE-DKEATTAIEAA--SSDALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
US-08-591-09-10
Sequence 10, Application US/08591079
Sequence 10, Application US/08591079
GENERAL INFORMATION:
APPLICANT: Zychlinksky, Arturo
TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 91; DB 2; Length 593; 28.7%; Pred. No. 0.58; tive 20; Mismatches 70; Indels
                                                                        APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Livrat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 1561-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSWH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acids
              Sequence 8, Application US/08591079
Patent No. 5972899
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 LDVKKTKDTKPVVKKEERQNVNT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 TDATVKAGTDAKAKAEKADNILT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.7%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-591-079-8
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
US-08-591-079-8
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67 DQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08762106
Patent No. 5948677
GENERAL INFORMATION:
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harris Brotman
STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.7%; Score 91; DB 2; Length 593
Best Local Similarity 28.7%; Pred. No. 0.58;
Matches 41; Conservative 20; Mismatches 70; Indels
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUUTER: Ploppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN RE-BASE #1.0, Version #1.30
CURRENT APPLICATION DAYR:
APPLICATION NUMBER: US/08/591,079
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SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWAN APPLICATION DATA:
APPLICATION NUMBER: US/08/762,106
FILING DATE: 09-DEC-1996
                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 1561-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELERAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 10:
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---AEVVQSDNAASDAW 118
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                                                                                                                                                                                                                             : || : || :|| :|| | :|| | :|| | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| 
Gaps
                                                                                                                     226 EKLAAAKETAKKHIDELKHLADKTKELAKRDIDSATTIDAINDIVARADVMERKLSEKET 285
                                                                                                                                                                                   72 LQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDV-- 129
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                                                             26 EKLALRNE--ERAIDELKKQAIEDKE-----ATTAIEA-----ASSDALEALADQTDA 71
   33;
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59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rubinfeld, Bonnee
APPLICANT: Polakis, Paul G.
APPLICANT: Ligenfelter, Carol
APPLICANT: Usong, Terilyn T.
TITLE OF INVENTION: MODULATORS OF BRCAL ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 91.5; DB 2; 23.3%; Pred. No. 0.81; tive 30; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------KKTKDTKPVVKKEERQNVNTLPTTGE 155
                                                                                                                                                                                                                                                                                                                                                                         342 KGLTLNIKFAGKKEKPEEP--KEEVTIKVNLIFADGK 376
   23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 QSEEAAVVKADNAASDALEALADQTDALQSEE---
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NAME: Glotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: 0NEXI
TELECOMUNICATION INFORMATION:
TELEPHONE: (510) 262-8710
TELEFRA: (510) 262-9758
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 835 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-968-751-4
; Sequence 4, Application US/08968751
; Patent No. 5948643
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   42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
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Best Local Similarity
Matches 37; Conserva
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STREET: 302.
TTTY: Richmond
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COUNTRY: US.
ZIP: 94806
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Trotter, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
                                                                                                                                                                                                                                                                                                        11.9%; Score 92.5; DB 4; Length 472; 22.2%; Pred. No. 0.3; tive 36; Mismatches 72; Indels 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AEKOKAAEATKVAEAEKOKAAEATKVAEAEKOK 370
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NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4901
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08446137B Patent No. 6162903
         TELEX: 904136
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 472 amino acids
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26.8%;
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                                                                                                                        : 472 amino acids
amino acid
GY: linear
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Best Local Similarity 22.28
Matches 34; Conservative
(202)672-5399
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                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-115-746-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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CITY: Seattle
STATE: Washington
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Best Local Similarity
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   TELEFAX:
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Ouery Match 11.9%;
Best Local Similarity 22.2%;
Matches 34; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-216-894-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: | :| | ::| | :|| 324 EESKKLTEKEKAELQAKLEAE--AKALKEQL-AKQAEELAKLRAGKASD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------VVKKEERQNVNTLPTTGEESNP 159
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Sequence 10, Application US/08216894

GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                  GENERAL INFORMATION:
APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                                                                                                                                                                                                                                                 STATE: Washington
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
SOFTWARE: PAtentin Release #1.0, Version #1.30
SOFTWARE: PAtentin Release #1.0, Version #1.30
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: US/08/795,475
FILING DATE: 11-FEB 1997
CLASSIFICATION NUMBER: US/08/795,475
FILING DATE: 11-FEB 1997
CLASSIFICATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.402D1
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: MANA and no acids
TYPE: amino acids
                                                                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.0%; Score 93; DB 2; Best Local Similarity 25.0%; Pred. No. 0.25; Matches 44; Conservative 27; Mismatches
US-08-795-475-6
; Sequence 6, Application US/08795475
; Patent No. 5965390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 LDVKKTKDTKP-------
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COMPUTER READABLE FORM:
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56 AASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAAS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%; Score 92.5; DB 2; Length 472; 22.2%; Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: Z4-MAR-1994
ATTORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 85326/102/DRLO
FELEPHONE: (2020/672-5300
TELEPHONE: (2020/672-5300
TELERX: (202)/672-5399
TELEX: (202)/672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 DAWEKA--ATPIA-LDVKKTKDTKPVVKKEERQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 AEKQKAAEATKVAEAEKQKAAEATKVAEAEKQK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 COLTY: Washington, D.C. ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
TITLE OF INVENTION: POLYEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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----LADAAEKTSRI 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 GAYVISTLIAEKLDGLKNSEELKEKIE----DAKKCNKAFTDKLKSSHAELGIANGAATD 154
                                                                                --- QTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAA-- 122
                                     102 GGIISSALGILGSFAAMNNAAKGAGEIAEKASSASSKAAGAASEVANKALVKATESVADV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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14 GGTLTNLLGNAPEKLALRNEERAIDEL--KKQAIEDKEATTAIEAASS---DALEALAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.0%; Score 93; DB 1; Length 212; 28.0%; Pred. No. 0.094; tive 30; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lym
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AWEKAATPIALDVKKTKDTKPVVKKE-ER--QNVNTLPTTGEES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,353
FILING DATE:
CLASSIFICATION: 435
(TTORNEY/AGENT TWILL)
                                                                                                                                                                                         123 TPIALDVKK-TKDTKPVVKKEERQNVNTLPTTGEES 157
                                                                                                                     162 AEEASSAMOKAMATTTKAASRASGVADDVAKATDFAED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UCT93-05
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08158353 Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CATTOIL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT
TELECOMMUNICATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617-861-9540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-158-353-2
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                                                                                                                                                                                                                                                                                             US-08-158-353-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Finlay, B. Brett
APPLICANT: Finlay, B. Brett
APPLICANT: Stein, Markus
TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN
FILE REFERENCE: 07422/01901
CURRENT APPLICATION NUMBER: US/09/171,517B
CURRENT FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: PCT/CA97/00265
PRIOR APPLICATION NUMBER: PCT/CA97/00265
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1996-04-23
NUMBER OF SEO ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 11
LENGTH: 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Score 95.5; DB 4; Length 312; 27.6%; Pred. No. 0.09; tive 20; Mismatches 70; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.0%; Score 101; DB 2; Length 900; Best Local Similarity 25.3%; Pred. No. 0.11; Matches 41; Conservative 34; Mismatches 65; Indels
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          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,069
                                                                                                                                                                                                                                                                                                                                     2618-17-C3
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                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,822
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMULICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-005-069-62
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US-09-171-517B-11
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ZIP: 80203
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 62, Application US/08630822A
Patent No. 5840695
GENERAL INFORMATION:
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25.3%;
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Best Local Similarity 25.3%.
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                  Colorado
                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                              CITY: Denver
STATE: Colora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 KEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA-E 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 VVQSDNAASDAW-----AATPIALDV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 QYANENGVDGVWTYDDATKTFTVTEMVTEVPGDAPTEPEKPEASIPLVPLTPATPIAKDD 593
                                                                                APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: JONSSON, Hans
APPLICANT: LINBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RANTAWAKI, Liisa K.
APPLICANT: RANTAWAKI, Liisa K.
APPLICANT: RANTAWAKI, Liisa K.
APPLICANT: RANTAWAKI, Liisa C.
APPLICANT: RANTAWAKI, Liisa C.
APPLICANT: RANTAWAKI, Liisa C.
APPLICANT: RANTAWAKI, Liisa C.
APPLICANT: MUELLER, HANS-PETER C.
APPLICANT: JONSSON CONTRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
13.5%; Score 105; DB 3; Length 664;
Best Local Similarity 23.9%; Pred. No. 0.029;
Matches 54; Conservative 21; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VDSPIEQP----RIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIED-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,408B
FILING DATE: 03-JUL-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION NUMBER: SE 9302855-3
ATION DATE: 06-SEP-1993
ATIONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29,769
REGISTRATION NUMBER: 29,769
REFERENCE/DOCKET UNMBER: 61743/102
TELECOMMUNICATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
               Sequence 2, Application US/08669408B Patent No. 6100055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 664 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 KKTKDTKPV-----
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20007-5109
                                                            GENERAL INFORMATION:
APPLICANT: GUSS, 1
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US-08-630-822A-62

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492 LEKQINDLOEK--LKGELEHNQKLKKQAVELRVAQSATEQLNNELQETWGGLQTQRDALQ 549
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Patent No. 5932470
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: WALLENFELS, INNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
ONNBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLESFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,822A
FILING DATE: II-APR-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: CONNELL, CARY J.
RECISTRATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2618-17-C3
FELECOMMUNICATION NUMBER: 2618-17-C3
TELECOMMUNICATION NUMBER: 32,020
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 mnino acids
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; Pred. No. 0.11;
34; Mismatches
                                                                                                                                                                                                   ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colorado
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US-09-171-517B-10
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Matches 45
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                                                                                                  206 AIEILKKYGIGDYYIKLINNGKTAEGVTALKDEILASKPAVIDAPELTPALTTYKLVI-- 263
                                                                                                                                                             ----KPVVKKEERQNVNTLPT 152
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Sequence 6, Application US/09171517B
Sequence 6, GDERAL INFORMATION:
CDERRAL INFORMATION:
APPLICANT: Finlay, B Brett
APPLICANT: Stein, Markus
TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN
FILE REFERENCE: 07422/019001
CURRENT APPLICATION NUMBER: US/09/171,517B
CURRENT APPLICATION NUMBER: US/09/171,517B
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1997-04-23
PRIOR FILING DATE: 1996-04-23
PRIOR FILING DATE: 1996-04-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                      Gaps
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                                                                 36 AIDELKKQAIED------KEATTAIE---AASSDALEALADQTDALQSEEAAVVK 81
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Patent No. 635524
GENERAL TORRAGATION:
APPLICANT: FINLBY, B. Brett
APPLICANT: Steln, Markus
APPLICANT: Steln, Markus
TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN
FILE REFERENCE: 07422/019001
                                  67;
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 Length 413;
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                                  Indels
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ch 14.7%; Score 114.5; DB 3;
1 Similarity 26.2%; Pred. No. 0.0019;
49; Conservative 15; Mismatches 56;
                                                                                                                                      82 ADNAASDALEALADQTDALQSEEA-EVVQSDNAASDAWE---
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US-09-171-517B-6
                  Local Similarity
                                                                                                                                                                                                                                                                              153 TGEESNP 159
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382 TGEGSNP 388
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US-09-171-517B-6
Query Match
Best Local S
Matches 49
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Sequence 10, Application US/09171517B

Sequence 10, Application US/09171517B

Sequence 10, Application US/09171517B

Setent No. 6355254

SENERAL INFORMATION:

APPLICANT: Finlay, B. Brett

APPLICANT: Stein, Markus

TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN

FILE REFERENCE: 07422/019001

CURRENT APPLICATION NUMBER: US/09/171,517B

CURRENT APPLICATION NUMBER: 07/CA97/00265

PRIOR APPLICATION NUMBER: 60/015,999

PRIOR FILING DATE: 1997-04-23

PRIOR FILING DATE: 1996-04-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATENTIN VOI 10

TENCOR: 20 10 NOS: 15

SEQ ID NO 10

TENCOR: 20 10 NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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CURRENT APPLICATION NUMBER: US/09/171,517B
CURRENT FILING DATE: 1998-10-20
FRIOR APPLICATION NUMBER: PCT/CA97/00265
FRIOR FILING DATE: 1997-04-23
FRIOR PRIOR APPLICATION NUMBER: 60/015,999
FRIOR FILING DATE: 1996-04-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 3.0
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ORGANISM: Escherichia coli
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US-09-171-517B-9
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Sequence 2 Sequence 2 Sequence 2

Sequence Sequence S

Sequence 2, Al Sequence 3, Al Sequence 23, A Sequence 23, A

Sequence 4, Sequence 4, Sequence 5, Sequence 4,

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FOR PRODUCING INHIBITOR-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE AUURCAS.
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DATORION DATA:
APPLICATION NUMBER: US/08/669,408B
FILING DATE: 03-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
FILING DATE: 06-SEP-1994
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENTY, Stephen A.
APPLICATION NUMBER: 29,768
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (202)672-5309
TELEFRAN: (202)672-5399
                US-08-319-795-2
US-08-468-985-2
US-08-072-070-2
US-08-072-070-2
US-08-469-434-2
US-08-468-718-2
US-08-468-718-2
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US-08-17-499A-2
US-08-127-499A-23
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APPLICANT: JONSSON, Hans
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: MATTHAWKI, Lilsa K.
TITLE OF INVENTION: METHOD AND MEANS FOR
TITLE OF INVENTION: PLASMAPROTEINASE IN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08669408B Patent No. 6100055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 413 amino acids amino acids
; MOLECULE TYPE: protein US-08-669-408B-10
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US-08-669-408B-10
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                                                                                                                       ; Search time 24.6578 Seconds
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1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-171-517B-6

US-09-171-517B-9

US-08-62-408B-2

US-08-630-82B-2

US-08-630-82B-2

US-09-005-069-62

US-09-105-108-11

US-08-158-353-2

US-08-158-475-6

US-08-158-475-6

US-08-115-746-110

US-08-115-746-110

US-08-115-746-110

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US-08-465-746-2
US-08-214-164-2
US-08-467-852A-3
US-08-246-636-2
                                                                                                                                                                                                                                                                                                                       231628 segs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
                                                                                                                       October 13, 2002, 04:45:42
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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311 AAGGGTACTGAGGCTGCTGAGGATTCTGAGGCTGATGAGGCTGCTGAGGATTTTGAAGGAT 252 q

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Search completed: October 13, 2002, 05:37:48 Job time : 1854.09 secs

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//t
                                                                                  Sugiyama, H., Yasumasu, S., Murata, K., Iuchi, I. and Yamagami, K. The third egg envelope subunit in fish: cDNA cloning and analysis, and gene expression

Dev. Growth Differ. 40 (1), 35-45 (1998)
                                                                                                                                                                                                                                                                                                            Submitted (08-APR-1999) Hitoshi Sugiyama, St. Marianna University School of Medicine, Department of Physiology; 2-16-1 Sugao, Miyamae-Ku, Kawasaki, Kanagawa 216-8511, Japan (E-mail:sugiyama@marianna-u.ac.jp, Tel:81-44-977-8111(ex.3405), Fax:81-44-977-0172)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 TIGAAGGATACIGAGGCIGCIGAGGATICIGAGGCIGCIGAGGTITITGAAGGATACIGAG 543
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Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 TTGAAGGGTACTGAGGCTGCTGAGGATTCTGAGGCTGATGAGGCTGCTGAGGTTTTGAAG
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/protein_id="BAA76901.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryzias latipes"
/db_xref="taxon:8090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="liver"
26. .1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Sugiyama, H. and Iuchi, I.
Direct Submission
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                                                         REFERENCE
AUTHORS
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MEDLINE
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                                                                                                                                                                                                                       CLEAR 14 LON-"EFRY GYSDYYKNLINNAKTVEGVKDLOAQVVESAKKARISEAT
DGLSDFLKSQTPAEDTVKS IELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVKDL
AGAQVVESAKKARISEATDGLSDFLKSQOTPAEDTVKSIELAEARVLANRELDKYGVKDL
GAQVVESAKKARISEATDGLSDFLKSQOTPAEDTVKSIELAEARVLANRELDKYGVKDL
YKNLINNAKTYBGYKALIDEILAALPKTDTYKLILMGKTLKGETTTEAVDATAEKVE
KQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLV
EAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLV
INGKTLKGETTTKAVDAFTAEKAFKQYANDNGVDGWTYDDATTYKLV
RKTLKGETTTKAVDAFTAEKAFKQYANDNGVDGWTYDDATKTFTVTEVPGD
APTEPERKPEASIPLYPOTTPAPTITAKDDAKKDDTKKEDAKKEDAKKETPTTG
EGSNPFTAAALAVMAGAGALAVASKKKED"
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'note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           choriogenin Hminor.
Oryzias latipes liver cDNA to mRNA.
Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063 GAAAAAGCCTTCAAACAATACGCTAACGACAACGGTGTTGATGGTGTTTGGACTTATGAT 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1180 CCAACTGAACCAGAAAACCAGAAGCAAGTATCCCTCTTGTTCCGTTAACTCCTGCAACT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         943 AAACCAGAAGTGATCGATGCGTCTGAATTAACACCAGCCGTGACAACTTACAAACTTGTT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1003 ATTAATGGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACTGCA 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 AspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAspAlaTrpGluLys-----AlaAlaThr 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                              /product="Protein having the same IgG specificity protein G from group G streptococci strain G148" //Ab_xref="G1:4526658"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGlu------Ala
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                              translation
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Fepetitive structures of 24 amino acids, A1, A2 and A3, are found interrupted by two unrelated repeats of 51 amino acids, B1 and B2. Further downstream, following a 12-residue unique 'spacer. region' (S), there is a stretch of 55 amino acids repeated three times, C1, C2 and C3. The latter regions are interrupted by two 15-residue regions, called D1 and D2. Directly following these repeats there is a region W, which consists of a repetitive, extremely hydrophilic, structure containing several proline residues. This region resembles a similar structure in the streptococcal M protein protein A, which is thought to mediate the binding of the protein to the cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus G 148 gene fragment for IgG-binding protein G. X04015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1469)
Glass B., Eliasson, M., Olsson, A., Uhlen, M., Frej, A.K., Jornvall, H., Flock, J.I. and Lindberg, M.
Structure of the IgG-blinding regions of streptococcal protein G
EMBO J. 5 (7), 1567-1575 (1986)
                                                                                                                                                                                                                             1167 AAAGCAGATAAAGCTTCAGGA------GCTCAAAAAACCA-----GAT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 ValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnValAsn 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------LeuProThrThrGlyGluGlu---SerAsn 158
                                                                                                 9
29 AlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLys 48
                                                                                               GluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGln
                                                                                                                                                                                              69 ThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAsp
                                                                                                                                                                                                                                                                                                89 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValVal
                                                                                                                                                                                                                                                                                                                                                                                               109 GlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAsp
                                                969 GATGCACGTAACGCTGAAAA-----GAAAAGCTCCAATCACAAGCA--
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/organism="Streptococcus
/strain="G 148"
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KQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTT
ENODATAERVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLV
INGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFTVTEWPEVPGD
APTEPERFERASIPLYPLTPATPITAKDDAKKDDTKKEDAKKEBAKKEDAKKAFTLPTTG
EGSNPFTTAAALAVWAGAGALAVASKRKED"
OAQVVESAKKARISEATDGLSDFLKSGTPAEDTVKSIELAEAKVLANRELDKYGVSDY
YKNLINNAKTVEGVKALIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 943 AAACCAGAAGTGATCGATGCGTCTGAATTAACACCAGCCGTGACAACTTACAAACTTGTT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                1003 ATTAATGGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACTGCA 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SeraspalaTrpGluLys-----AlaAlaThr 123
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                                                                                                                                                                                                                                                                                                                                  41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGlu.......Ala 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAla 94
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Al2446.1 GI:491352
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44
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Mismatches:
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Patent: WO 8705631-A 4 24-SEP-1987;
Location/Qualifiers
1. 1469
//organism="synthetic construct"
//b_xref="taxon:32630"
1. 1443
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Matches:
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1 (bases 1 to 1469)
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Best Local Similarity:
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ORIGIN
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KEELDTLSKALTDTIEKKIESENAYKKELGGEKAAARSAEARARIDALNNKNKOISDLT
NENAGLKEATEGYVOTIONASREIAAKQOELAAAKSGLEAKKAREIEALKQODASKTEE
TAKLQSEAATLENLLGSAKHELTDLQAKLDTATAREKAKLESOYTLENLLGSAKRELT
DLQAKLDARNARKEKLGSQAAALEKQLEATKELADLQAKLAATNOEKEKLEBEAKAL
KEQLTKQAEELAKLKADKASGAQKPDTKPGNKEVPTRPSQTRINTNTAPMAQTKRQLP
STGEETTNPFTTAAALTVIASAGVLALKKEEN*
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RDLEASRAASKELEAEHQKILKEEKQISDASRQGLSRDLEASREAKKYVEADLAALTAE
HQKLKEEKQISEASRQGLSRDLEASREAKKYVEADLAALTAEHQKLKEEKQISDASRQ
GLSRDLEASRERAKKYVEADLAEANSKLQALEKLINKELEEGKKLSEKEKAELQARLEAE
AKALKEQLAKQAEELAKLKGNQTPNAKVAPQAANSSRSAMTQOKRTLPSTGETANPFFT
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GASRTITSSENISKLYDENSKLIEERADLLGKLEEKEDKLESVERHYLRTLDQEYKEH
                                                                                                                                                                    protein; Allele: 50; M-related protein"
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Matches:
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123. .1400
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Submitted (21-MAR-1996) Susan K. Hollingshead, Microbiology, Univ.
of Alabama at Birmingham, 845 19th Street South BBRB 406/6,
                                                                                                                                                                                                                                                                                           Db 104506 GTCCCCAAT-------ATAAATAGTCAGCCCAGAAAATGGATGTG 104468
                                                                                                                                                                                                                                                                                                                                                                                                                            104407 GAGCTIGAAAACGAICAAGAGGAATTIAICAAAGAGGAIICACCAAIICCGCAIICCGAI 104348
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Yung, D.L. and Hollingshead, S.K.
DNA sequencing and gene expression of the emm gene cluster
MSO group A streptococcus strain virulent for mice
Infect. Immun. 64 (6), 2193-2200 (1996)
                                                                                                                                                                                                                                                                                                                                                                       31 ArgAsnGlu-------GluArgAlaIleAspGluLeuLysLysGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 IleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSer.....SerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 LysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 LysAspThrLysProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
                           146491
                                                          37
60
60
60

    .4469
    /organism="Streptococcus pyogenes"

                                                                             Conservative:
Mismatches:
                                                       Matches:
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                                                                                                                                     Indels:
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Hollingshead, S.K. and Yung, D.L.
Direct Submission
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Db 104050 GACGAGAAGCA 104036
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VERSION
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15851. 1567.
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7792. .7948
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8071. .8364
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AC019950 146491 bp DNA Linear HTG 03-JAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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SM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (Dases I to 146491)

S Adams, M. and Venter, J.C.

Direct Submission

L Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA

This sequence was identified as CDM:10211502 by the submitter.
For more information on this record e-mail to fly@celera.com.

* This sequence will be replaced

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

roce
                                                                                                                                                                                                                                                                                                                         Db 117684 GCAGAAGAAGAAGAAGCA-----GAAGAAGCAGAAGCAGAAGCAGAAGAAGAAGAAGAA 117631
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                                                                                                                                                                                                                                                                                          26 GluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIle 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaaspGlnThraspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla 85
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/db_xref-"taxon:7227"
41452 a 32191 c 31484 g 41364 t
                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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16682. .16939
/rpt_family="L1"
17009. .17747
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Direct Submission
Submitted (05-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Submitted (06-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                Db 206709 GGATCACTACAAATTCACGTCAGTCTTATGTACAAACATAATCAGTCTACAAAGAGTGTC 206650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                      Db 206826 GCAGAGGCAGAGGCAGAGGAGGCAGAGGCAGAGGCAGAGGCAGAGGCAGAGA 206767
                                                                                                                                                      AlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrp 118
                                                                                                                                                                                                                              119 GluLysAlaAlaThrProlleAlaLeuAspValLysLysThrLysAspThrLysProVal 138 ::::::||| ::: |||| |||
SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 78
                                                                                                                                                                                                                                                                                                                                                                                            167227 bp DNA linear PRI 10-JA ACO20662.6 GI:17386508
                                                                          79 ValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 167227)
Waligorski,J., Cotton,M. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-461M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhini 1 (bases 1 to 167227) Sulston J.E. and Materston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
3 (bases 1 to 167227)
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                                                                                                                                                                                                                                                                                                              139 ValLysLysGlu 142
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The RCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-341H1, 2000 bp overlap; the clone sequenced to the right is RP11-289K3. Actual start of this clone is at base position 162181 of RP11-341H1; actual end is at base position 1672Z7 of RP11-461M18.
                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                     clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Data from AC016725 and AC017031 was used to finish this clone, AC020602. There is a tandem repeat from base position 33099 t 33933.
site: http://genome.wustl.edu/gsc
                      Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0461M18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://bacpac.med.buffalo.edu)
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8850. .3229
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490. .3796
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/clone_lib="RPCI-11"
250. .316
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260. .3347
rpt_family="ERVL"
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/rpt_family="MIR"
1376. .1470
/rpt_family="MIR"
2361. .2391
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878. .923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3516
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repeat_region

Center: Washington University Genome Sequencing Center

Center code: WUGSC

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Db 206997 GAGCACCTACGGGTCCGGCCAGAGAAGAGGATGCAGCAAGAGGGGAAAGAGGGCAGACAGTA 206938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 GluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIle 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 GluAspLysGluAla-------ThrThrAlaIIleGluAlaAlaSer
1987 221006: gap of unknown length
1007 222304: contig of 1298 bp in length.
Location/Qualifiers
Location/Qualifiers
/organism="Mus musculus"
/strafi="CS7BL6/J"
/db.xref="taxon:10090"
/chromosome="15"
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Matches:
Conservative:
Mismatches:
Indels:
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67135. .868mbly_name:Contig66"
/note="assembly_name:Contig64"
103999. .121819
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219741. .220986

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149370. .157963
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157984. .167921
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/note="assembly_name:Contig52"
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/note="assembly_name:Cont1g57"
192864. .200562
                                                                                                                                                                                1. .44872
/note="assembly_name:Contig67"
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                                                                                                                                               /clone="RP23-274F23"
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167942. .178841
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218163. .219720
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                                                                                                                                                                   /sex="male"
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50.81%
29.03%
14.74%
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221007
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Best Local Similarity:
Query Match:
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                                        FEATURES
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                                 Tobses 1 to 222304)
Montgomery, K.T., Grills, G., Li, L., Brown, W.A., Chiu, D., Decker, J., Fusina, W., Haider, A., Keller, A., Perera, A., Shim, C., Thomas, E., Zencheck, W., Xi, C., Juels, P. and Kucherlapati, R.
Direct Submission
Submitted (21-DEC-2001) Harvard Partners Center for Genetics and Genonics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: agarose-FP - N/A Quality coverage: 7.6 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as a truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                            contig of 19703 bp in length gap of unknown length contig of 17121 bp in length gap of unknown length length gap of unknown length contig of 17821 bp in length contig of 17821 bp in length gap of unknown length gap of unknown length contig of 18758 bp in length gap of unknown length gap of unknown length contig of 8594 bp in length gap of unknown length contig of 9938 bp in length contig of 9938 bp in length gap of unknown length
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gap of unknown length
contig of 22222 bp in length
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of 13982 bp in length
                                                                                                                                                                                                                                                                                                                         Center project name: ALG
Sequencing vector: pSMART, AF399742
Sequencing vector: pSMART, AF399742
Chemistry: Dye-terminator Big Dye: 100%
*Consensus quality: 213980 at least 020
*Consensus quality: 21998 at least 030
*Consensus quality: 209034 at least 040
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 221944 - sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
of 7699 bp in length
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bp in length
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                                                                                                                                                                                                                                                                                                            Contact: gnktm@capecod.bwh.harvard.edu
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 TITLE
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AUTHORS
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202744: contig of 1113 bp in length 202744: contig of 1128 bp in length 204092: contig of 1328 bp in length 204102: contig of 1328 bp in length 204112: gap of unknown length 205425: contig of 1313 bp in length 20550: contig of 1205 bp in length 205670: gap of unknown length 207282: contig of 1205 bp in length 207302: gap of unknown length 208250: contig of 948 bp in length 208250: contig of 812 bp in length 208020: contig of 812 bp in length 20902: gap of unknown length 209102: gap of unknown length 2104047: contig of 1385 bp in length 210507: gap of unknown length 210507: gap of unknown length
                  f unknown length
g of 1113 bp in length
f unknown length
g of 1328 bp in length
f unknown length
g of 1313 bp in length
f unknown length
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132382. .141581

Moote-"assembly_name:Contig126
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vector_side:left'

clone_end:T7

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AC104834 22-3AN-2002
Mus musculus chromosome 15 clone RP23-274F23 strain C57BL6/J,
WORKING DRAFT SEQUENCE, 19 unordered pieces.
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Montgomery, K.T., Grills, G., Li, L., Brown, M.A., Chiu, D., Decker, J., Fusina, M., Haider, A., Keller, A., Perera, A., Shim, C., Thomas, E., Zencheck, W., Xi, C., Juels, P. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 109356 GGATCACTACAAATTCACGTCAGTCTTATGTACAAACATAATCAGTCACAAAAGAGTGTC 109415
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                                                                                                                                                                                                                                                                        632 others
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36
27
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11
                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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AC104834.3 GI.18030119
HTGS_PHASE1: HTGS_DRAFT.
House mouse.
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114.50
50.81%
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Best Local Similarity:
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                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC023354 210791 bp DNA linear HTG 25-JAN-2002 Mus musculus chromosome 15 clone RP23-384L8 strain C57BL6/J, WORKING DRAFT SEQUENCE, 29 unordered pieces.
SADGEADAIRKRAQAEADAIKLRGEALRQNPNVMELEAINKWNGQLPQYMTEGANTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 210791)
Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Gordon, M., Goltz, J.S. and Kucherlapati, R., Ferera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R., Unpublished to 2 (bases 1 to 210791)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39784 GTCGATACCATTGAGTCGGAGTCCTCAAAGGCTCTGGCTGCAGCCGCCAGATCGGAAGCA 39725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39604 CGGGCAAGCAAAGAGGCTGCCGCAGCATCAAACAGCTTACAAAGTGAGCAGGTT 39545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39544 GCAGCCGCCCATGCAGACTCCGCGAAGAGTGAAGCGA------ 39500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 AlaLeuAspValLysLys-----ThrLysAspThrLysProValValLysLysGlu 142
                                                                                                            /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 IleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrAlaIleGluAla
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Conservative:
Mismatches:
Indels:
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                                                    complement(2427, .2459)
/gene="HCM2.0006c"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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31.01%
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Best Local Similarity:
                                                          misc_feature
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http://wchanning.bwh.harvard.edu:9088/hpcgg/jsp/hpcgg/Sequence/mous
e.html
Montgomery,K.T., Grills,G., Han,J., Lee,E., Long,J., Pomerantz,R., Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A., Gordon,M., Goltz,J.S. and Kucherlapati,R.
                                                                            Submitted (14-FEB-2000) Department of Molecular Genetics, Albert Laintein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA On Jan 9, 2002 this sequence version replaced g1:11094415.
                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: agarose-FP - N/A Quality coverage: 4.8 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown length
contig of 26812 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
of 13371 bp in length
unknown length
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of 14560 bp in length
                                                                                                                                                                                                                                                                                                 Center project names. Control Body 1008
Chemistry: Dye-terminator Big Dye; 1008
*Consensus quality: 198418 at least Q30
*Consensus quality: 195838 at least Q30
*Consensus quality: 191563 at least Q40
Estimated insert size: agarose-FP - N/A
Every Converse: agarose-FP - N/A
Ouality coverage: agarose-FP - N/A
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                                                                                                                                                 Center: Harvard Partners Genome Center
                                                                                                                                                                                                                                                         Contact: gnktm@capecod.bwh.harvard.edu
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21876:
48688:
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complement(1647. .2489)
/gene="HCM2.0006c"
complement(1647. .2489)
/gene="HCM2.0006c"
complement(1647. .2489)
/gene="HCM2.0006c,
possible lipoprotein, len: 280 aa;
/note="HCM2.0006c,
possible lipoprotein, len: 280 aa;
/note="HCM2.0006c,
possible lipoprotein (28 aa), fasta scores;
protein-related protein from plasmid pMT1 (276 aa),
fasta scores; E(): 0, 97.5% identity in 280 aa overlap and
TR:068763 (EMBL:AF074611), Y1114, Yersinia pestis KIM5
hypochetical protein from plasmid pMT1 (276 aa), fasta
scores; E(): 0, 97.5% identity in 280 aa overlap and
posstible N-terminal signal sequence and an appropriately
posstioned PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1113...1484)

complement(1113...1484)

complement(1113...1484)

complement(1113...1484)

complement(1113...1484)

complement(1113...1484)

/gene="HCM2.0005c"

/note="HCM2.0005c"

/note="HCM2.0005c;

process: E(1): 8.5e-15,

45.6% identity in 114 aa overlap. Highly similar to
TR::CB855230 (EMBL:AL17211), YPM1.46C; Versinia pestis

CO-92 hypothetical protein from plasmid pWT1 (123 aa),
fasta scores: E(): 0, 87.8% identity in 123 aa overlap
and TR::QSGGV (EMBL:AF074611), Y1115, Yersinia pestis KIM5

hypothetical protein from plasmid pWT1 (123 aa), fasta

scores: E(): 0, 87.8% identity in 123 aa overlap

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/protein_id-"cAD09873.1"
/db_xxeff-"GI:165059873.7"
/tb_xxeff-"GI:165059873.7"
/tb_xxefa-"GI:165059873.7"
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VFQTYRKGVDDITDTDLRQKIADSLNRLASRMTTDTFIDGGKASLLDNALKDIQAEMS
PVGIEVISLSWYGRPDYPDTVIESINAKVTANQKTLQRQQEVEQRKABANMLREQAEG
/gene="HCM2.0004c" hypothetical protein, len: 136 aa; highly similar to TR:CAB55229 (EMBL:AL117211), YPWT1.47C, Yersinia pestis CO-92 hypothetical protein from plasmid pMT1 (136 aa), fasta scores: E(): 0, 97.8% identity in 136 aa a overlap and TR:O695026 (EMBL:AF074611), Y1116, Yersinia pestis KIM5 hypothetical protein from plasmid pMT1 (136 aa), fasta scores; E(): 0, 97.8% identity in 136 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MKKLYDAANAALDVVDTBIAQGFPEPEWATQLREAIAEMNAPEP
SEDEADWQRFIRMYAEEVGPTPTAEQAMLLKYFKEAGENLPVDDTPHWFHAAWRKFDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical protein"
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/db_xref-"GI:16505985"
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/note="repeat 1; 57 bp repeat"
complement(1647. .2489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1137. .1141)
/gene="HCM2.0005c"
/note="possible RBS"
complement(1492. .1497)
/note="possible RBS"
1565. .1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFRAAMTVFLLMQEKKHEETV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .232
// note="55.7% identical to Yersinia pestis CO-92 plasmid pm71 (EMBL:ALI17211) bases 48304. .48535"
complement(29. .334)
/gene="HCM2.0002c"
complement(29. .334)
/gene="HCM2.0002c"
complement(29. .334)
/gene="HCM2.0002c"
/note="HCM2.0002c"
/note="HCM2.0
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//gene="HCM2.0003c"
//gene="HCM2.0003c, hypothetical protein, len: 91 aa;
//note="HCM2.0003c, hypothetical protein, len: 91 aa;
//gersinia pestis CO-92 hypothetical protein from plasmid
pMT1 (91 aa), fasta scores; E(): 0, 94.5% identity in 91
aa overlap and TR:Q92CX9 (EMBL:AF074611), Y1117, Yersinia
pestis KIM5 hypothetical protein from plasmid pMT1 (91
aa), fasta scores; E(): 0, 94.5% identity in 91 aa
overlap.
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/db_xref="G1:16505983"
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FYVRDDRVLSSPYLTRRNGKLSGVGEDKFVYNKSGDVXGVHAKNASYLFDDCKEVG"
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MDADSVYVDDDGVCWHNGSCWYVDDTWTVSDEDAAHLERILGISTFE"
                                                                                                                                                                                                        /gene="HCM2.0001c"
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/note="HCM2.0001c, hypothetical protein, PWT1.45C,
highly similar to TR:CAB55227 (EMBL:AL17211), YPWT1.45C,
PWT1.01 aa), fasta scores: E(): 5.9e-25, 93.3% identity
in 60 aa overlap and TR:068760 (EMBL:AF074611), Y1119,
Versinia pestis KIM5 hypothetical protein from plasmid
pWT1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity
in 60 aa overlap. Spans the end of the sequence"
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/transl_table=11
/product="hypothetical protein"
/protein_id="CAD09870.1"
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/db_xref="G1:16505982"
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/gene="HCM2.0004c"
complement(719. .1129)
             /db_xref="taxon:90370"
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/note="possible RBS"
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224. .6722
                                                  /gene="HCM2.0001c"
                                                                                                                                        complement(1. .29)
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LeuGluAlaLeuAlaAspClnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
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STYPPHCM2/c
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VTRLNEEKMARDAVDKAIAADAAAFSELKDAQLKAYEDLAKLAADTDLDLDVAKIIND
YTKVENAKTARDVKK FEESONEVTRITREKAKAAALAKARADAE BILKKYGIGDY
YTKVENAKTARDVKK TEESONEVTRITREKAKAAALAEKAADAE BILKKYGIGDY
YTKILNNGKTARDVKTKDELTAPALTTYKLVINGKTLKGETTTKA
VDAETAEKAFKQYANENGVUATYDDATKTETVYENYTEVPGDAFTERKKPERASIPL
VPLITATPIAKDDAKKDDTKKDDTKKEDAKKPEAKKEEAKKAATLPTTGEGSNPFFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="aAA26921.1"
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                                                         BCT 16-AUG-1994
                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     962
                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="binding of macroglobulin, albumin and IgG" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of macroglobulin, albumin and IgG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1555)
Jonsson, H., Frykberg, L., Rantamaeki, L. and Guss, B.
MAG, a novel plasma protein receptor from Streptococcus
Db 94243 CAACTCGCCGCCAATACTAACACCTTGAAGACTGCCACTGATTCGAACAAC 94193
                                          Streptococcus dysgalactiae (mag) gene, complete cds. L27798. L27798.1 GI:475117

    1555
    /organism="Streptococcus dysgalactiae"

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49
15
56
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Mismatches:
Indels:
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Matches:
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                                                                                                                             Streptococcus dysgalactiae DNA. Streptococcus dysgalactiae
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                                                                                                                                                                                                                                                                       Location/Qualifiers
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/product="unnamed"
242 c 305 g
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94259307
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/gene="mag"
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288. .1529
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249. .254
264. .269
276. .281
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34.22%
26.20%
14.74%
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Query Match:
                                                                                                               mag gene
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-10_signal
-10_signal
RBS
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ACCESSION
VERSION
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SOURCE
ORGANISM
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MEDLINE
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                             RESULT 31
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Salmonella enterica subsp. enterica serovar Typhi.

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

Balmonella.

I (bases 1 to 106516)

Parkhill,J., Dougan,G., James,K.D., Thomson,N.R., Pickard,D.,

Wain,J., Churcher,C., Mungall,K.L., Bentley,S.D., Holden,M.T.G.,

Sebalita,M., Baker,S., Basham,D., Brooks,K., Chillingworth,T.,

Farrar,J., Feltwell,T., Hamlin,N., Haque,A., Hien,T.T., Holroyd,S.,

Jagels,K., Krogh,A., Larsen,T.S., Leather,S., Moule,S., O'Gaora,P.,

Parry,C., Quail,M., Rutherford,K., Simmonds,M., Skelton,J.,

Stevens,K., Whitchead,S. and Barrell,B.G.

Complete genome sequence of a multiple drug resistant Salmonella

enterica serovar Typhi CTIB

Nature 413 (6858), 848-852 (2001)
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Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18
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Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/S_typhi/).
                                        -----AATGGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACT 1130
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8.1
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/strain="CT18"
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* 10976 21831: contig of 10846 bp in lead 21822 21836: gap of unknown length 21837 30764: contig of 8928 bp in len 30765 30779: gap of unknown length 37501 37515: gap of unknown length 47191 47205: gap of unknown length 47206 57255: contig of 9675 bp in len 47206 57255: contig of 10050 bp in len 57256 57270: gap of unknown length 47206 57270: gap of unknown length 57251 57271: gap of unknown length 68425 68425 68439: gap of unknown length 68425 68439: gap of unknown length 79779 79779: contig of 11339 bp in len 68440 79778: contig of 11339 bp in len 68425 68439: gap of unknown length 79779 93036: contig of 13343 bp in len 79779 93036: contig of 13343 bp in len 79779 93037: gap of unknown length 79779 79778: contig of 13343 bp in len 79779 79778: contig of 13243 bp in len 79778: contig of 3417 bp in len 1000000000000000000000000000000000000	25ProGluLysLeuAlaLeuArg	0y 86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
13433   CGCATCGCTCCACATTTGGTTGAAGCTGTCAACGATGTTCCAGCCAG	RESULT 30 ACO06902 LOCUS LOCUS LOCUS LOCUS LOCUS DEFINITION Caenorhabditis elegans clone Y74A11Y, *** SEQUENCING IN PROGRESS ACCESSION ACO06902.2 G1.4309900 KEYWORDS HG; HTG. LOCUS Caenorhabditis elegans. Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis Caenorhabd	66. 15 18 18 19 11]

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Submitted (23 FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Materston, R.H.
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FVETVNRKKAILTRRENNEDEIRESTEDMEECHSTIEGWQSTEIEELRAEWIKLSE
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*** SEQUENCING IN PROGRESS ***,
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      Join(19676, .19768,20094. .20690)
/gene="T03Al.3"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                          /evidence-not_experimental
/protein_id-"AAC17551.1"
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HTG; HTGS_PHASE1.
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39.09%
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source
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AUTHORS
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                                                                                      COMMENT
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Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

E | (bases 1 to 35318)

Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,

Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,

Coulson,A., Craxton,M., Dear,S., Duz,Z., Durbin,R., Favello,A.,

Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jer,M.,

Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,

Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,

O'Callaghan,M., Parsons,J., Percy,C., Rikhen,L., Roopra,A.,

Standers,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,

Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,

Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INV 28-MAY-1998
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                                                                                                                                                                                                                                                                                                                                2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAsp 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 VallysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnValAsn 148
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                                                                                                                                                                                                                                      33 GluGluArgAlaileAspGluLeuLysLysGlnAlaileGluAspLysGluAlaThrThr 52
                                                                                                                                                                                                                                                                                                          53 AlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 72
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36
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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Indels:
/clone_lib="RPCI-23"
31267 c 30172 g 40659 t
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Caenorhabditis elegans cosmid T03Al.
                                                                                    Length:
Matches:
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Du, 2. and Scheet, P.
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116.50
53.49%
25.58%
14.99%
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Query Match:
                44661 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSSSPPARPCCVCFRFRPHEDEKAQKNTFTRWINFHLEEHSSSG
RIEDLFEDIRDGVLLCHLIEVLTGEALAPIHKLNYWESTNAVHKGRVSKRVHHIANLT
TALTVLRRRGLELINNNAADIADGNPRIVLGLIWQIILHFQIETNMILLREWGWAATG
                                                                                                                                                                                                                      USA
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VLDRQCSHIMSVTQDH"
19676. .20690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"contains similarity to actinin-type actin-binding domains (Pfam: actinin-binding.hmm, score: 106.64 and 88.64)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(11113. .11167,11680. .11741,12385. .12480,13819. ..
13915. .14091,14713. .15405,15634. .16163,16314. .16441,
16912. .17234,17324. .17665)
                                                                                                                                                                 Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                         Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                 Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
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/protein_id="AAC17552.1"
/db_xref="GI:3158507"
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11113. 17665
/gene="T03A1.4"
3 (bases 1 to 35318)
Waterston,R.
Direct Submission
Submitted (22-MAY-1998) De
University, 4444 Forest Pa
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23073 GACGTGGCTAAGGACGACGCTAACAAACTCAAGGCTACTGTAGAGCAACTTACCAAGCTG 23132 22953 AACATCCAAAAGACTGGTGACGATGAAAAGCGCGCGGATGAACTAGAAGAACGATGTCGGA 23012 22893 GAGCCTTCAGCCGTCGCTTTGCGTGATCGTGCCTAAATTCGTTTCTGATCTTGAAAAG 22952 54 65 23013 AATGCGGTCAAGAACGTGGAAGATGTTGTTTCGAAATACCAAAATCAACCTCAACCTC -----AsnGluGluArgAlaIleAspGluLeuLysLysGlnAla--------LysGluAlaThrThrAlaIle ArgllelleProAsnGlyGlyThrLeuThrAsnLeuLeuGlyAsnAla--Length: Matches: Conservative: Mismatches: ---ProGluLysLeuAlaLeuArg-----Indels: US-09-847-539A-6 (1-159) x AC006834 (1-54126) Gaps: 45.2 117.00 39.09% 24.87% 15.06% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: σ 25 32 45 Score: 셤 ò ô g g a ò õ à

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Direct Submission

Submitted (19-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Hunquery(Sanger-ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 30, 2001 this sequence version replaced gi:16444787.

During sequence assembly data is compared from overlapping clones, Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGU4U63 146759 bp DNA linear ROD 29-NOV-2001
Mouse DNA sequence from clone RP23-467J12 on chromosome ll,
complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 146759)
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from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                               23193 AAGGCTAAGGAATTGCTTCAGGCTCTTGAAAAAGCCATTCCACAAGAGGACGCTATTCGT 23252
                                                                                                                                                                                                                                                                                                         23301 CTTACCAAGGTG-----GATGAGTTCAAACCAGAGGATGCACTTCCAATTGTT---GAC 23351
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                                                                                                                                                                                                                                                                102 SerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAla 121
                                                                                                                                                                                                                                                                                                                                                                                                  122 AlaThrProileAlaLeuAspValLysLysThrLysAspThrLysProValValLysLys 141
                                                                                                                              86 AlaSer-----AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla 85
                                     23352 CAACTCGCCGCCAATACTAACACCTTGAAGACTGCCACTGATTCGAACAAC 23402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 GluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGluSerAsn 158

    .146759
    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /chromosome="11"

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Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                  Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
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Missouri 63108, USA
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investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
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On Oct 5, 2001 this sequence version replaced gi:4263104
Submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Genetics,
Park Avenue, St. Louis,
                                                                  (bases 1 to 54126)
Gattung, S., Goela, D. and Broy, M.
The sequence of C. elegans cosmid ZK973
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University, 4444 Forest
8 (bases 1 to 54126)
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University, 4444 Forest
7 (bases 1 to 54126)
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Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation) Location/Qualifiers

FEATURES

1. .54126 /organism="Caenorhabditis elegans" /Strain="Bristol N2" /db_xref="taxon:6239" /chromosome="I"

/gene="ZK973.6"

/clone="ZK973" 11. .25772

gene

join(11. 103,170. .209,1232. .1563,1609. .1736,1764. .1940, 1993. .2127,2196. .3029,3082. .3300,3352. .4719,4757. .5015, 5065. .9450,9629. .12490,12669. .15377,15556. .18264, 1843. .21151,21330. .24038,24217. .24654,24700. .24843, 24890. .25021,25098. .25586,25635. .25772) TDLVVVALILSFRRRQLGSEGEPEVEELRRALREIIARPITEPRDVSPDAIVADILRM KDEKKRDEKTIDEIQATTLTDEQRASFAPLIEDYRRRADRHRIVFEHLVMIYLDWLSR QFDELEDEIGMIIQTSRADDLRRMNSTEWNKWTDLANIEROVGPDTKKALSAELADL LUKVWINKPRKYVECELIDSSREGSPOERREKKKVWWSNTITTIHWVEELLESS LUSRNPDVQQKLVAVKENLRELDTTYVTPHPPSINSPLGTENRNDLEEVKRLAAEIDR DITASSAYREDAPTDEDALKSAIHLLDDQKVTLNHHWYVEGSTPEKNEDDRTDAIDIA SSVGEKLGNIKSAVEEVYEEVLASTRPVKEDPPLOHQEVOTTPAGGSWWDTDEFSRO PPVLSDERIELKTDPSAIDKFEVRSDEDPVPKIIDLFGQLQTAVNEASPLACEGTDDV EEIEREINGSLEAFEAEPLIAKIOELREAKRYGDEARSAAHDOIVALEKEAEDVTAKE SAKKKKKDKKKSPQEMIDELSAKVVEAKALIPKIEEAAKNENLPADDKPKAEQLVSNL EAFVKDVETQVSEKQDELDKLNNANDAIKRLGDALDDAEKTVVPSSVPALSEFKDRIA AVKNVEDVVSKYQNOPOPLDVAKDDANKLKATVEQLTKLÄESSDKIDPQVAKDIKDSK TKAKELLGALEKAIPOEDAIRREQAEINDRLNNLEKELTKVDEFKPEDALPIVDQLAA NTNTLKTATDSNNEKAVAPSSLISHDDLVVGLPEKVFOLQHAIDDKKQALNKAAAVNE IAPKLQLVSQQLQSVPQEVPASLDEQKQLLEDVENOKHNLENLLANLPENDFTADELR QKSQWDLSRLKDLLKQLGSAVGDKLAALAAFNAARKNAEDALLDITREDGGDDNKSPD ELIDDLAKKEETVAKLLDTVSGVKPDELDDKERAEYNDLLARLATAADVLKNKRAELE KAVIANAPSSDAHVQQLEQAVATAETLIPDLEERARLWNEFLAARNDIDALIEQLQQP LDAVLAQPKRSAEEAAQDVENLRNNSQQLSDLDNKIANLQRISELLDPLESAYADVRF FDVDAEQTRHQYDDVLNDVAAELEDETLLKQSASQVANEIDDISKMIDSTDPERSILD /translation="MELFRRLONFCDAVKILRSONTKWNGIKISOCCKRGGGEYIIGS ECGFAEFAEFGKFGNLRTSLVSCFQIYLCLFSQOKLVISRVLFLSKLIETTCGCPLLF HRKRDSMEARINKŸ LTHSAKINAKLTOFEKWLNAIEEDIEQTEROFEDPERSYRFGSE HEVALAKQRLVAKLERLNVANKEEVLRLCERYHTIMHKLTPFQTAVGLPLHVSTNLDR NGPFQSQİSVSSIASSELERPESVMSLTSSIGVIPADVAELSPFEAKINKLLQKLHII EDSYLKGPRPIDTVREDVKQLEKYRNRGAETILQQLSTSNIEDAEKEGLKHRFVLMLNN YDDILRSIENEIRDDNELTAKNQEILAELSNAEQTLQNSPLEDLDISAELDRLQMQLD PHLATLVEAVNDVPASVEPSAVALRDRAAKFVSDLEKNIQKTGDDEKRADELKNDVGN **QAVKAKADEKSLHDSVDRIVSRLVPLVRESDELRHNAEAVPTQYAPKAEELKKEVEAA** EAKALIPKIEEAAKNENLPADDKPKAEQLVSNLEAFVKDVETQVSEKQDELDKLNNAN DAIKRLGDALDDAEKTVVPSSVPALSEFKDRIAPHLATLVEAVNDVPASVEPSAVALR DRAAKFVSDLEKNIQKTGDDEKRADELKNDDGNAVKNVEDVVSKYQNQPQPLDVAKDD LIVRLDEEWTQDANQLRAELASIHGSFFQLEFDRLNEKLNMLIHDKDKLRELMYHRRH YLTAANELITDSKTDLAQRATSSDHPDDILRATDEVTKALDIKGEELRRLGELAEMNI TIAKSDIPALKAQINRIKDRIVNADASRKHVTTDPKIAEDLDNKLAKLQTELDDAIKT SSTCRRSPSLTLMSLFQKSAIYHITRLFLSQRRGLQDWNANRTRETHLKHESKSEIDT /note="contains similarity to myosin-like proteins; codec for by the following C. elegans cDRAs: cm5bl2, cm10f6, cm15g2, yk2f4.3, yk2f4.5, yk7el0.5, yk7el0.5, yk19b4.3, yk19b4.5, yk32c4.3, yk3c4.5, yk36b3.3, yk36b3.5, CEESO66F, CEMSA37F, CEMSH10F, yk25all.5, yk8f4.5, yk752h02.5, yk87lh03.5, yk87d55.5, yk88f5c06.5, yk444g3.5, yk533e4.5, yk542g12.5, yk369e5.5, yk88lh02.3, yk533e4.3" /product="Hypothetical protein ZK973.6" /protein_id="AAF40010.2" /db_xref="GI:15967153" /gene="ZK973.6"

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/db_xref="G1:775217"
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FSVAVGPPPFSLRTY PEEDMCMAWARFCDPSDIKVVILGQDPYHGGQANGLA
FSVAVGPPPFSLRTYAELHRSLPEFSPPDHGCLDAMASGGVLLLWTITTVGVKGKPG
SHADIGWAWFTDHIIALLSERLKACVPMLWGAKAGDKASLINSKKHLVLTSQHPSPLA
OOTSTRKSAOOKFVGNNHFVLANNFLREKGLGEIDWRL"
                                                                                                                                                                                                                                                                                          /proteIn_id="AAA66376.1"

AbxareF="G1:775218"

/translation="MAWFLKSEGFSRRSQRLLSEDEETSRGSSFTLGSOPPOATGE

EEVSFPESDYSEEDEIDLEERE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        712 GAGCAGGAGGAAGCGGTGCAGGAGCAGGAGCGGTGCAGGAGCAGGAGGAAGCGGTG 771
                                                                                                                                                                                        3019. >3222
/note-similar to BKRF4 of EBV, Swiss-Prot Accession
Number P30117"
/citation-[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIle------AspGluLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 GCCCCGGTCCCCGCCCCAATAAAAACGCCGAAGCTGCGTCGGCTGCAAAGGAGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysalaaspasnalaalaSeraspalaLeuGlualaLeuAlaaspGlnThrasp----
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The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for
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Caenorhabditis elegans cosmid ZK973, complete sequence.
AC006834 GI:15967151
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditia
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Caenorhabditis elegans
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Best Local Similarity:
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GDWPYAVWYGPKNSCYNLRRCLGCCVPWCRLIPLSRLPYGHSWGTGPEPTPLMESCV
SYFLVFLPTGQSAECVKDALVDYISTRPQPTSSVKVTFCTFDPPVMLPIFYPPPEAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MHAAIRVFVSLSLVALFVLPTWGNWAYPCCHVTOLSQQHHLALE
NISDIYLVSNKTCDGFSLASLNSPKNGSNQLVISRCANGLNVASYFIAVLRRSRSALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viral episome"
/note="similar to EBNAl of Epstein-Barr virus, Swiss-Prot
Accession Number P03211"
                                                                                                                                                                                                                                                                                                                                                                                                                    -1. _294
/note="similar to BRRF2 of Epstein-Barr virus, Swiss-Prot
Accession Number P03210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 force—"The 21-bp repeat unit encodes the heptapeptide Gly-Gly-Ser-Gly-Ala-Gly-Ala; approximately seven and one-half copies of this repeat in strain 594-S encode a mino acid repetitive domain."

//citation=[1]
//unction=encodes heptamer repeat of Gly, Ser and Ala //rpt_family="analogous to IR3 of EBV"
                                                                                                                                                                                      Submitted (31-MAR-1995) John L. Yates, Department of Human Genetics, Roswell Park Cancer Institute, Elm and Carlton Streets, Buffalo, NY 14263, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EBV,
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/note-similar to BKRF3 of EBV encoded by GenBank
Accession Number V01555; similar to to EBV uracil DNA
glycosylase, Swiss-Prot Accession Number P12888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="binds to or1P to permit replication of the
                                                                                                                                                                                                                                                                                                                             /specific_host="Paplo sp."
/db_xref="taxon:10394"
/clone="p701 (5.4 kbp Sall to EcoRI HVP DNA insert)"
/lab_host="Paplo sp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1843. .2259
/note="potential 15kDa protein; similar to BKRF2 of
Swiss-Prot Accession Number P03212"
Yates,J.L., Camiolo,S.M., Ali,S. and Ying,A. Comparison of the EBNAl proteins of Epstein-Barr virus and Virology 222 (1), 1-13 (1996)
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2241, 3009
                                                                                                                                                                                                                                                                                      /organism="Herpesvirus papio"/strain="594-S"
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/product="EBNA1"
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/db_xref="GI:775215"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA66372.1"
/db_xref="GI:775214"
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/db_xref="G1:775216"
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/rpt_un1t=612. .622
612. .770
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1843. .2259
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Yates, J.L.
Direct Submission
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DEARSLGLNVTRLRFVLIVCATLITASTVAIAGIIGWVGLVVPHIARLLTGHNHQQLL
PMAMCTGAILLLTDTLARSIGTTEIPLGILTAFVGAPFFLLLLLLRGGRQ"
complement(5834. .6856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 111796 CGTCGTTTTGAACTGATGGTGGAAGCGGCGGGTCACGCTGACGTGAGGGGAAGAAGAAT 111855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1111856 GCCGGAGAGGCGGAGACGTCCGCGAGGAATGCCGGCATATCAGCCAGTCAGGCAGAAGAG 111915
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                                                                                                                                              /note="probable ABC transporter, weakly similar to iron (iii) ABC transporter, ATP-binding protein {Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
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Herpesvirus papio
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
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/product="hypothetical protein"
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ALKADNYBLIORAMEEDWSDLPRCDIAVASRSTLVADMRQAMSKLNNQARLRYTTHL
VSTSFVSPAIQRAAGREWIELPNYIFALNVLYQMGIYAHVDFTRGQNCQQDNST"
complement(4099 . 4857)
/gene="ECs1697"
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/product-"utative ABC transporter permease protein"
/product-"utative ABC transporter permease protein"
/product-"13361163"
/db_xref-"01:13361163"
/translation-"MRIVNGCILILAAISTTFAAVSGAYHLDMQOLLALILRQENVPV
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ILMGLSYYIQLVAFCGGLMVAGWULTRRYTRHDPILTLVLVGTALGTLCGGGST
IKTLADPYTQLPSITFWLLGGLSTVTLRDLCYAAPIILIGSLPLFFLRWRMNLTLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"probable ABC transporter protein (permease), similar to ABC transporter permeases e.g. [Haemophilus influenzae] gi[2501391|sp][057130|YE71_HAEIN percent identity 40 in 323 aa"
CVSGVSVACKMLTTLGLTIDDAVSDGSQANAGORLIRAQGNAAALHOGWKAIONVLEW
SCGVSDYLDQMLALLRERYPDGNIACTRKAIPGTRLLASQAILAAGGLIHRAGCAETI
LLFANHRHFLHDNQDWSGAINQLRRHAPEKKIVVEADTPKEAIAALRAQPDVLQLDKF
                                                                                                                                                                                                                                                                                     /evidence-not_experimental
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/protein_id="BaB35118.1"
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/translation="MPTLILSVDKIANRITAPRNVLSRTSAGVLARLTTMSVSGYIAG
INNKMLVPSPLPAATGRSSGGIAYRRHCDDFPFSGTNRCVTSGRYPGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTLLAVRHASLGYSRHPVLRDVSFTLSQGTICCLLGANGCGKTT
LMRSTLGYPELKGEVLLDSLPVQTLSHRQRAQAIAWVPQAHDGIFAFSVLDMYLMGL
PATIGAFSVPGKQERLKATEQLEKLGILLLAARRRWNTLSGGERQLALIARALVQOPRL
LLLDEPASSLDFGHQICLLDTLAQLKNNGMMLMSTHHPLHANAIADSIIQVEPDGRV
TQGLPTEQLTTNKLAALYRVSADQIHHHLSAISH"
                                                                         SPOOATEIAQIAPSLAPHCTLALIGGINLTTLKNYLDCGIRLFITSAPYYAAPADIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unknown,similar to hypothetical proteins e.g. Orf2 [Escherichia coli CFT073] gi|3661479|gb|AAC61711.1| percent identity 98 in 214 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //note-"probable ferric enterobactin transport, similar ferric enterobactin transport ATP-binding protein [Escherichia coli CFT073] gil3661480|gb|AAC61712.1| percent identity 79 in 148 aa" //transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="putative ferric enterobactin transport
ATP-binding protein"
/protein_id="BAB35120.1"
/db_xref="GI:13361162"
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3445, .4089)
/gene="ECs1696"
complement(3445, .4089)
/gene="ECs1696"
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/gene="ECs1698"
complement(4854. .5834)
/gene="ECs1698"
                                                                                                                      complement(3219, ,3500)
/gene="ECs1695"
complement(3219, ,3500)
/gene="ECs1695"
                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                                              /note="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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CDS

and

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DDKRG TYKLGFTPRENDEYTLYTIKOGGEKDNPPYSONSGOKSRYWOWPEYDKESFYY
OGTTOLNDFRFTLKSRLYRDFFENTLAMYNSLADLKRKKGSYSHYSDYSOSGCLGLAAD
VRENDLLTFAVNWKDDVHREKGAPHAAYDRYEDRYWSLASEYGWAAADNVDVVAGISY
DWRDSYBAKHBEKDGSTHYDDNNGSAFNWOWMGKYHFVNEDTLALSYYDRKRFPTLK
ERYTTSKPAYNOIAIVNPQLKPERARGVDLTWNGAFTHDWGFEVSYYYNRYSDAILSH
OLDADTIQNONSGTVDYSGLDAGIKGKISNILDVGLSYALIHADAKRKDIGKTTDLPT
OTWTAMMTLKPWEPLESYLLSEEARSSSYSNSOCSOKAAGFAVTHIRADYTLGHGFSVN
ASVNNLFDTQYASEGFVEEGRNFWAGVEYTF*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="putative TonB dependent outer membrane receptor"
/product="putative TonB dependent outer membrane receptor"
/product="13451516.1"
/db_xxef="GI:13451158"
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DOPTMARLDKONVAQALSVPGVVLQXSGSRREDQVKRGFDSRQVPVPDGVPIYVP
YDGNUDLARILTNULGAVEVSKGYSSLLQGPNQMGGAINITTQKPTKPLEASLCFRQG
WSRSQDNAYDMHASFAASSELGYLQVSGSQLKODFLGLPHGVNNDIAGKHGKMINSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MGIIAWIIFGLIAGIIAKLIMPGRDGGGFFLTCILGIVGAVVGG WLATWFCIGGSISGFNHSFLVAVVGAILVLGVFRLLRRE" complement(430, .2400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor, similar to TonB dependent outer membrane receptor Prra [Escherichia coli CFT073] g1|3661477|gb|AAC61709.1| percent identity 97 in 656 aa"
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                                                                                                                                                               Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:kendegen-Info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6679-2047)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to YMGE_ECOLI gl|1787445 percent identity in 84 aa (Conserved in E.coli K-12)"
                                                5 (bases 1 to 291136)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H.
Hayashi,T.
0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(430, .2400)
/gene="EC31693"
/note="probable TonB dependent outer membrane
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/db_xref="GI:13361159"
                                                                                                                                                                                                                                                                                                                                                                                              1. .291136
/organism="Escherichia coli 0157:H7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_strain="RIMD 0509952"
/db_xref="taxon:83334"
126. 380
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complement(2426. .3280)
/gene-"ECs1694"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126. .380
/gene="ECs1692"
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/gene="ECs1692"
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                                                                                                                                                                                                                                                                                                                                        genome project.
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Escherichia coli 0157:H7 DNA, complete genome, section 7/20.
AP002556 BA000007
AP002556.1 GI:13361156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasakawa,C. and Shinagawa,H.
Complete nuclectide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin i genes of the enterohemorrhagic Escherichia coli 0157:17 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
                                                           DD 184996 ACGGCAGCCGCGAAGAAGTCAGCCAGCGATGCCAGCACCATCAGCCGCGAAGC 185055
                                                                                                                                                                        185056 CATGCGACTGATGCTGCGGACTCAGCACGCGCGCACACGTCAGCCGGACAGGCCGCG 185115
                                                                                                                                                                                                                                                                                                         TCGTCGCCTCAGTCAGCGTCTTCCAGCGCAGGAACGCCATCAACAAAGGCTACTGAAGCA 185175
                                                                                                                                                                                                                                                                                                                                                                                              ||| :::||||||:::
------TGAAAAGTGCTGCCGCTGCAGAGTCCTCAAAAAGCGGGGGGTACC 185223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 185224 AGTGCCGGTGCGGCGAAAACGTCAGAAACGAATGCGGCAGTGTCACAATCAGCCGCC 185283
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Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishil,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnish,M., Hayashi,T., Yasunaga,T., Honda,T.,
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Yokoyama, K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                  SerAspAlaLeuGluAlaLeuAlaAspGln---ThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                            106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 AlaLeuAspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGln 145
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Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                           86
                                  --- AlaLeuGluAlaLeuAla
                                                                                                                                      AspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 185284 ACTTCTGCATCCACGCGACCACG 185307
                            ThrThrAlaIleGluAlaAlaSerSerAsp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ASNValASnThrLeuProThrThr 153
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                         /translation="MRRGATSYLPMNKTTEYIDAMPIAASEKAALPKTDIRAVHQALD
AEHRTWAREDDSPQGSVKARLEQAWPDSLADGQLIKDDEGRDQLKAMPEAKRSSMFPD
PWRTNPVGRFWDRLRGRDVTPRYLARLTKEEQESEQKWRTVGTIRRYILLILTLAQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VATWYMKTILPYQGWALINPMDMVGQDLMVSFWQLLPYMLQTGILILFAVLFCWVSAG
FWTALMGFLQLLIGRDKYSISASTVGDEPLNPEHRTALIMPICNEDVNRVFAGLRATW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mRLIVVSIMVTLLSGCGSIISRTIPGQGHGNQYYPGVQMDVRDS
AWRYVTILDLPFSLVFDTLLLPIDIHHGPYE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MMTMYATLEEAIDAAREEFLADNPGIDAEDANVQQFNAQKYVLQ
DGDIMMQVEFFADEGEEGECLPMLSGEAAQSVFDGDYDEIEIRQEWQEENTLHEWDEG
                                      /note="similar to membrane glycosyltransferase MDOH_ECOLI
gi|1787287 percent identity 100 in 847 aa but differs at
N-ter (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gi|1787289 percent identity coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 184936 CGCCGTTTTGAGCTGATGGTGGAAGAGGTGGCGCGTAACGCGTCCGCGGTGCCACAGAAC 184995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"identical to YCEK_ECOLI g1|1787288 (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LysLeuAlaLeu
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45
21
69
13
                                                                                                                                                                                                                                                                /product-"membrane glycosyltransferase"
/protein_id="BAB34850.1"
/db_xrefe"GI:13360891"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"hypothetical protein"
/protein_id-"BAB34851.1"
/db_xref="G1:13360892"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyThrLeuThrAsnLeuLeuGlyAsnAlaProGlu-----
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/db_xref-*GI:13360893"
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/gene="ECS1429"
/note="similar to MSYB_ECOLI
99 in 125 aa (Conserved in E.
                                                                                                                                                                                                                                 /evidence-not_experimental
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/gene="ECs1429"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /os2. .8059
/gene="ECS1428"
/832. .RNE^
                                                                                                                                                           /codon_start=1
/transl_table=11
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/gene="ECs1428"
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119.50
44.59%
30.41%
15.38%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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LISIHAGNGFWINRPLANPKHLAVSSFSMENPOGFGLLQRGRDFSRRFEDLDDRYDLRPS
AWYTPKGEWGKGSVELYPINDETNDNIVAYWPTPDQLPEPGKEMNFKYTIFSRDED
KLHAPDNAWYQGTRSTGDVKGSNLTROPPGGTAFVVDFTGAEMKLPEDTPYTAQTS
IGDNGEIVESTVRYNPVTKGWRLVMRVKVKDAKKTTEMRAALVNADQTLSETWSYQLP
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/product-putalive
/product-putalive
/product-id-"aba14846.1
/db_xref-"G1:13360887.1
/db_xref-"G1:13360887.1
/db_xref-"GI:THTHYQGDITKLAVDVIVNAANPSLMGGGGVDGAIHRAAGP
/LIDACLKYRQQOGCPTGHAYUTLAGDLPAKAVVHTVQFVWRGGEQNEDQILQDAYI
NSLRLVAANSYTSVAFPAISTGVYGYPRAAAAEIAVKTVSEFITRHALPEQVYFVCYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAGE ALON-MANUPPAQUERFLDSIRAMIMILGIPFHISLIYSSHTWHVNSAEP SLWLTLFNDFIHSFRQVFFVISGYSYMLFLRYPLKKWWKVRVERVGIPMLTAIPLL SLWLTLFNDFIHSFRYGYKGAESWPGLSLYDKKNTLAMELISHWFTLLYVWTTLCYWIFKRI RNNLENSDKTNKKFSWYKLSVIFLCLIGGYAVIRRITIFIYYPPILSNGTFNFIVWQTL FYLPFFILGALAFIESWYKLSYTFPSRGCTLAAALAFVAYLLNQKSGGDAWYETES VITWVLGLWMVNVYFSFGHRLLNFQSARVTYFVNASLFIYLVHHPLTLFFGAYLTPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MMKRTPTSTKDSLPNKEMNDLPRLASAVLPLCSOHPGQCGLFPL
EKSLDAFAARYRLAEMSEHTLDVQYYIWQDDMSGRLLFSALLAAAKRGVRVRLLLDDN
NTPGLDDILRLLDSHPRIEVRLFNPFSFRLLRPLGYITDFSRLNRRMHNKSFTVDGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSIDGKTVFIGSFNFDPRSTLLNTEMGFVIESFTLAGLIDKRFIGSGYDAAWGLRLDR
WGRINWYDRHAKKEIVLKKEPATSFWRRVMVRLASILPVEWLL"
complement(2038. .3195)
/gene="ECS1425"
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SNLPSVFRDMKYADYQQIQFNHDKAYWNNLKTPFKLEFYHQGMYFDTPVKINEVTATA
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GAGQVYGLSARGLAIDTALPSGEEFPRFKEFWIERPKPTDKRLTIYALLDSPRATGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLVGGRNIGDAYFGAGEEPLFSDLDVWAIGPVVEDVADDFARYWYCKSVSPLQQVLDV
PEGEMADRIELPASWHNDAMTHRYLRKMESSPFINHLVDGTLPLIWAKTRLLSDDPAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEGKAKRHSLLPQRLFDIMGSPSERIDIISSYFVPTRAGYAQLLRMYRKGVKIAILTN
SLAANDVAVVHAGYARWRKKLLRYGVELYELKPTREQSSTLHDRGITGNSGASLHAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(20038. .3195)
/gene="ECS1425"
/note="similar to MDOC_ECOLI gi|3025226sp|P75920 percent identity 99 in 385 aa (Conserved in E.coli K-12)"
/codon_starte.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to YMDC_ECOLI gi|1787284 percent identity 99 in 493 aa (Conserved in E.coli K-12)"
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/product-glucans blosynthesis protein"
/protein.id="BAB34848.1"
/db_xref="Gl:13360889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence-not_experimental
/product="putative synthase"
/protein_id="BAB34847.1"
/db_xxef="G1:13360888"
                                                                                                                                                                                                                                                                    EENAHLYERLLTQQGDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/gene="ECs1426"
3588. .5123
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/gene="ECs1424"
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/gene="ECs1426"
                                                                                                                                                                                                                                                                                                                                              'gene="ECs1424"
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Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Makino, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T., Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and Shinagawa, H. Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coll 0157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
MRL.http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                     AP002555 222605 bp DNA linear BCT 07-MAR-2001
Escherichia coli 0157:H7 DNA, complete genome, section 6/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (sites)
Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ECs1423"
74. .607
/gene="ECs1423"
/note="similar to B1045_ECOLI g1|1787283 percent identity
100 in 177 as (Conserved in E.coli K-12)"
/codon_start=1
                                                                                                                                      (strain:0157:H7, sub_strain:RIMD 0509952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (sites)
Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 (bases 1 to 222605)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                   Escherichia coli 0157:H7
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete genome sequence of enterohemorrhagic Escherichia coll 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Escherichia coll 0157:H7"
/strain="0157:H7"
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1, ,222605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Residues 1 to 289 of 296 are 84.42 pct identical to residues 1 to 289 of 292 from GenPept 118 : g1/7162108 [emb[CAB76676.1] (Y19180) putative catalase [Salmonella typhimurium]"
                                                                                                                                                                                                                                       /translation="MAFRMSEOPRTIKIYNLJTGTNEFIGEGDAYIPPHTGLPANSTY
IAPPDIPAGFVAVFNDESSWHLVEDHRGKTYYDVASGDALFISELGSLPENYTWLSP
EGEPOKWNGTAMYKDAEAEKLFRIRBAEETKNSLMQVASEHIAPLQDAVDLEIATEEE
SZLLEAWKKYVLLNRVDTSTAPDIEWPVIPEV"
/gene="21921"
                                                 ť
                                                                                                                                                           /transl_table=11
/product-*putative tail fiber protein of prophage CP-933x"
/protein_id="AAG56009.1"
/db_xref="G1:12514849"
                                          /note="Residues 1 to 191 of 193 are 94.76 pct identical residues 1 to 191 of 191 from GenPept 118 : gil2367120|g91AAC74619.11 (AE000252) orf, hypothetical protein [Escherichia coll]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4754 CATGCGACTGATGCTGCGGACTCAGCACGCGGCCAGCACGACGCCGGACAGGCCGCG 4813
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/protein_id="AAG56010.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GluvalvalGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProlle 125
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function="orf; Other or unknown (Phage or Prophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ThrThralaIleGluAlaAlaSerSerAsp-----AlaLeuGluAlaLeuAla
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/protein_id="AddSoon.com"/
// Add_xref="G1:12514847"
// CLanslation-winnavkiscurce_protein_of_propriege_cr_553A
// Clanslation-winnavkiscurce_protein_of_protein_of_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavkiscurce_winnavk
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SDDLNGINVKYRYEFMDALGLITSFSYANAEDEQKTRYSDTRWHEDSVRNRWFSVWAG
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GGGVQPNFXSEVAIDIAYEGSGSGDWRTDGFIVGVGYKF"
4319. 7240
                                                                                                              /note="Residues 1 to 199 of 199 are 75.87 pct identical to residues 1 to 199 of 199 from GenPept 118 : gi|7532789|gb|AAF63231.1|AF151091_2 (AF151091) Lom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGWFKLATYTWPQASSVVSITLIGGAGFNVGSPQQAGISELVLRAGNGNPKGITGAL
WQRTSTGFTRFAWVNTSGDTYDIYVALGNYATGVNIQMDYTSNASVTHTSPAYSANK
BGGLTDGTYYSLYTPSEQFYPPGAPIPWPSDYVPSGYALMQGQTFDKSAYPKLAAAYP
SGVIPPMRGWTIKGRASGRAYLSQEQDGIKSHTHSASASSTDLGTKTTSSFDYGTKS
TNNTGAHTHSVSGTAASAGHTHSVTGASAVSQWSQNGSVHKVVSAASVVTSAAGAHT
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PALVDAALADNAAAVFEPAAAEALCSAAVSEDLAFVSDVLAAFAELPAAVAEEAALLA
LEAALVSDDFAASFEADASLAEEAASDAFVVAVDAEVAADCCDTAAFVSDVFAAPALV
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                          /function="putative membrane; Other or unknown (Phage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Residues 1 to 498 of 973 are 95.78 pct identical residues 1 to 498 of 1122 from GenPept 118 : gi|1787636|gb|AAC74454.1| (AE000234) putative membrane protein [Escherichia coli]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="putative membrane protein of prophage CP-933X"
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/protein_id="AAG56008.1"
/db_xref="GI:12514848"
                                                                                                                                                                                                                                                                                                                                                                                      /product-"putative outer membrane protein of prophage CP-933X"
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7240. .7821
7240. .7821
7240. .7821
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complement(4822. .5571)
/gene="21919"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:12514846"
                                                                                                                                                                                                                                                                             [prophage P-EibA]"
                                                                         Prophage Related)"
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/transl_table=11
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/gene="21918"
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LASVILDNLPPRPFNIRMYRETADSTTDQLQNRTLHGSYTEIIDVKQCYPNTAIVGLO
VDABOFGGOMTVNYHIRGRIIQYPSNYDPRKRTYSGIWDGSLKPAYSNNPAMCLWDM
LTHPRYGMGKRLGAADVDKWALYAIAQYCDQTVPDGFGGTEPRNTFNAYLSQQRKAWD
VLSPCSAMRCMPWNGQTLTFVQDRPSDVWPTPAVWWWMITAWGFATASAP"
1245. .3593
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NLNSMWAVKLQQMQDGRLYIAGIGAGIENTPAGMQSQVLLAADRIAMINPANGNTKPM
FVGGGDQIFWNEVFLKYLTAPTITSGGNPPAFSLTPDGRLTAKNADISGNVNANSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Residues 8 to 366 of 388 are 81.05 pct identical to residues 11 to 369 of 1132 from GenPept 118 : 91|215|125|9b|AAA96553.1| (302459) J (tail:host specificity;1132) [bacteriophage lambda]"
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SELTISGKGTDARLVTATATEHRSGLPLGEYTLLVRAINSYGQGGEPATTFRI
AAPAAPSRIELTPSTOITAPHLAVYDPTVQFEFWFSERRIADIRQVETAARYLGSA
LYWIAASINIKPGHDYYFYIRSVNTVGKSAFVBAVGRASDDARGYLDFFKGEIGKTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function "putative structure; Structural component (Phage
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NKTPLTDTDGNPVIHGVTAVWRAGEQEQTPPEGFESSGAETALGVEVTKAKPVTRTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNVTINENCRVLGKLSANQIEGDLVKTVGKAFPRDSRAPERWPSGTITVRVYDDQPFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="0-island #52; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655" 130. .1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Residues 1 to 781 of 782 are 62.37 pct identical to residues 376 to 1131 of 1132 from Genept 118 : gi[21515] gpl[AAA96553.1] (J02459) J (tail:host specificity;1132) [bacteriophage lambda]"
Grotbeck, E.J., Davis, N.W., Lim.A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
Direct Submission
Submitted (22-007-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
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CP-933X"
                                                                                                                                                                                                                                                                                                                                                       1. .10432
/organism="Escherichia coli 0157:H7 EDL933"
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3661. .4260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /serotype="0157:H7"
/db_xref="taxon:155864"
/note="enterohemorrhagic"
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/db_xref="G1:12514844"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="EDL933"
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/gene="21917"
3661.
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/gene="Z1916"
1245. .3593
/gene="Z1916"
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130. .1296
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/gene="Z1915"
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/gene="21917"
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FEATURES

Similarity:

Best Local

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/function="putative structure; Structural component (Phage or Prophage Related)"
//note="Residues 61 to 451 of 451 are 96.93 pct identical to residues 1 to 391 of 391 from Genpept121:
dbj|BAB19563.11 (AP000400) host specificity protein J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="putative factor; DNA packaging, phage assembly (Phage or Prophage Related)"
/note="Residues 1 to 224 of 226 are 92.85 pct identical to residues 1 to 224 of 225 from Genpept121: dbj|BAB19564.1|
(AP000400) tall assembly protein I [Escherichia coli
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/function="putative factor; DNA packaging, phage assembly (Phage or Prophage Related)"
/note="Residues 1 to 223 of 224 are 92.37 pct identical to residues 24 to 246 of 247 from Genpepti21: dbj|BAB19565.1|
(AP0000400) tail assembly protein K [Escherichia coli
                         EKEAIVDNGARFEPQSGSLNSVIPPAVQHLTVEVSAADGQYLAQAKWDTPRVVKĞVRF
SLRLTSGKGTDARLVTTAITADTEHRFSGLPLGEYTLTVRAINSYGQGEPATTTFRI
AAPAAPSRIELTPGYRQITATPHLAYDPTVOFFWSEKRIADIROYETAARYLGSA
LYWIAASINIKPGHDY YISSVUTVGKSAFVGRASDAREGYLDFRKGEIGKTHL
AQEUWTOIDNGOLAPDLAEITRSTRWSNETTQTVRKKLENDSAAIQQIQKVQVDTNN
NLNSWWAVKLQQMQDGRLYIAGIGGIENTPAGMGSQVLLAADRIAMINPANGNTKPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="aak16946.1"
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//tb_xref="G1:13259575"
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OSILVNRTPLTDTDGNPVIHGVTAVWRAGEQEQTPPEGFESSGAETGLGVEVTKAKPV
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TTSQPLASYLLDNLPERPFNTRWYRETADSTSDQLQNKTLWSSYTEIJDVKQCYPNTA
TVGLQVDADFOFGGQOMTVNTIRGRITADSTSDQLONFEKRTYSGLWDGSLKPAYSNNPAM
CLWDMLTHPRYGMSKILGAADVDKWALTALAQYCDGTVPGFGGTEPRHTFNAYLSQD
RKAWDVLSDFCSAMRCMPVWNGQTLTFVQDRPSDVVWPTPAVMWWMITAWGFATASA
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/db_xref="G1:13259576"

/translation="MATTNAFSLASPPLARICLHGDLQRFGRRLSLYWNTAAEAIRAL
SLQVPGFRRENNEGWYOITARSYDTAPEARYARLHEQLGEGTVIHIVPRLAGAGGGGT
QIVLGAAAIVGSFFFARASAALWGSALAAGGFSATTWLFSLGASWILGGVAQULAPKA
KTPDYRATDNGRPYFSSLDNMIAQGNPMPVPYGEMLVGSRRISQDISTRDEGGGT
                                                                                                                                                                                                                                 FVGGCDOIFWNEVFLKYLTAPTITSGGNPPAFSLTPDGRLTAKWADISGNVNANSGTL
WYVINBURYLKLSANQISGDLVKTVGKAFPRDSRAPERWPSGTITVRVYDDOPFD
ROIVIPAVAFSGAKHEKEHTDIYSSCRLIVRKNGAEIYNRTALDNTLIYSGVIDMPAG
HGHMTLEFSVSAWLIVNWYFPASISDLLVVYMKKATAGITIS'
TAHPAPDRIQVSTLPDGVETYGVWGLSLPSLCRRLFRCVSVRENTDGTFAITAVQHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative tail component of cryptic prophage
CP-933p"
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complement(5588. .6943)
/gene="26030"
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/gene="26031"
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/transl_table=11
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9331 50 21

Length: Matches: Conservative:

4.76 119.50 38.59%

Percent Similarity:

Alignment Scores: Pred. No.:

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AE005333 10432 bp DNA linear BCT 21-MAR-2001 Escherichia coli 0157:H7 EDL933 genome, contig 2 of 3, section 2 of
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Pose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfal, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Genome sequence of enterchaemorrhagic Escherichia coll 0157:H7 Nature 409. (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 10432)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
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                                                                                                                                                                2163 CGTCGTTTTGAACTGATGGTGGAAGAAGCGGCGTCACGCTGAGGAGGGCGAAGAAGT 2104
                                                                                                                                                                                                                                                                                                                                     2103 GCCGGAGAGGCGGAGACGTCCGCGAGGATGCCGGCATATCAGCCAGTCAGGCAGAAGAG 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1983 GAAAGTGCAGCCGCTGCAAAGCAGTCAGAGGAGGGTCCTCGTCGTCCTCGGCCTCTGCGGCC 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1923 GCTCAAAAAGCCAGTGAGTCATTACAAAGTGCAACAGATGCTGAGTTGTCAAAAAAGACG 1864
                                                                                                                                                                                                                                                                                                                                                                                                                      2043 AACGCTGCAAATGCTGACACTTCAGCAGGGGATGCATCGGAGTCAGCCCGGCAGGCGGCA 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AlaLeuAspValLysLysThrLysAspThrLysProValValLysLysGluGluArg--- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GlnAsnValAsnThrLeuProThrThr------GlyGlu 155
                                                                                                                                                                                                                                                                                              4 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla 85
                                                                                                                                                                                                            31 ArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu--- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
  66
47
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  Mismatches:
Indels:
                                                                                                                           GlyThrLeuThrAsnLeuLeuGlyAsnAlaProGlu-
                                           Gaps:
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/transl_table=11
/product=*putative Lom-like outer membrane protein of
cryptic prophage CP-933P*
/protein_id=*AAK1694.1*
/db_xref="GT:1329573"
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IPEQDRVITQVVILDADRKQIQCVVRPLQILRADGTWENIGGMK"
complement(1159. .2472)
/gene="L6027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OAAESAAAAKOSEEASSSSASAAAOKASESILOSATDELSKKTAESAAGNAARDATTA
AEKARESAESAOSAEOSRIAAEEAVNRIPTVVGPPGPKGEPGPAGPOGPKGEKGETG
TGPAGATGERGFAGDAGPAGPOGPKGDRGERGETGLTGNAGPGGPKGDTGAAGPAGPG
GPKGETGAAGPVGATGPGPGKGDPGETQLTRINSHGWFPGTDAAGPAGP
TFLAPKDTTRYQGFFQDGFKGDPGTOIRFRIGPASIIETNSHGWFPGTDGALITGL
TFLAPKDTTRYQGFPGILQVRRGDGPWQDVKGLDEVGSDTGRTGE*
COMPLEMENT (2624. . 3223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prophage Related).
// Anote="Residues 1 to 199 of 199 are 96.48 pct identical to residues 1 to 199 of 199 from GenPept121: dbj|BAB19561.1|
(AP0000460) outer membrane protein Lom precursor [Escherichia coli 0157:H7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or Prophage Related)"

Anote-"Residues 1 to 782 of 782 are 99.87 pct identical to residues 25 to 806 of 806 from Genpept121: dbj|BAB19562.1|
(AP000400) host specificity protein J [Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AaK16945.1"
\/Larailation="WYUDDNOYERYSFSALKDRHTAVEVNYTDPQNGWGTSTELVED
/translation="WYUDDNOYERYSFSALKDRHTAVEVNYTDPQNGWGTSTELVED
PEAILRYGRNLLKMDAFGCTSRGQAHRAGLWVIKTGLLETQTVDFTLGSGGLRHTPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or Prophage Related)"

Anote-"Residues 1 to 437 of 437 are 94.96 pct identical to residues 1 to 437 of 437 from GenPeptl21: dbj|BhB19560.1|

(AP0000400) tail fiber protein [Bscherichia coli 0157:H7]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative structure; Structural component (Phage
                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="putative structure; Structural component (Phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MTVKISGVLKDGTGKPVQNCTIVLKARRTSSTVVVNTVASENPD
EAGRYSMDVEYGQYSVILLVEGFPPSHAGTITVYEDSQPGTLNDFLGAMSEDDVRPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRRFELMVEEAARHAEEAKKNAGEAETSARNAGISASQAEENAANADTSAGDASESAR
residues 41 to 129 of 129 from Genpept121:
gb|AAD25465.1|AF125520_60 (AF125520) hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
/product="putative tail fiber protein of cryptic prophage
CP-939P*
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                                                                                                                                  /product-"unknown protein encoded by cryptic prophage
CP-933p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAK16943.1"
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                                                                                                                                                                                                        /protein_id-"AAK16942.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="26028"
complement(2624. .3223)
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/gene="26029"
                                                                                                                                                                                                                                                                                                                                                                         complement(1159. .2472)
/gene="26027"
                                                         Bacteriophage 933W]"
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/trans1_table=11
                                                                                                                      /transl_table=11
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Telftygrnnopealadramlsmlsbsgsagsgsiqdkisqckrpvssgnkqcppesi
QCPITLERPEEGVFVKNSDSSAVCCLFDFDAFSRLASEGSYHPLTREPITASMIISPD
RCVYDPIKGNFIIRDS"
                                                                                                                                                                                                                                                                                                                                                                                                           AE006458 9331 bp DNA linear BCT 21-MAR-2001 Escherichia coli 0157:H7 EDL933 genome, contig 2 of 3, section 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Residues 53 to 176 of 176 are 37.50 pct identical to residues 13 to 140 of 140 from GenPept121: dbj|BAA36750.1| (AB016764) ORF4 [Escherichia coli]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Residues 1 to 89 of 89 are 92.13 pct identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases i to 9331)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-FEB-2001) Laboratory of Genetics, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706-1577, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                         2456 CCCGAGGAAGAGGTGAAAGAGTCAGAGGCCCCTGTTGCACCTGAAGCTAAGAAGCCCCA 2515
                                                                                                                                                    /codon_start*1
/transl_table=11
/product="unknown protein encoded by cryptic prophage
   114 AlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThrLys 133
                                                                                                                   134 AspThrLysProValValLysLysGluGluArgGlnAsnValAsnThrLeuProThrThr 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="orf; Other or unknown (Phage or Prophage
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/servef="a0157:H7"
/db_xref="taxon:155864"
/note="enterohemorrhagic"
complement(201. .731)
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/db_xref="G1:13259570"
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Escherichia coli 0157:H7 EDL933
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complement(888. .1157)
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/gene="26025"
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Plunkett, G. III.
Direct Submission
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AE006458/c
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                                                    AUTHORS
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    JOURNAL
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Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.
U19361
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Hyperoartia;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Hyperoartia;
Eutomyzontiformes; Petromyzontidae; Petromyzon.
1 (bases 1 to 3763)
Jacobs, A.J., Kamholz, J. and Selzer, M.E.
The single lamprey neurofilament subunit (NF-180) lacks
multiphosphorylation repeats and is expressed selectively in
projection neurons
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                                                                                                                                                                                                                                                                                                                                 31 ArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu---
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                                                                                                                             297816
49
22
66
47
5
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                                                                                                                                                              Conservative:
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                                                                                                                               Length:
Matches:
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Best Local Similarity:
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EEPEESPTEEEPKKPAAAKPAKAPAKPKPAPKAEAEEKPEPAKPAQAKPAPAEEEED
EKEDDEEEEEVEEVKPEDAKPVKSKPAPAKEEEDEPKPAKOPPKPKRPARPKEEPE
DKAEPAKEKHSPVEERKPIKEIAKPAKAAPKADKEPEAAEPKKIEVKKVVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSYTESSVTCSYRRAYADASRGGSKRLLSTPSSGFRSQSWCRGS
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DVIDDINGEKTTVQIEQEHLDEEI QRLREKTDDEVRLNETEALINAFRKNVDDTSLV
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GQLEGQSARNIETAEEWFKGKFSQLTEAAEQNNDAIRSAKEEITEHRRKLQMRCTELD
ALAGTKESLERQLSEMEERHQSDVGNLQDAAQQLENELRNTKWEMARHLREYQDLLNV
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                                                                                                                                      Jacobs, Department of Neuroscience,
Stemmler Hall, 3600 Hamilton Walk,
                                                                                                                                                                                                                                                                  /organism="Petromyzon marinus"
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/clone="clones LIF5, LIF13, and LIF22"
/tissue_type="central nervous system"
/clone_lib="Lambda gtil cDNA library from larval Lamprey CNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2276 AAGTCAGATGCTGAAGAAGCTGAGGGTGAGAGCAGAAGAGGCTGCAAGTCAGAGGG 2335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAla 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAlaValValLysAlaAspAsnAlaAla-----SerAspAlaLeuGluAlaLeuAla 94
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     Res. Mol. Brain Res. 29 (1), 43-52 (1995)
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/note="180 kDa neurofilament subunit"
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Matches:
Conservative:
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Indels:
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                                                                               Jacobs, A.J.
Direct Submission
Submitted (03-JAN-1995) Alan J. J
University of Pennsylvania, 452 s
Philadelphia, PA 19104-6087, USA
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Brain Res. Mol. Brain
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GTAACPPYHIAFVVGGLSADQTLKIAKLASTKYYDNLPTSGNDQGAFRDIELEKWLL
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EKEHNROGVITASLARENHAAGHVOLDINRPLBADWODLARLEVGTRYSUSGPTVVAR
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MRAVWHWENSPRLAPRILVDDKGNNFFSQFEQQHRCASCPAGH*
COMP.Lenient (6092.7372)
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NFFMPGTGINEVAHGAETTGYVAAEPFTLKVFISHAPPTSIVDAMAHBEILQIVVFSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mearisterhyQRQQKLKEQVDTRVAAaiekKGILIVFTGNGKG
KSTAAFGTVTRAVGHGKTVGVAQYIKGQWDNGEYNLLQPLGVEFHIMGTGFTWETQNR
QADIDAAKEVWSESKRMLADKRYDLVVLDELTYMLAYHYLDTEEVIASLQNRPAQQSV
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/protein_id="BaB341B1.1"
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   NGPRFDLLSMLIAAVRSNLGVALLPRFAIQHDLDSGDMVIPCDVPIRTGNRFIMTWQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4332..5984)
/gene="ECs0757"
/note="probable fumarate hydratase, similar to fumarate hydratases e.g. fumarate hydratase class I, aerobic (fumarase) - Escherichia coli gill20598|sp|P00923|FUMA_ECOLI percent identity 68 in 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="probable transport protein, similar to
glutamate/aspartate transport proteins (proton glutamate
symport proteins) e.g. [Bacillus stearothermophilus]
gi|121467|sp|p24943|GirT_BACST percent identity 38 in 416
aa,also similar to C4-dicarboxylate transpor"
                                                                                                                                                                                /note-"probable cob(1)alamin adenosyltransferase, similar to cob(1)alamin adenosyltransferases (corrinoid adenosyltransferases) e.g. [Escherichia coli) gi|115148|sp|p13040|BTUR_ECOLI percent identity 67 in 200
                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/product="putative cob(1)alamin adenosyltransferase"
/protein_id="BAB34179.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVTGROCHSOLLKMADTVSEIRPVKHAFDNGIQAQPGIDW" complement(4332, .5984)
/gene="ECS0757"
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/product="putative funarate hydratase"
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                                   EKSDSPHLQQFREWLLAKSVVPQEM'
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/gene="ECs0758"
                                                                                                                                .4322)
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                                                                                                                      complement(3720./gene="ECs0756"
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complement(7533.
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/transl_table=11
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/transl_table=11
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RELAFKLGLEGKLVQOFTKIFWGLATIFLERDLALIEINPLVITKQGDLICLDGKLGA
DGNALFRQPDLREMRDQSQEDPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTWDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLHGGEPANFLDVGGGATKERVTEARKILSDDKVKAVLVNFGGIVRCDLIAGIIG
AVAEVGVNVPVVVRLEGNNAELGAKKLADSGLNIIAAKGLTDAAQQVVAAVEGK"
1245. .2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSILIDKNTKVICQGFTGSQGTFHSEQAIAYGTKMVGGVTPGKG
GTTHLGIPVENTVREAVAATGATASVITVPAAPFCKDSILEAIDAGIKLITITEGITPT
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AAYIKEHVTKPVVGYIAGVTAPKGKRMGHAGAIIAGGKGTADEKFAALEAAGVKTVRS
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BEFLRTPLFSHSKRRIPLUDYCKYYLGJVKETVIKLERQYTTJWTWGPTVQVIELAVN
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LFEEELLPVCSGSLLAMSDQKLSVAELLTELPLLHQSTRITGWERMFALSGVSSPLVN
                                                                                                                Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:kendgen-life.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
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VKCQVHAGGRGKAGGVKVVNSKEDIRAFAENWLGKRLVTYQTDANGQPVNQILVEAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /hote="similar to SUCC_ECOLI gil1786948 percent identity 100 in 388 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"similar to SUCD_ECOLI gi|1786949 percent identity
100 in 289 aa (Conserved in E.coli K-12)"
/codon_start=1
                                                             Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence-not_experimental
/product-succiny1.coa synthetase alpha subunit"
/protein_id="BAB34177.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                 Cocation/Qualifiers
1. .297816
/organism="Escherichia coli 0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="0157;H7"
/sub_strain="RIMD 0509952"
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1245. .2114
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/gene="ECs0754"
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79. .1245
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/gene="ECs0755"
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1 (sites)
Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokwa,K., Ishil,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
Shinagawa,H.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Hayahl,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
Shinagawa,H.
Complete genome sequence of enterohemorrhagic Escherichia coll
Ol57:H7 and genomic comparison with a laboratory strain K-12
DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                           126 AlaLeuAspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGln 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comparative analysis of the whole set of rRNA operons between a enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                  86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                        146 Asn.------GlyGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete nucleotide sequence of the prophage VT1-Sakai carryli
Shiga toxin i genes of the enterchemorrhagic Escherichia coli
0157:H7 strain derived from the Sakai outbreak
Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297816 bp DNA linear BCr U/-M
H7 DNA, complete genome, section 4/20.
                                                                                                                 1277 GCTCAAAAAGCCAGTGAGTCATTACAAAGTGCAAAGAGGCGGAGTTGTCAAAAAAGACG
                                                                                                                                                                106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle
                                                                                                                                                                                                            1337 GCAGAAAGTGCAGCCGGTAATGCAGCCAGGGATGCA--------
                                                                                                                                                                                                                                                                                                          1373 ACGACCTCAACAGAAAAAGCCCGGGAATCAGCAGAAAGCGCACAGTCAGCGGAACAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derived from the Sakai outbreak
Genes Genet. Syst. 74 (5), 227-239 (1999)
20198780
23/816 h
hia coli 0157:H7 DNA,
BA000007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 GluSerAsnPro 159
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KVGARTYRYVATDBKFCVTRESHSGCFTNLLHRLGWPKGEISRKIEVMLNASPVSAAM
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IDAENHRGTGSDFHCNLNAVEYPCGEGISVVDFHATIVFHELLHVFHNLNGERLKVES
SRAESQKYSPLLLEEARTVGLGAFSEEVLSENKFHEEIGMPRRTSYPXDSALIHDDNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="WKLISWILEDGDKLPHRHVFNCMGYDGDNISPHLAWDDVPAGTK
SFVVTCYDPDAPTGSGWWHWVVVNLPADTRVLPQGFGSGLVAMPDGVLQTRTDFGKTG
YDGAAPPKGETHRYIFTTFYHALDVERIDVDEGASGAMYGFNVHFHSLASASITAMFS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pct identical to
coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1097 GCCGGAGAAGCAGAGACGTCCGCGAGGAATGCCGGCATATCAGCCAGTAAGGCGGAAGCG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
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                                                                                                                                                                                                                                                        function "orf; Other or unknown (Phage or Prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LysLeuAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="orf; Unknown function"
/note="Residues 1 to 158 of 158 are 99.36
residues 1 to 158 of 158 from Escherichia
MG1655: B0773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="orf, hypothetical protein"
/protein_id="AAG55144.1"
/db_xref="G1:12513759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 GlyThrLeuThrAsnLeuLeuGlyAsnAlaProGlu-----
                                                                                                                                                                                                                                                                                                       'note-"No significant matches"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7668. .8144)
/gene="ybh8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="bloA"
/note="20993"
complement(8203. 9492)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSLGFQQVRLHPLL"
complement(7668..8144)
/gene="ybh8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8203. .9492)
                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                              /gene="20990"
6462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                            5462. .7160
/gene="20990"
                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="20992"
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128.50
38.59%
26.63%
16.54%
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JOURNAL MEDLINE PUBMED REFERENCE

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SARQAAESAASAKKSEEASSSASEAAQKASESLOSATDAELSKKTAESAAGNAARDA
TTSTEKARESAESAGSAGSAEDSRIAAEDAVNRIPTVVOEPGFKGEPGFAGFOGFKGDKGE
RGDTGPAGATGERGPGGDTGAGCPGCPKGDRGERGTGLTGNAGFOGPKGDTGAAGPA
GPQGFKGETGAAGPVCATGPOGPKGDPCETGTRFKLGPMRIIETNSYGWFPGTDGALI
TGLTFLDPKDATQVQGMFQHLQVRFGDGPWQDVKGLDEVGSDTGRTGE"
7/Gene="20984"
2004. . 2312
                                                                                                                                                                                                                                                                                                                             /note="kesidues 1 to 102 of 102 are 98.03 pct identical to residues 28 to 129 of 129 from Genbept 118 : 9114585437|gb|AAD25465.1|AF125520_60 (AF125520) hypothetical protein [Bacteriophage 933W]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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/protein_id="AAGS5139.1"
/bcotein_id="AAGS5139.1"
/translation="wwwavtoaelendmulrklmoslcGcckHdDcenGRS17AQLR
/translation="wwwavtoaelendmulrklmoslcGccKHdDcenGRS17AQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QWFEDNDERYKKDEVPIVNTKQHPYLDNVTNAARIESDRAIGIFVDGDFSVNOKTAFS
KLERDFENVALIYREDDDFSKYDRKLSDTYHDIJCEORLRFTEDKRDFYLLNLLEKELR
EISAGDGLISMYAKKRNHAWFDFFRNLALLKAGEIFRCTYNYKNHGISFGEGLIYLD
MDMILTGKLGTIYABDGISKHYDDRRNDSWNIENSAIIVNRSNHPALLEGLSFWHSKVD
AHPYYDGLGKGVKKYFNFTPLHNYNHFCDFIEFNHPNIIMNTSQYTCSSW"
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SAADLSNVYESVIRAVHDSRSRLIDQHTVDMIGNTVLDALSRSQTFRDAVSYGIHNEK
VHIGCIKYRNEYELNEESSVKIDDIQSLTCNELYEYDVGQEPIFPICEAGENDNEEPY
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WSVPDFKGYAEPEREAHLRLRNINALRQAAMRHEENERAFFERLGTTSDRYEASPDFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MLSPIRTTFHNSVNIVQSSPCQTVSFAGKEYELKVIDEKTPILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Residues 13 to 326 of 326 are 55.73 pct identical to residues 18 to 331 of 336 from GenPept 118: gil65603671gblAAR73527.11 (AR170176) hypothetical predicted by Glimmer [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYSAVSNIGYGFIQQHDFPGLAINDNLQDANQIQLYHGAPYIFTFGDVDKHNQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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/protein_id="AAG55141.1"
/db_xref="G1:12513756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=1.
/product="unknown protein encoded by prophage CP-933K"
/protein_id="AAG55142.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="orf; Other or unknown (Phage or Prophage
Related)"
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                                                                                                                                                                                                                                                                        /function="orf; Other or unknown (Phage or Prophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Z0985"
2489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/gene="20989"
5350, .6231
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/gene="Z0989"
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                                                                                                                                                                                                                   2004. .2312
/gene="Z0984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3530. .4522
/gene="Z0986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3530. .4522
/gene="Z0986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2489. .3469
/qene="Z0985"
                                                                                                                                                                                                                                                                                                          Related)"
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                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41. 7576
/note="0-1sland #36; Region of the EDL933 chromosome not
homologous to E. coll K-12 MG1655; Cryptic prophage
CP-933K; includes one copy of the 13 bp direct repeat that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="Aag55137.1"
/db_xref="G1:12513752"
/translation="MRKVGATLSAAICLAVSGVPAWASEHQSTLSAGYLHASTDAPG
SDDLMGINVKYRYEFTDTLGLITSFSYANAEDEGKTHXSDTRWHEDYVRNRWFSVWAG
PSVRVNEWFSAXYAMGAVAXSRYSTFSGDYFRYTDUKRKTHDVLTGSDDARKYSNTSLAW
GAGVQFNPTESVAVDVAYEXSGSGDWRTDGFIVGVGKKF"
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NPDEAGRYSMDVEYGQYSVTLLVEGFPPSHAGTISVYEDSQPGTLNDFLGAMTEDDAR
PEALRRFEQWVEEAARHAEEAKKNAGEAETSARNAGISASKAEASAANADTSAEDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Residues 164 to 440 of 440 are 68.79 pct identical to residues 381 to 645 of 645 from Genept 118 : gil4585436|gb|AAD25464.1|AF125520_59 (AF125520) putative tall fiber protein [Bacterlophage 9338]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="putative membrane; Other or unknown (Phage or
                                                    Rose, D. J., Mayhew, G. F., Evans, P. S., Gregor, J., Kirkpatrick, H.A., Bose, D. J., Mayhew, G. F., Evans, P. S., Gregor, J., Kirkpatrick, H.A., Grofai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E. J., Davis, N. W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T. S., Lin, J., Yen, G., Schwartz, D. C., Welch, R. A. and Blattner, F. R.
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7 Nature 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Residues i to 199 of 199 are 72.86 pct identical residues i to 199 of 199 from GenPept 118 : g1/7532789|gb|AAF63231.1|AF151091_2 (AF151091) Lom [prophage P-EibA]"
                                                                                                                                                                                                                                                                                                                                                        Coases 1 to 13501)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grobeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
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/protein_id-"AAG55138.1"
/db_xref-"GI:12513753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"putative outer membrane protein of prophage CP-933K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (22-OCT-2000) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Escherichia coli 0157:H7 EDL933"/strain="EDL933"
                                  1 (bases 1 to 13501)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="enterohemorrhagic"
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719. .2041
/gene="20982"
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                               REFERENCE
AUTHORS
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JOURNAL
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   Twenty
              start
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                                                                                                                                          INV 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved sequences flank variable tandem repeats in two S-antigen genes of Plasmodium falciparum (call 40, 775-783 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF7] S antigen gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Aplcomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 3838)
Cowman, A.F., Saint, R.B., Coppel, R.L., Brown, G.V., Anders, R.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                       219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAla 113
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                                                                                                                                                                                                                                                                                                                                                                                                             LysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGlu-----AlaAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                59 SerAsp------AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                         74 SerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 GCGGATCAAGCAAATACTGCTAAAGCAGAAGCAGATGAACTTGCAAAGGCAGAAAAAAA
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                                                                                                                                                                                                                                                       969
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36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CAAGCTGCTCTAAAAGAATTCGATCGTTATGGTGTGAGC
                                                                                                          /product="albumin-binding protein"
/protein_id="AAA26847.1"
/db_xref="G1:153555"
                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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Infect. Immun. 60, 3601-3608 (1992) 92363555
                                    1. .yby
/organism="Streptococcus
/isolate="DG12"
/db_xref="taxon:1329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9838 bp
Plasdmodium falciparum (isolate
M10130
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                      Location/Qualifiers
                                                                                                  /transl_table=11
                                                                                        /codon_start=1
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55.65%
33.91%
17.82%
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Best Local Similarity:
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PFASA7
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/procein_ii="aaa29758.1"
/db_xref="GI:160671"
/db_x
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Escherichia coli 0157:H7 EDL933 genome, contig 1 of 3, section 82
of 155.
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Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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degenerate tandem repeats of twentyfour base pairs each at position 953 and end at 1432.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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734 .1591
/product="S antigen"
                                                                                                                                                                                         /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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Conservative:
Mismatches:
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/note-"S antigen precursor"
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1 bp upstream of EcoRI site.
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AE005258.1 GI:12513751
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Pred.
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1 (bases 1 to 798)
Fahnestock,S.R.
CLONED PROTEIN G VARIANT GENES AND THE PROTEIN G VARIANTS EXPRESSED
THEREFROM
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                                                                                                                                                                                                                                                                                              84 -----AsnAlaAlaSerAspAlaLeuGluAla---------LeuAla 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                -----LeuGluAlaLeuAla
                                                                                                                                                                                                         AspGlnThr------AspAlaLeuGlnSerGluGluAlaAla
                              AsnLeuLeuGlyAsnAla.........-ProGluLysLeuAlaLeu
                                                                                             TCTAAAGATAAAGAAGCATTAGATGAAAGAAATAAAGTTCTGGAAGCAAGTCGTACCCGT
                                                                                                                   -------GlnAlaIleGluAspLysGluAlaThrAlaIleGluAlaAla
                                                                                                                                                                                    PAT
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                                                                       31 ArgAsnGluGluArgAlaIleAspGluLeuLysLys--
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109107
                                                                                                                                                                                                                                                     ValValLysAlaAsp------
        US-09-847-539A-6 (1-159) x SSCMLB1 (1-1380)
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1. .798
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161 c 177 g
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Alignment Scores:

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STRABP 969 bp DNA linear BCT 26-APR-1993
Streptococcus canis (group G) albumin-binding protein gene, partial
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340 GITGACGGIGAATGGACTIACGACGATGCGACTAAGACCTITACAGITACTGAAAAACCA 399
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Streptococcus canis (group G) (individual_isolate DG12) DNA.
Streptococcus canis
                                                                                                                                                                                                                                                 220 AAGACTGACACTTACAAATTAATCCTTAATGGTAAAACATTGAAAGGCGAAACAACTACT
                                                                                                                                                                                                                                                                                           LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln------SerGluGluAla
                                                                                                                                                                                                                                                                                                                                                                                                          400 GAAGTGATCGATGCGTCTGAATTAACACCAGCCGTGACAACTTACAAACTTGTTATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                    85 AlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 GGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACTGCAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GluLys-----AlaAlaThrProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580 ACTAAGACCTTTACGGTAACTGAAATGGTTACAGAGGTTCCTCGAGGTGATGCACCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700 GCTAAAGATGACGCTAAGAAAGACGATACTAAGAAAGAAGATGCTAAAAAACCAGAAGCT
                                                                                                                                                                     AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 Ala---GluvalvalGlnSerAspAsnAlaAlaSerAspAlaTrp-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group;
798
58
24
64
84
          Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                         52 ThralaileGluAlaAlaSerSerAsp---------
  Length:
                                                                Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                78 AlavalvalLysAlaAsp------
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1 (bases 1 to 969)
Sjobring, U.
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M95520.1 GI:153554
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25.22%
17.89%
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                       Percent Similarity: .
Best Local Similarity:
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0.00155 Length: 1576 154.50 Matches: 80 26.45% Conservative: 16 22.04% Mismatches: 62 19.88% Indels: 206 1 Gaps: 7	) x SG148PG (1-1576)	eGluGlnProargIleIleProAsnGlyGlyThrLeuThrAsnLeu 	LeuGlyAsnalaProGluLySLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu	LysLysGlnAlaileGluAspLysGluAlaThrThrAlaileGluAlaAlaSerSerAsp	scréadaticrescasca-	AlaLeuGlualaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal		   AAAGAATTCAACATAGAATTTTTAGCTGCATTACCTAAGACTGACACTTACAAATTA			::: GCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTTGACGGTGAATGGACTTAC		GACGATGCGACTAAAGACCTTTACAGTTACTGAAAAACCAGAAGTGATGGATG		TTAACACCAGCCGTGACAACTTACAAACTTGTTATTAATGGTAAAACATTGAAAGGCGAA		ACAACTACTGAAGCTGTTGATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAAC				GAAAAACCAGAAGTGATCGATGCGTCTGAATTAACACCAGCCGTGACAACTTACAAACTT		GTTATTAATGGTAAAACATTGAAAGGCGAAACAACTACTAAAGCAGTAGACGCAGAAACT		GCAGAAAAAGCCTTCAAACAATACGCTAACGACAACGGTGTTGATGGTGTTTGGACTTAT		GATGATGCGACTAAAGACCTTTACGGTAACTGAATAAGGTTACAGAGGTTCCTGGTGATGC	ACCAACTGAACCAGAAAACCAGAAGCAAGTATCCCTCTTGTTCCGTTAACTCCTGCAAC
Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	-539A-6 (1-159)	ValAspSerProIl 	LeuGlyAsnAlaP            CTGGGGAATTCAG	LysLysGlnAlaI	ACAGCAGCAGCGG		LysAlaAspAsn	AAAGAATTCAACA	ATCCTTAATGGTA	AspGln	::: GCAGAAAAAGTCT		GACGATGCGACTA		TTAACACCAGCCG	ThrAspA	ACAACTACTGAAG	AspAsnAlaAlaSerAspAlaTrp-	GACAACGGTGTTG,		GAAAAACCAGAAG		GTTATTAATGGTA	GluLysAla-	GCAGAAAAAGCCT		GATGATGCGACTA	ACCAACTGAACCA
Pred. No.: Score: Percent Sim Best Local Query Match	-847	1 391	21	41	511	61 570	81	627	85	95	747	96	807	96	867	97	927	111	987	118	1047	118	1107	119	1167	121	1227	122
Pred. Score Percer Best 1 Query DB:	0S-09	9 d	g g	φ	QQ	Oy Op	ογ	q	දු දු	ò	qq	ô	qq	ò	qq	οy	q	οy	QQ	οy	qq	δ	qq	٥y	qq	ογ	q	og G

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/evidence-experimental
/product-*multiple ligand-binding protein 1*
/protein_id=*CAA59349.1*
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Streptococcus sp.serotype C mlbl gene for multiple ligand-binding
protein 1.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Direct Submission
Submitted (23-FBB-1995) S.R. Talay, GBF Gesellschaft
Submitted (23-FBB-1995) S.R. Talay, GBF Gesellschaft
f.Biotechn.Forschung mbH, National Research Centre for Biotechn.,
Mascheroder Weg 1, D-38124 Braunschweig, FRG
C (bases 1 to 1380)
Z Talay,S.R., Grammel,M.P. and Chhatwal,G.S.
Structure of a group C streptococcal protein that binds to
fibrinogen, albumin and immunoglobulin G via overlapping modules
Biochem. J. 315 (Pt 2), 577-582 (1996)
                                                                                                             123 rProlleAlaLeuAspValLysLysThrLysAspThr-------LysPr 137
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103
103
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X84989.1 GI:1403574
mlbl gene; multiple 11gand-binding protein.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1. .1380
//organism="Streptococcus sp."
/strain="serotype C"
/isolate="C20"
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61. .168
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/gene="mlb1"
61. .1380
/gene="mlb1"
61. .1380
/gene="mlb1"
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151.50
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us-09-847-539a-6.std.rge

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/db_xref="G1:51862"
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TYDDATKFTVTEKLVINGKTLKGETTTEAVDAATAEKVFKGYANDNGVDGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MEKEKKVKYFLRKSAFGLASVSAAFLVGSTVFAVDSPIEDTPII
RNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGQQLGKQRQQQM
                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus sp. 'group G'.
Streptococcus sp. 'group G'
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                  ---SerAspAlaTrpGlu-------LysAlaAlaThrProIleAlaLeu 127
GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla--- 114
                                                                               914 AAAGAATTCAACAAATATGGAGTAAGTGACTATTACAAGAATCTAATCAACAATGCCAAA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Protein G'gene"
/note="Truncated gene; Start codon TTG not ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1576)

Goward.C.R., Murphy,J.P., Atkinson,T. and Barstow,D.A.

Expression and purification of a truncated recombinant

streptococcal protein G

Blochem. J. 267 (1), 171-177 (1990)
                                                                                                                                                                                                                                                                       128 AspValLysLysThrLys-----AspThrLysProValValLysLysGlu 142
                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'group G'"
                                                                                                                                                                                                                                                                                                                                          SG148PG 1576 bp DNA lin
Streptococcus G148 protein G' structural gene.
X53324
                                                 81 LysAlaAspAsn----AlaAlaSerAspAlaLeuGluAlaLeu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Streptococcus sp./strain="G148"
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/db_xref="GI:288359"
/db_xref="SPTREMBL:Q54180"
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292. .601
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/note="Truncated gene"
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/clone="pspG3"
292. .1262
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1. .1576
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/transl_table=11
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FEATURES
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AUTHORS
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               LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 40
                                                                             41 LysLysGlnAlaileGluAspLysGluAlaThrThrAlaileGluAlaAlaSerSerAsp 60
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Fahnestock.5.R.
CLONDED STREPTOCOCCAL GENES ENCODING PROTEIN G AND THEIR USE
CONSTRUCT RECOMBINANT MICROORGANISMS TO PRODUCE PROTEIN G
Patent: WO 8705025-A 2 27-AUG-1987;
Location/Qualifiers
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ANDNGVDGEWTYDDATKTFTYTERPVINSASELTPAYTTYKLYINGKTLKGETTTEAV
ANDREWFKYGYANDNGVDGEWTYDDATKTFTYTERPVINSASELTPAYTYKLVING
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/product="mature G protein (AA 1 - 560)"
694. .765
/note="repetitious region 1"
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hote="coll-wall spanning region"
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/note="membrane spanning region"
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Matches:
Conservative:
Mismatches:
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/note="repetitious region 4"
1462. .1626
/note="repetitious region 3"
1627. .1671
/note="repetitious region 4"
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2157. .2165
/note-"inverted repeat A"
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/note-"inverted repeat A'"
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/note="repetitious region 1"
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/note="repetitions region 3"
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/note="repetitious region
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/note="repetitious region
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/note="repetitious region
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                                                                  /db_xref-"taxon:1324"
 Location/Qualiflers
1. .2456
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Fahnestock, S.R.
CLONED STREPTOCOCCAL GENES ENCODING PROTEIN G AND THEIR USE.
CONSTRUCT RECOMENANT MICROORGANISMS TO PRODUCE PROTEIN G
Patent: WO 8705025-A 4 27-AUG-1987;
Location/Qualifiers
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Olsson.A., Eliasson.M., Guss.B., Nilsson,B., Hellman,U.,
Lindberg,M. and Uhlen,M.
Structure and evolution of the repetitive gene encoding
streptococcal protein G
Eur. J. Blochem. 168 (2), 319-324 (1987)
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G protein; IgG receptor.
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Streptococcus sp. G148
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Query Match:
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ValAspSerProlleGluGlnProArgIleIleProAsnGlyGlyThrLeuThrAsnLeu
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Mismatches:
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| /note="A2 repeated sequence"
| 1344. | 1446
| /note="A3 repeated sequence"
| 1483. | 1647
| /note="1918 | repeated sequence"
| /note="210 bp duplication"
| /rote="210 bp duplication"
| /rote="1708. | 1918
| 1693. | 1857
                                                                               /note="Al repeated sequence" 986. .1435
/note="225 bp duplication" //rpt_unit=1211. .1435
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/note="B2 repeated sequence"
1903. 2067
/note="B3 repeated sequence"
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                               /product="protein G"
886, .996
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ALAKAKADALKEFNKYGVSDYYKNLINNAKTVBGVKDLQAQVVESAKKARISEATDGL
SDELKSQTPAEDTVKSTELAEAKVLANRELDKYGVSDYKNIINNAKTVBGVKDLQAQ
VVESAKKARISEATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRELDKYGVSDYYKN
LINNAKTVEGVKALIDEILAALPKTOTYKILINGKTLKGETTTEAYDAATARKYFKQY
ANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAYTYKLVINGKTLKGETTTEAY
DAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAYTYKLVING
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EPEKPEASIPLYPLTPATPIAKDDAKKDDTKEDAKKPEAKKEDAKKAETLPTTGEGS
NPFFTAAALAVWAGAGALAVASKRKED"
676. 2355
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/translation="MEKEKKVKYFLRKSAFGLASVSAAFLVGSTVFAVDSPIEDTPII
                                                                                                                                                                                                                                                                                                                                                                                                                       111 ::: 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
797 ACAGCAGCAGCGGTAGCCGATACTGTGGCAGCGGCAGCTGAAAATGCTGGGGCAGCA 856
                                                                                     96 GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla--- 114
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Submitted (12-CCT-1987) Fahnestock S.R., Genex Corp., 16020
Industrial Dr., Gaithersburg, MD 20877, USA
1 (bases 1 to 2384)
Filpula,D., Alexander,P. and Fahnestock,S.R.
Nucleotide sequence of the protein G gene from Streptococcus GX7805, and comparison to previously reported sequences
8015586
                                                                                                                                                            81 LysAlaAspAsn-----AlaAlaSerAspAlaLeuGluAlaLeu-----AlaAsp
                                                      61 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
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    2384
    /organism="Streptococcus sp. GX7805"
    /strain="GX7805"

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/transl_table=11
/product="protein G precursor"
/protein_id="CAA66489.1"
/db_xref="GI:47101"
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/gene="spg"
577. .675
/gene="spg"
577. .2358
/gene="spg"
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1 (bases 1 to 2384)
Fahnestock, S.R.
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RNGGELTHLLGNSETTLALBNEESATADLTRAAUADTVAAAAAENGGAAAREAAAAD
ALAKAKADALKEFNKYGUSDYKNLINNAKTUGE (NDLQAQUVESAKKARISEATDGL
SDELKSGTPAEDTYSE IELARUKKULANRELDKYGUSDYKNLINNAKTUGEVELIDE
ILAALPKTDTYKLILNGKTLKGETTTEAUDAATAEKUFKQYANDNGVDGEWTYDDATK
TETVTEKPER VIDASELTPAUTTYKLINGKTLKGETTTKANDATAEKTOYANDNG
VDGVWTYDDATKTFTUTWRYTYKLINGKTLKGETTTKANDATAEKKOYANDNG
VDGVWTYDDATKTFTUTWRYTYKLINGKTLKGETTKANDATAEKKOYANDNG
                                                                                                                                                                                                                                       BCT 23-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Draft entry and computer-readable sequence of [1] kindly provided by S.R.Fahnestock, 07-NOV-1986. The -35 and -10 regions are located at positions 465-470 and 487-492 respectively and an SD sequence at 565-570.
                                                                                                                                                                                                                                                                                                     constant region; Immunoglobulin binding protein.
Streptococcus sp. (Lancefield group G; strain GX7809) DNA, clone
mGX4547.
                                        STRSPGIGP 1950 bp DNA linear BCT 23-F
Streptococcus sp. (Lancefield group G) spg gene encoding an
immunoglobulin G binding protein.
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                                                                                                                                                                                                                                                                                                                                                                        Streptococcus.
1 (bases 1 to 1950)
Fahnestock, S.R., Alexander, P., Nagle, J. and Filpula, D.
Gene for an immunoglobulin-binding protein from a group
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/note="1gg binding protein signal
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J. Bacteriol. 167, 970-880 (1986)
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                                                                                                                                                                                                        914 AAAGAATTCAACAAATATGGAGTAAGTGACTATTACAAGAATCTAATCAACAATGCCAAA 973
                                                                                                                                                                                                                                                                                                                  96 GlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAla--- 114
                                                                                                                                                                                                                                                                                                                                                                                    115 ---SerAspAlaTrpGlu-------LysAlaAlaThrProIleAlaLeu 127
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                                                                                                                  41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
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                                                                                                                                                                                   AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal
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JOURNAL Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden Location/Qualifiers 1.717 Source //Organism="Extreptococcus pyogenes" //Strain="MRTG" //Strain="MRTG" //Ab.xref="taxon:1314" mat_peptide 1.7717 mat_peptide 1.7717	misc_feature 1.174 /note="Region: alpha2-macroglobulin-binding A domain" CDS <1>717	/note="grab" /codon_start=1 /transl_table=11	/product="GRAB precursor" /protein_id="AAD26341.1" /db_xref="GI:4589085"	/translation="VDSPIEQPRITPNGTLTNLLGNAPEKLALRNEERALDELKKQA IEDKEATPAIEARADOADALQSEEAAVVKADNAASDALEALADQTDALQS EEAAVVKADNAASDTLEALADQTDALQSEEAAVVKADNAASDTLEALADQTDALQSEE AAVVKADNAASDTLEALADQTDALQSEEAAVVQSDNAASDTHEALADQTDALQSEE AAVVKADNAASDTLEALADQTDALQSEEAEVQSDNAASDAWGKAATPIALDVKKTKD	TKPVVKKERRONVNTLPTIGE" misc_feature 175.594	misc_feature 595. 717 /note="Region: cell-wall attachment"  BASE COUNT 257 a 140 c 163 q 157 t	NI	Alignment Scores: 3.09e-45 Length: 717 Pred. No.: 692.00 Matches: 153 Percent Similarity: 64.02% Conservative: 0	: 64.02% Mismatches: 89.06% Indels: 1 Gaps:	-09-847-539A-6 (1-159) x AF124402 (1-717)  1 ValAspSerProlleGluGlnProArgllelleProAsnGlyGlyThrLeuThrAsnLeu	1 GTTGACTCACCTATCGAACAGCCTCGAATTATTCCAAATGGCGGAACCTTAACTAATCTT 21 LeuGlyAsnAlaProGluLySLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 1	01 CITGGCAATGCTCCAGAAAAACTGGCATTACGTAATGAAAAAGGGCCATTGATGAATTA 41 LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp	DD 121 AAAAAACAAGCTATTGAGGATAAAGAAGCTATAGAAGCTATAGAAGCTCAGATTCAGAT 180  QY 61 Ala	241 CAATCAGATAACGCTGCTAGTGACGCCTTAGAAGCATTGGCGGATCAAACAGACGCTTTA	Db 301 CAATCAGAAGGTGCGGTTGTTAAAGGGGATAACGCTGCTAGTGACACTTTAGAAGCA 360 Oy 61	Db 361 TTGGCGGATCAAACAGACGCTTTACAATCAGAAGAAGCTGCGGTTGTTAAAGCGGGATAAC 420 . Qy 62	Db 421 GCTGCTAGTGACACTTAGAAGCATTGCGGATCAAACAGACGCTTTACAATCAGAAGAA 480  Qy 77 AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln 96
	Db         181 GCCTTAGAAGCATTAGGGGATCAAGCAGACGCTTTACAATCAGAAGAAGCTGCAGTAGTT 240           Qy         58	241 CAATCAGATAACGCTGCTAGTGACGCCTTAGAAGCATTAGCGGATCAAGCAGACGCTTTA	dy 58	Qy 58 58 Db 361 TTGGCGGATCAAACAGACGTTTACAATCAGAAGAAGCTTCGGTTGTTAAAGCGGATAAC 420	Qy 58 58	Db 421 GCTGCTAGTGACGCCTTAGAAGCATTGGGGGATCAAACAGACGCTTTACAATCAGAAGAA 480 Qy 59SerAspAlaLeuGluAlaLeuAlaAspGln 68	481 GCTTCGGTTGTTAAAGCGGATAACGCTGCTAGTGACGCCTTAGAAGCATTGGCGGATCAA	Oy 69 ThraspalaLeuGInSerGluGlualaalaValValLysalaaspasnalaalaSerasp 88 	Oy 89 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValVal 108 	Oy 109 GInSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAsp 128 	Qy 129 VallyslysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnValAsn 148 	Qy         149 ThrLeuProThrThrGlyGluGlu 156           b	5 AF124402 ION Streptococcucts. ON AF124402	Cooteants	group, streptor lates proteolvs	bacterial surface by binding alphá2-macroglobulin J. Biol. Chem. 274 (22), 15336-15344 (1999) 99269061	FURENCE 2 (bases 1 to 717) AUTHORS Rasmussen,M., Muller,H.P. and Bjorck,L. TITLE Direct Submission

361 GCAGCAACTCCAATGCTTTAGATGTTAAGAAAACTAAAGATACAAAACCTGTAGTTAAA 420

Rasmussen, M., Muller, H.P. and Bjorck, L.

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21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu 40
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Streptococcus pyogenes
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Rasmussen.M., Muller,H.P. and Bjorck,L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology, Molecular
Submitted (28-JAN-1999) Cell and 221 00, Sweden
Location/Qualifiers
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Protein GRAB of streptococcus pyogenes regulates pacterial surface by binding alpha2-macroglobulin J. Biol. Chem. 274 (22), 15336-15344 (1999) 99269061
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1 (bases 1 to 804)
Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin
J. Biol. Chem. 274 (22), 15336-15344 (1999)
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                                                                                                                                                                                                                                                               AF124403 804 bp DNA linear BCT 14-AUG-2000 Streptococcus pyogenes strain AP49 GRAB precursor, gene, partial
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Rasmussen,M., Muller,H.P. and Bjorck,L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular
Pathogenesis, Soelvegaten 39, Lund 221 00,
Location/Qualifiers

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Matches:
Conservative:
Mismatches:
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/note="Region: repeat motif"
679. .804
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IEDKEATATERASSDALEALADOTDALOSEERAVVKADNAASDALEALADOTDALOS
EERAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE"
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Streptococcus pyogenes
Bacteria, Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Streptococcus pyogenes strain AP1 GRAB precursor, gene, partial
                                                                                                                                                                                                                                                                                                                                                                  /note="Region: alpha2-macroglobulin-binding A domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLys
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156
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Matches:
Conservative:
Mismatches:
Indels:
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/note="Region: repeat motif"
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AF124400.1 GI:4589080
               <1. .>468
/note="grab"
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1 (bases 1 to 469)
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Best Local Similarity:
Query Match:
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No.:
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AF124400
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Rasmussen, M., Muller, H.P. and Bjorck, L.
Direct Submitssion
Submitted (28-JaN-1999) Cell and Molecular Biology, Molecular Pathogenesis, Scelbegatan 39, Lund 221 00, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 468)
Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates pacterial surface by binding alpha2-macroglobulin J. Biol. Chem. 274 (22), 15336-15344 (1999)

    .468
    .70ganism-"Streptococcus pyogenes"
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    Length:
Matches:
Conservative:
Mismatches:
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                                                                                US-09-847-539A-6 (1-159) x AE006573 (1-10029)
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1. 174
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AF124401
AF124401.1 GI:4589082
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Best Local Similarity:
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                                               Query Match:
DB:
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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JOURNAL
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AF124401
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BCT 14-AUG-2000

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MTQONIRRYLVKGGLLIVGDRETIOLLALENHNAILVTGGFPVSKRVIEMANNORIPV
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VEPTMIDSAGNMSNGVISEFLKEISIRALTKKHOKNIIIEQMMVYFLHAIQIEDELKI
YPKIITENRRSSTIDIEIFVDDQVIAKAIITTKIN"
COMPLEMENL(5148. .5690)
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/product="protein GRAB (protein G-related alpha 2M-binding
protein)"
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DALGSEEAAVVKADNAASDALEALADOTDALGSEEAEVVOSDNAASDAMEKAATPIAL
DVKKTKDTKPVVKKEERQNVNTLPTTGEESNPFFTAAALAIMVSTGVLVVSSKCKEN"
COMPLEMENT ( (939. .8198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVTHYDTFTVATMINHALSNIRIKTDLKTVEQVMIPITDYGYLCEDSSVEEFNTLIKK
TRQVRFPVLDYKRKVIGVVSMRDVVDQLPTTKLTKVMSKNPITARPNTSLANISQKMI
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UDP-N-ACETYLGLUGOSAMINE 1-CARBOXYVINYLTRANSFERASE 2
(ENOYLPYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUGOSAMINE
ENOLPYRUVYL TRANSFERASE) (EPT) >91|2127264|pir||G32354
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC
>5.1.7) murz Beachlus subtilis
>91|85767|emb|CAA89875.1| (249782)
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
(Bacillus subtilis) >91|6363245|emb|CAB1877.1| (299122)
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
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(AF008220) YtoI [Bacillus subtills]
>gi|2635392|emb|CAB14887.1| (Z99118) ytoI [Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Best Blastp hit = emb|CAA03913.1| (AJ000084) putative acetyl transferase {Proteus mirabilis]"
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(AF124401) GRAB precursor [Streptococcus pyogenes]"
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                                                                                                                                                                                                                                 hypothetical protein"
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complement(5928. .6581)
/gene="grab"
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complement(5148. .5690)
/gene="SPy1356"
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/note="SPy1358"
complement(6939. .8198)
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                                                                                                                                                                                                                             /product-"conserved
                                                                                                                                                                                   /transl_table=11
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LVGPQQLTAQBITVPCDISSAAFWLVAGLIIPGSELLLKNVGVNPTRTGILEVVEKMG
AQOYYEDMIKKRQVYTDILLASWGANKGTIISGGLIPRLIDELPIJALLATQAQGTTCIK
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MYRTEKAVIGNRIGDIGAAVORARSPYTGCLADSCANAYOCTPSDEIKQLMDYTKEA
MYRTEKAVIGNRIGDIGAAVORARSPYTGCHAD
                                                                                                                                                                                                                                                             SYNTHASE) (EPSPS) >91|1075724|pir||552580

3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)

- Lactococcus lactis >91|683583|emb|CAA55180.1| (X78413)

5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mkrmklrtnagplogtiovpddksishravilgavakgetrvkg
LLKGEDVLSTIQAFRNLGVRIEEKDDQLVIEGGGFGGLNAPCQTLNMGNSGTSNRLIA
GLLAGQPFSVKMIGDESLSKRPMDRIVYPLKOMGVEISGETDRQFPPLQLQGNRNLQP
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ytoI - Bacillus subtilis >gi||2293258||gb||AAC00336.1|
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ANIOPEPTIDASE (MAP) (PEPTIDASE M)
ANIOPEPTIDASE (MAP) (PEPTIDASE M)
SQ1|11264635|pti|1744465 methionyl aminopeptidase (EC 3.4.11.18) map [imported] - Bacillus halodurans
Sq1|4512426|dby|BAA75293.1| (AB017508) map homologue
(identity of 81% to B. subtlils) | [Bacillus halodurans]
Sq1|10172768|dby|BAB03875.1| (AP01507) methionine
aminopeptidase [Bacillus halodurans]
                                                                                                                            /note="Best Blastp hit = sp!P43905|AROA_LACLA
3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE
(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Best Blastp hit = dbj|BAB07074.1| (AP001518) unknown conserved protein [Bacillus halodurans]"
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/note="SPy1354"
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/translation-*MTKVLLGFMGVGKTTVSKHLSMHCKDMDAIIEAKIGMSIAAFFE
QHGEIAFRTIESQVLKDLLFANDNSIIVTGGGVVVLQENRQLLRKNHQHNILLVASFE
TLYQRLKHDKKSQRPLFLKYSKEAFYEFYQQRMVFYEGLSDLVIRVDHRTPEEVANII
                                                                                                                                                                                                                                                                                                                           AE006573 10029 bp DNA linear BCT 01-JUN-2001
Streptococcus pyogenes M1 GAS strain SF370, section 102 of 167 of
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Kr1335 [imported] - xytella fastidiosa (strain 9a5c)
>gi|9106332|gb|AAR84144.1|AE003966_5 (AE003966) shikimate
kinase [xytella fastidiosa]*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae,
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Direct Submission
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Only of 10-APR-2001) Department of Microbiology and Immunology,
University of Oklahoma Health Sciences Center, 940 SL Young Blvd,
Oklahoma City, OK 73104, USA
Oklahoma City, OK 73104, USA
1. 10029
/organism="Streptococcus pyogenes MI GAS"
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Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Oian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
340 AAAGCGGATAACGCTGCTAGTGACGCCTTAGAAGCATTGCGATCAAACAGACGCTTTA 399
                                                                            121 AlaAlaThrProIleAlaLeuAspValLysLysThrLysAspThrLysProValValLys 140
                                                                                                                                                                                                                141 LysGluGluArgGlnAsnValAsnThrLeuProThrThrGlyGluGluSerAsnPro 159
                                                                                                                                                         460 GCAGCAACTCCAATCGCTTTAGATGTTAAGAAACTAAAGATACAAAACCTGTAGTTAAA
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Streptococcus pyogenes M1
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1 (bases 1 to 10029)
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/product="GRAB precursor"
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DOVKRYKDTKPVVKKEERQNVNTLPTTGEESNPFFTAAALAINVSTGVLVVSSKCKEN"
                                                                                               proteolysis at the
                Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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/note="Region: alpha2-macroglobulin-binding A domain"
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Basanussen,M., Muller,H.P. and Bjorck,L.
Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biology,
Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden
Location/Qualiflers
1..832
                                        1 (base 1 to 832)
Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates p
Bacterial surface by binding alpha2-macroglobulin
J. Biol. Chem. 274 (22), 15336-15344 (1999)
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/strain="ATCC700294"
/db_xref="ATCC.700294"
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/note-"Region: membrane-spanning"
/ note-"Region: membrane-spanning"
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Conservative:
Mismatches:
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  Streptococcus pyogenes

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Compugen Ltd
GenCore version
Copyright (c) 1993 - 2002
```

OM protein - nucleic search, using frame_plus_p2n model

October 13, 2002, 04:49:23 ; Search time 1561.09 Seconds (without alignments) 2131.407 Million cell updates/sec Run on:

US-09-847-539A-6 777 1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159 Title: Perfect score:

Sequence:

0.5 7.0 7.0 BLOSUM62 Xgapop 10.0 , Xgapext C Ygapop 10.0 , Ygapext C Fgapop 6.0 , Fgapext 7 Delop 6.0 , Delext 7 Scoring table:

1797656 segs, 10463268293 residues Searched:

3595312 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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-MODEL-frame+pan.model.verxlh
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gb_v1:*
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em_ln:* em_pat:* em_ph:* em_pl:* em_ro:* em_or:* em_om: * Gen Emb1:* Database

em_vi:*
em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htgo_inv:* 33. 33. 33.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SUMMARIES	-	000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000	C. 1970 CD 4	o -	400 AF124400	103 AF124403	102 AF124402	3IGP M13825 Streptoco	109115	Y00428 Streptoco	I08537	x06173	108536		1001001	M95520 Streptoco	M10130	AE00525	AP002553	U19361 Pe	AE006458	AE005333	AP002555	_ 5	AC00683	i3 AL604063	AF067614	784 ACUU6/84 Caenornab	L27798 St	AL513384	AC023354	AC104834 Mus n	AC020602	AC019950	U52008 S		A12446 1	367 AB025967	X69324 S.	97 AY060997	061 AF32406	VECTVOC.
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## ALIGNMENTS

RESULT 1

AF124399 B32 bp DNA linear BCT 14-AUG-2000 Streptococcus pyogenes strain ATCC700294 GRAB precursor, gene, AF124399 AF124399.1 GI:4589078 complete cds: LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE AF124399

Streptococcus pyogenes

em_sts:* em_un:*

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Eukaryotta Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 483)
Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Baxter,E., Berman; B., Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Calniker,S. and Rubin,G.M.

BDGP/HHMI Ar Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11570937.
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AT.121-AT.319: DH5-alpha TonA
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from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
and the potB7. Plasmid CDNA library."
Drosophila melanogaster cDNA clone AT22627 5 similar to CG7289:
FBan0007289 located on: 2L 22B8-22B8;: 04/09/2001, mRNA sequence.
BF487636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: AT.226 row: C column: 3
High quality sequence stop: 465.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-847-539A-6_COPY_59_86 (1-28) x BF487636 (1-483)
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                                                                                                                                                                                          Drosophila melanogaster
                                                                                                    BF487636.2 GI:13753351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Stapleton, M.
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Query Match:
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ô g

27 Ala 27

δ

119 GCC 127

Search completed: October 13, 2002, 03:33:12 Job time : 338.257 secs

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E 1 (bases 1 to 40.L., Ashlock, D.A, Wen,T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks

L Unpublished (2001)

Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS BF487636 483 bp mRNA linear EST 23-APR-2001
DEFINITION AT22627.5prime AT Drosophila melanogaster adult testes pOTB7
MEST10-D08.T7-1 ISUM4-TN Zea mays CDNA clone MEST10-D08 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 ACCCAGGCTCTGAAATCTCTGTTGGAGGAGCAATTCAAGTAGAGAGGCAGCG 265
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Mismatches:
Indels:
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T7-1 (AA TAC GAC TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: schnable@tastate.edu
                                                                                                                  GI:14206770
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BF487636/c
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KEYWORDS
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ORGANISM
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera: Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases i to 797)

2 Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Change, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)

On Dec 6, 2000 this sequence version replaced gi:11577746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="lb="AT Drosophila melanogaster adult testes pOTB7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 29-MAY-2001
                                BF494445
797 bp mRNA linear EST 19-APR-2001
A703046.Sprime AT Drosophila melanogaster adult testes pOTB9
Drosophila melanogaster CDNA clone AT03046 5 similar to CG7289:
FBan0007289 located on: 2L 2288-2288;: 04/07/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev.stage="0-3 day old Ore-R males"
//dev.stage="0-3 day old Ore-R males"
//dab_host="Plates AT.10-AT.120: DH5-alpha. Plates
//dab_host="139: DH5-alpha TonA"
//note="Organ: ADULT testess; Vector: pOTB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into porB7. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AspalaLeuGluAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21 | 111 | 111 | 111 | 111 | 111 | 112 | 114 | 114 | 115 | 114 | 115 | 114 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003584; arm:2L [1824960,2149443]
estimated-cyto:22B4-22D2: 04/07/2001
Plate: AT.30 row: D column: 10
High quality sequence stop: 699.
Location/Qualifiers
1. 797
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Mismatches:
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Drosophila melanogaster
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US-09-847-539A-6_COPY_59_86 (1-28) x AZ699109 (1-666)
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53.85%
42.31%
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Best Local Similarity:
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSS: RRCI-23-224J19.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note—10.0gan: Kidney/Brain: Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
163 c. 150 g. 150 t.
                                                                                                                                                                                                                                                 AZ699109 666 bp DNA linear GSS 24-JAN-2001
RPCI-23-224J19.TV RPCI-23 Mus musculus genomic clone RPCI-23-224J19
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S., Nlerman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musil (bases 1 to 666)
                                                                                    2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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Conservative:
Mismatches:
Indels:
                                 US-09-847-539A-6_COPY_59_86 (1-28) x AI062753 (1-666)
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/clone="RPC1-23-224J19"
/clone_lib="RPC1-23"
/sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
 Gaps:
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1. .666
                                                                                                                                                                                                                                                                                , DNA sequence.
AZ699109
AZ699109.1 GI:12416865
                                                                                                                                                                       167 GTACGAGGAGATCGTGCC 150
                                                                                                                                        22 ValLysAlaAspAsnAla 27
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68.18%
50.00%
39.53%
                                                                                                                                                                                                                                                                                                                                                           house mouse.
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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
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                                                                                                                                                                                                                              AZ699109/c
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JOURNAL
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                              RESULT 36
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B1637204
SD1913.5prime SD Drosophila melanogaster Schleider L2 cell culture port2 Drosophila melanogaster CDNA clone SD19151 5 similar to CG7289: FBan0007289 GO:|| located on: 2L 2288-2288:: 05/19/2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="1519151"
/clone=11b="550 Drosophila melanogaster Schneider L2 cell
/clone=11b="550 Drosophila melanogaster Schneider L2 cell
/clone=10pT2"
/lab_host="Welor: poT2; Site_1: EcoRI; Site_2: Xho1; Sized
fractionated cDNAS were directly ligated into poT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophillae; Drosophila.

I (bases 1 to 710)
Harvey, D., Broketein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                           Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic A8003584: amm:2L [1824960,2143443] estimated-cyto:22B4-22D2: 05/19/2001 Plate: SD.191 row: E column: 3 High quality sequence stop: 578.
1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-847-539A-6_COPY_59_86 (1-28) x BI637204 (1-710)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid cDNA library."
a 203 c 170 g 1
                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BI637204
BI637204.1 GI:15539414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
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FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                      APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Hamilton, Paul T.
APPLICANT: Hamilton, Paul T.
APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Richard J. Rodrick, Becton Dickinson and STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: 451.747
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 2034..2147
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 222..425
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTR: NS

ZIP: 07417

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: APPLICATION NUMBER: US/08/508,004
FILING DATE: 27-JUL-1995
CLASSIFICATION NUMBER: US 08/402,282
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: FUGIt, Donna R.
RECISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: 32,135
RECISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: 9-3283
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                      RESULT 18
US-08-608-004-3
US-08-608-004-3
Sequence 3, Application US/08508004
Patent No. 5582969
GENERAL INFORMATION:
APPLICANT: Paarson, Sobert E.
APPLICANT: Dickson, Julie A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                        5703 CTGCGG 5708
22 ValLys 23
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CITY: Fr
STATE: N
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 4855..5376
OTHER INFORMATION: / function= "potential coding
OTHER INFORMATION: / product= "L5 gp37 homolog"
FRATURE:
NAME/KEY: misc_feature
LOCATION: 5382..5747
OTHER INFORMATION: / function= "potential open reading
OTHER INFORMATION: / function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8033.8236
COTHER INFORMATION: /function- 'potential open reading
OTHER INFORMATION: frame"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 824,9443
OTHER INFORMATION: /function- 'potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 10371..10586
OTHER INFORMATION: /function* "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 2747.3109
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3109.3444
OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: 3731.4855
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OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 5837.6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 6403.7770
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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LOCATION: 7770..8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450.1024
OTHER INFORMATION: /function= "potential open reading
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LOCATION: 1115..11786
OTHER INFORMATION: /function= "potential open reading
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LOCATION: 344..3728
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 1109..2014
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 2747.3109
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 3444.3728
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: frame"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3731.4855
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
FEATURE:
                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 222-425
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109.3444
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OTHER INFORMATION: frame"
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LOCATION: 5382..574
LOCATION: 5382..574
OTHER INFORMATION: frame" potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 4855..5376
OTHER INFORMATION: /function= "potential coding
OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= "L5 gp37 homolog"
                 NAME: FUGIT, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-326
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOCY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-847-539A-6_COPY_59_86 (1-28) x US-08-508-004-3 (1-15664)
                                                                              NAME/KEY: misc_feature
LOCATION: 12748..1449
OTHER INFORMATION: function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1771..15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 15154..1544..154
OTHER INFORMATION: frame" potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

: LOCATION: 15429..1564

: OTHER INFORMATION: /function= "potential open reading

US-08-508-004-3
                   OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,066
FILLING DATE:
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.66e+03
42.00
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36.36%
32.56%
LOCATION: 11917..12741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5703 CTGCGG 5708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ValLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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US-08-402-066-3
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5643 GAGGGCCTGGCCAACATGCAGGACAAGCTCGACGTGTTGCAAGCAGAACACGCGGCCGCG 5702
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LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 222.445
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Pearson, Robert E.

APPLICANT: Hamilton, Julie A.

APPLICANT: Hamilton, Paul T.

APPLICANT: Little, Michael C.

APPLICANT: Little, Michael C.

APPLICANT: Little, Michael C.

APPLICANT: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive CITY: Franklin Lakes CITY: Franklin Lakes COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07417

ZIP: 07417

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
ATTORNEY-AGENT INFORMATION:
NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-326
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                               Sequence 3, Application US/08402068 Patent No. 5633159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                  5703 CTGCGG 5708
                                                     22 ValLys 23
                                                                                                                                               RESULT 20
US-08-402-068-3
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                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 8244.9443
COCATION: 8745.943
OTHER INFORMATION: frame"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9450.10244
OTHER INFORMATION: function- "potential open reading
OTHER INFORMATION: function- "potential open reading
OTHER INFORMATION: frame"
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| NAME/KEY: misc_feature
| LOCATION: 15429..15664
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LOCATION: 7770..8006
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
FRATURE:
NAME/KEY: misc_feature
LOCATION: 8033..8236
OTHER INFORMATION: /function- "potential open reading
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LOCATION: 11115..11786
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: 14771..15154
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 15154..15426
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 6403..7770
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 10371..10586
COTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 11917..1274
OCTHER INFORMATION: function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 12748..1449
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.66e+03
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63.64%
36.36%
32.56%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
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NAME/KEY: misc_feature
LOCATION: 1109..2014
OTHER INFORMATION: function= "potential open reading OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 2034..2747
OTHER INFORMATION: frame"
PEATURE: FEATURE: frame"
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MANEKER: misc_feature

OCEATION: 277.3109

OTHER REPORTING: /function - potential open reading

OTHER REPORTING: /function - potential open reading

OTHER REPORTING: /function - potential open reading

OTHER REPORTING: /function - potential open reading

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OTHER REPORTING: /function - potential ope
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APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Roses
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
TILE OF INVENTION: GERES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICANT: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 1
LENGTH: 68750
COTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: frame"

NAME/KEY: misc_feature
LOCATION: 12748..1449
COTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: frame"

NAME/KEY: misc_feature
COTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: frame"

FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: /frame"

SEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: /frame"

SEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: /function= 'potential open reading OTHER INFORMATION: /frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-847-539A-6_COPY_59_86 (1-28) x US-08-402-068-3 (1-15664)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-335-409-1
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59.26%
37.04%
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63.64%
36.36%
32.56%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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US-09-335-409-1
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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-969-1
  LENGTH: 68750
                                                                                                            Alignment Scores:
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US-09-568-480-1
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                                            2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal
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Patent No. 6355457

GENERAL INFORMATION:

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Cyr, Devon

APPLICANT: Goetlach, Joern

APPLICANT: Goetlach, Joern

TILLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4.3058.A

CURRENT APPLICATION NUMBER: US/09/567,969

CURRENT APPLICATION NUMBER: 09/335,409

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MINDIAR: SISTVAN
APPLICANT: ZIKLE, ROSS
APPLICANT: ZIKLE, ROSS
APPLICANT: ZIKLE, ROSS
APPLICANT: ZIKLE, ROSS
APPLICANT: Cyr. Devon
APPLICANT: Gerlach, Joern
ITTLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4.30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
US-09-847-539A-6_COPY_59_86 (1-28) x US-09-335-409-1 (1-68750)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                Sequence 1, Application US/09568102
Sequence 1, 6346404
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 53883 GCTCGGCGCGACGATGTCGCT 53903
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42.00
59.26%
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Best Local Similarity:
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LENGTH: 68750
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2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Like, Ross
APPLICANT: Qirkle, Ross
APPLICANT: Qirkle, Poson
APPLICANT: Gyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERBACE: 4.30582A
FURRENT FILING DATE: 2000-05-10
PRIOR PLICATION NUMBER: US/09/568,480
PRIOR PLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
                                                                                                                                     US-09-847-539A-6_COPY_59_86 (1-28) x US-09-567-969-1 (1-68750)
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Mismatches:
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Sequence 1, Application US/09568486
Patent No. 6355459
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09568480 Patent No. 6355458
                                                                                                                                                                                                                                                                                     Db 53883 GCTCGCCGCCACGATGTCGCT 53903
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CRGANISM: Sorangium cellulosum
US-09-568-480-1
                                                                                                                                                                                                                                                    22 ValLysAlaAspAsnAlaAla 28
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42.00
59.26%
37.04%
32.56%
1.65e+04
42.00
59.26%
37.04%
32.56%
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SEQ ID NO 1
LENGTH: 68750
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Best Local Similarity:
Query Match:
                                         Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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53823 GATGCCCTCCGGTCCATGGCCGAGGCTGGCGCGGAGGTGCAGATCGTGGAGGCCGACGTG 53882
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TELEX: 246633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERICS:
LENGTH: 1129 base pair
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MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
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PCT-US93-01676A-3
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                                                                                                                            RESULT 27
PCT-US93-01676A-3
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US-07-876-280-8
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APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: PATENTIN CONTACT OF THE BIOSYNTHESIS OF EPOTHILONES
SOFTWARE: PATENTING DATE: 1999-06-17
SOFTWARE: PATENTING DATE: 1999-06-17
SOFTWARE: PATENTING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09568472

Patent No. 635819.

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Molnar, Istvan

APPLICANT: Tirkle, Ross

APPLICANT: Generach, Joern

TITLE OF INVENTION: Genes FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT FILING DATE: 2000-05-10

PRIOR FILING DATE: 2000-05-10

PRIOR PLICATION NUMBER: 09/335,409

PRIOR PLICATION NUMBER: 09/335,409

NUMBER OF SEQ ID NOS: 30

SCOFTWARE: PatentIn Ver. 2.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
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; ORGANISM: Sorangium cellulosum
US-09-568-472-1
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Sorangium cellulosum
Molnar, Istvan
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Best Local Similarity:
Query Match:
DB:
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LENGTH: 68750
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Sequence 3, Application PC/TUS9301676A
GENERAL INFORMATION:
APPLICANT: Stambrook, Peter J.
TILE OF INVENTION: MUTAGENICITY TESTING USING REPORTER
TITLE OF INVENTION: GENES WITH MODIFIED METHYLATION FREQUENCIES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
IP: 20004
COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
COMPUTER: PATENTIN RELEASE
SOFTWARE: PATENTIN RELEASE
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: PCT/US93/01676A
FILLING DATE: 19930226
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Mismatches:
Indels:
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Matches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842,644
FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
                                                Db 53883 GCTCGGCGCGACGATGTCGCT 53903
22 ValLysAlaAspAsnAlaAla
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, LOCATION:
US-08-049-783-5
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Sequence 8, Application US/07876280
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Bayne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Gangley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE BAND R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GlualaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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                                                                                                                                                                                                                                                                                                                                                 COMPUTEN KEALBABLE FURM:

COMPUTEN KEALBABLE FURM:

COMPUTEN IBM PC COMPALIBLE

COMPUTEN: IBM PC COMPALIBLE

COMPUTEN: APERITIN Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/876,280

FILING DATE: 19920430

CLASSIFTCATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

RECISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: M/S 104

TELEPHONE: 904-372-5800

TELEPHONE: 904-372-5800

INFORMATION FOR EGO ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1185 base pairs

TYPE: NUCLEIC ACID

STRNDEDRESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
CLONE: E. COLI NM522(PMYC2317) NRRL B-18816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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Gaps:
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; Patent No. 5439881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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40.91%
31.78%
                                                                                                                                                                                                                                                                       STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide LOCATION: 1.1185
                                                                                                                                                                                                                                                          Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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751 GAGAAT 756
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US-07-876-280-8
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US-08-049-783-5
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APPLICANT: Narva, Kenneth E
APPLICANT: Schwab, George E
APPLICANT: Schwab, George E
APPLICANT: Payne, Jewel M
TITLE OF INVENTION: Gene Encoding No. 5439881el Nematode-Active
TITLE OF INVENTION: Toxins Cloned from Bacillus thuringlensis Isolates
NUMBER OF SEQUENCES: 18
CORRESSONDENCE ADDRESS:
ADDRESSES: Jeff Lloyd
STREET: 2421 N.W. 41st Street
CITY: Gainesville
STATE: FT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIF: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,783
FILING DATE: 19930419
CLASSIFICATION: 435
ATFORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
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Sequence 9, Application US/08316301A

Patent No. 575349.

GENERAL INFORMATION:

APPLICANT: Schwepf, Harry E.

APPLICANT: Schwab, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1185 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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40.91%
31.78%
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LOCATION: 1..1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.00
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Query Match:
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LIBRARY: LAMBL
CLONE: PS69DIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751 GAGAAT 756
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5 GlualaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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Patent No. 5874288
GENERAL INFORMATION:
APPLICANT: Thompson, Mark
APPLICANT: Cardineau, Guy
TITLE OF INVENTION: Bacillus thuringlensis Toxins With Improved
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                            US-09-847-539A-6_COPY_59_86 (1-28) x US-08-316-301A-9 (1-1185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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INDIVIDUAL ISOLATE: PS69D1
IMMDIATE SOURCE:
CLONE: E. CO11 NM522(pMYC2317) NRRL B-18816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik STREET: STREET: 421 N W. 41st Street, Suite A-1 CITY: Gaines/ille STATE: Florida
             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZCOUNTW: . USAN
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPPLICATION DATA:
APPLICATION NUMBER: US/08/904,278
FILING DATE:
CLASSIFICATION: 424
ATTORREY/AGRET INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/POCKET NUMBER: MA-702
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 9:
SEQUENCE CHRACTERISTICS:
LENGTH: 1185 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
             31.78%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
1..1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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751 GAGAAT 756
                                                                                                                                                                                                       25 AspAsn 26
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US-08-904-278-9
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                  US-08-904-278-9
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FEATURE:
           Query Match:
DB:
                                                                                                                                                              g
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APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Foncerrada, Luis
TITLE OF INVENTION: No. 5753492el Nematode-Active Toxins and Genes
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOCTAME: PAPLICATION DATA:
APPLICATION NUMBER: US/08/316,301A
FILING DATE: 30-SEP-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/871,510
FILING DATE: 23-APR-1992
CLASSIFICATION NUMBER: 07/693,018
FILING DATE: 03-MAY-1991
CLASSIFICATION NUMBER: 07/65,544
FILING DATE: 10-AUG-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/65,544
FILING DATE: 10-AUG-1997
CLASSIFICATION: 435
FILING DATE: 11-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/084,653
FILING DATE: 11-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/0830,050
FILING DATE: 31-JAN-1992
CLASSIFICATION: 435
FILING DATE: 31-JAN-1992
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
CLONE: E. COll NM522(PMYC2317) NRRL B-18816
                                                                                                                                                          ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Libyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MA20CCCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904.775-8100
TELEFAX: 904.372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9 (PS69D1):
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat_peptide
LOCATION: 1..1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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COUNTRY: USA
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Sequence 9, Application US/09076137B

Sequence 9, Application US/09076137B

Sequence 9, Application US/09076137B

Sequence 9, Application US/09076137B

GENERAL INFORMATION:
APPLICAMT: Schnepf, Harry E.
APPLICAMT: Payne, Jewel M.
APPLICAMT: Narva, Kenneth E.
APPLICAMT: Norcerrada, Luis
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
                                                                5 GlualaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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Sequence 9, Application US/0922594
Sequence 9, Application US/0922594
Sequence 9, Application
Sequence 9, Application
Sendra Normanion
APPLICANT: Thompson, Mark
APPLICANT: Routh, Mark
APPLICANT: Cardineau, Guy
TITLE OF INVENTION: Bacillus thuringiensis Toxins With Improved
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-847-539A-6_COPY_59_86 (1-28) x US-09-076-137-9 (1-1185)
US-09-847-539A-6_COPY_59_86 (1-28) x US-08-904-278-9 (1-1185)
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MA-20CCCD2
CURRENT APPLICATION NUMBER: US/09/076,137B
CURRENT FILING DATE: 1998-05-12
EARLIER PPLICATION NUMBER: 08/316,301
EARLIER FILING DATE: 1994-09-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 9
LENGTH: 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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US-09-076-137-9
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59.09%
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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751 GAGAAT 756
                                                                                                                                         751 GAGAAT 756
                                                                                                               25 AspAsn 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AspAsn 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-847-539A-6_COPY_59_86 (1-28) x US-09-222-594-9 (1-1185)
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS69D1
IMMEDIATE SOURCE:
CLONE: E. Coli NM522(pMYC2317) NRRL B-18816
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                      OPERATING SYSTEM: PC-LUJS/MS COFTWARE: PAtentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/222,594
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/904,278
FILING DATE:
APPLICATION NUMBER: 39,355
FILING DATE:
ATONEV/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: MA-702
FERENCE/DOCKET NUMBER: MA-702
TELEPHONE: (352) 375-8800
TELEPHONE: (352) 375-8800
TELEPHONE: (352) 375-8800
TELEPHONE: (352) 375-8800
TELEPHONE: CARRACTERISTICS:
LENGTH: 1185 base pairs
TELENGTH: 1185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pCT-US92-03624-9
; Sequence 9, Application PC/TUS9203624
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.00
59.09%
40.91%
31.78%
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LOCATION: 1..1185
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Best Local Similarity:
Query Match:
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ORIGINAL SOURCE
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STREET: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08252965B
Patent No. 5624818
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hurlin, Peter J.
APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
TITLE OF INVENTION: Mad or Max
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-847-539A-6_COPY_59_86 (1-28) x PCT-US92-03624-9 (1-1185)
           COMPUTER: REALBABLE FORM:
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03624
FILING DATE: 19250501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAliwanchik, David R.
RECISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 904-375-8100
TELLEPAN: 904-375-8800
INFORMATION FOR SEQ ID NO: 9 (PS69D1):
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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Mismatches:
Indels:
Gaps:
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CLONE: E. coli NM522(pMYC2317) NRRL B-18816
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS6901
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59.09%
40.91%
31.78%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: mat_peptide
LOCATION: 1..1185
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101-2347
COMPUTER READABLE FORM:
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STATE: Washington
COUNTRY: USA
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Best Local Similarity:
Query Match:
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PCT-US92-03624-9
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2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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Sequence 2, Application US/08140729A
Sequence 2, Application US/08140729A
Setent No. 56587B-2
Sequence 2, Application US/08140729A
Setent No. 56587B-2
Sequence 3, Applicant Amara, Susan G
APPLICANT: Amara, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Matches:
Conservative:
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Indels:
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                             CURKENT APPLICATION DATE:

CURKENT APPLICATION DATE:

FILING DATE: 01-JUN-1994

CLASSIFCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Shelton, Dennis K.

REFISTRATION UNBER: 26,997.

REFERENCE/DOCKET NUMBER: 26,997.

SEQUENCE CHARACTERISTICS:

LENGTH: 1242 base pairs

TYPE: nucleic acid

STRANDEDNESS: 31ngle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: clone 10; see Figure 24
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658782nan, Kevin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08546666
Patent No. 577674
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
APPLICANT: Arriza, Jeffrey L
TITLE OF INVENTION: Anino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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10 South Wacker Drive, Suite 3000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/140,729
FILING DATE: 20 OCT 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5776774nan, Kevin E
REGISTRATION NUMBER: 35,303
             REFERENCE/DOCKET NUMBER: 93,509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER: 35,303
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1626..1680
                                                                                                                                                                                                                                                                                                                    CDS
31..1626
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MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                           NAME/KEY: 5'UTR
LOCATION: 1..30
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Best Local Similarity:
Query Match:
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CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
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                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
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; LOCATION:
US-08-140-729A-2
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5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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Sequence 2, Application US/08916745
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
APPLICANT: Arriza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses; NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
Indels:
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
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APPLICATION NUMBER: US 08/140,729
FILING DATE: 20-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/916,745 FILING DATE: 19-AUG-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: NO. 5840516nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509
                                    TELEFAX: 312-715-1234
TELEFX: 910-221-3317
INFORMATION FOR SEQ 1D NO. 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: 3'UTR
LOCATION: 1626..1680
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1..30
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Best Local Similarity:
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COUNTRY: USA
ZIP: 60606
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LOCATION:
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FEATURE:
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US-08-546-666-2
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Score:
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Patent No. 5919628
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
APPLICANT: Arriza, Jeffrey L
TITLE OF INVERTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,929
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Conservative:
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Indels:
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/140,729
FILING DATE: 20 OCT 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5919628Nan; Kevin E
REGISTATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509
TELECOMMUNICATION INFORMATION:
                               TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATORE:
NAME/KEY: 5'UTR
LOCATION: 1.30
TELECOMMUNICATION INFORMATION:
                 : 312-715-1000
312-715-1234
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LOCATION: 1626..1680
US-08-916-745-2
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31..1626
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APPLICANT: Arriza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
CORRESPONDENCE: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,661
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Matches:
Conservative:
Mismatches:
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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CLASSFETCATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/140,729
FILING DATE: 20 OCT 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5919699nan, Kevin E
REGISTRATION NUMBER: 35,303
REPERRENCE/DOCKET NUMBER: 93,509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-546-661-2/c
; Sequence 2. Application US/08546661
; Patent No. 5919699
; GENERAL INFORMATION:
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            41.00
56.52%
43.48%
31.78%
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1626..1680
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                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                       NAME/KEY: 5'UTR
LOCATION: 1..30
                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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LOCATION:
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; LOCATION:
US-09-042-929-2
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| TELEFAX: 312-715-1234 |
| TELEX: 910-221-5317 |
| INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1680 base pairs |
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| TYPE: LENGTH: 1680 base pairs |
| TYPE: LENGTH: 1080 |
| TYPE: CDNA |
| TOPOLOGY: linear |
| MALECULE TYPE: CDNA |
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| LOCATION: 1..30 |
| FATURE: NAME/KEY: 3'UTR |
| LOCATION: 31..1626 |
| FATURE: NAME/KEY: 3'UTR |
| LOCATION: 1626.1680 |
| SCOIE: NAME/KEY: 3'UTR |
| LOCATION: 1626.1680 |
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Search completed: October 13, 2002, 03:45:56 Job time : 674.134 secs

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GenCore version 5.1.3
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Listing first 45 summaries
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| 15 46 35.7 705 22 AAG90301 16 45 34.9 502 21 AAG90301 17 45 34.9 502 21 AAG90301 18 45 34.9 1362 20 AAG90301 19 45 34.9 1447 20 AAG81029 20 44 34.1 274 21 AAG61028 21 44 34.1 274 21 AAG61028 22 44 34.1 284 22 AAG61028 23 44 34.1 284 22 AAG61022 24 44 34.1 284 22 AAG61026 25 44 34.1 284 22 AAG61027 26 44 34.1 284 22 AAG61027 27 44 34.1 284 22 AAG61026 28 44 34.1 371 22 AAG61026 29 44 34.1 371 22 AAG61026 29 44 34.1 371 22 AAG61026 31 34.1 371 22 AAG61026 33 44 34.1 162 20 AAG61026 34 43 34.1 162 20 AAG61026 34 43 34.1 162 20 AAG61026 35 44 34.1 162 20 AAG61026 36 44 34.1 1630 22 AAG61026 37 44 34.1 1630 22 AAG61026 38 44 34.1 1630 22 AAG61026 39 44 34.1 1630 22 AAG61026 39 44 34.1 1630 22 AAG61026 30 44 34.1 1630 22 AAG61026 31 33.3 258 22 AAG61026 32 AAG61036 33 34.1 1630 22 AAG61036 34 33.3 258 22 AAG61036 35 AAG61038 36 AA 33.3 258 22 AAG6103 37 A4 43 33.3 258 22 AAG6103 38 AA71038 Standard; peptide; 28 AA.  AA71038 AA771038 Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein Grein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 14       | 47         | 36.4         | 258          | 20   | AAY36771              | Chlamydia trachoma                       |
| 16 45 34.9 502 21 AAV55580 AA 45 34.9 1467 20 AAW99481 M 45 34.9 1467 20 AAW99481 M 45 34.9 1467 20 AAW99481 M 45 34.9 1637 22 ABB60342 DD 44 34.1 42 22 ABG01077 N 82 44 34.1 274 21 AAG58292 AA 44 34.1 296 21 AAG58292 AA 44 34.1 296 21 AAG58292 AA 44 34.1 296 21 AAG58291 AAG58291 AA 44 34.1 296 21 AAG58291 AAG58291 AA 34.1 358 21 AAG58291 AAG58291 AA 44 34.1 358 21 AAG58291 AAG58291 AA 44 34.1 358 21 AAG58291 AA 44 34.1 421 22 AAM981028 BB 44 34.1 1412 22 AAM981028 BB 44 34.1 1412 22 AAG92957 CC 33 44 34.1 1420 20 AAW81028 BB BB AA 33.3 32.3 AAV89562 AA AAG1028 AA 33.3 32.3 AAV89562 AA AA 34.1 1530 22 AAG92957 CC 34 33.3 32.3 AA AA 34.1 1530 22 AAG92957 AA 44 34.1 1530 22 AAG92957 AA 44 34.1 1530 22 AAG92957 AA 44 34.1 1530 22 AAW81028 AA 44 34.1 1530 22 AAR81028 AA 44 33.3 33.3 258 22 AAW81025 AA AA 33.3 33.3 258 22 AAW81025 AA AA 33.3 33.3 26 21 AAV505072 AA AA 34.1 1530 2A AAV505072 AA AA 34.1 1530 2A AAV505072 AA AA 33.3 33.3 34.1 50.0 AAV505072 AA AA 34.1 1530 2A AAY505072 AA AA 34.1 1530 2A AAY505072 AA AA 34.1 1530 2A AAY505072 AA AA 33.3 33.3 34.1 50.0 AAY05072 AA AA 33.3 34.1 50.0 AAY05072 AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA AA 34.1 1530 2A AA 34.1 1530 2A AA 34.1 1530 2A AA 34.1 1530 2A AA 34.1 1530 2A AA 34.1 1530 2A AA 34.1 1530 2A AA 34.1 1530 AA AA 34.1 1530 AA AA 34.1 1530 AA AA 34.1 1530 AA AA 34.1 1530 AA AA 34.1 1530 AA 34.1 1530 AA AA 34.1 1530 AA 34.1 1530 AA AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34.1 1530 AA 34 | 15       | 46         | 35.7         | 705          | 22   | AAG90301              | C qlutamicum prote                       |
| 17 45 34.9 1362 20 AAM89481 18 45 34.9 1447 20 AAW89481 20 44 34.1 22 ABG01077 21 44 34.1 274 21 AAG58293 22 44 34.1 274 21 AAG58292 23 44 34.1 274 21 AAG58292 24 43 34.1 296 21 AAG58292 25 44 34.1 296 21 AAG58292 26 44 34.1 358 21 AAG58292 27 44 34.1 358 21 AAG58291 28 44 34.1 358 21 AAG58291 29 44 34.1 358 22 ABB6896 30 44 34.1 358 22 AAG88291 31 34.1 429 22 ABB6896 32 44 34.1 152 20 AAW81028 33 44 34.1 152 20 AAW81028 34 44 34.1 152 20 AAW81028 35 44 34.1 152 20 AAW81028 36 44 34.1 152 20 AAW81028 37 44 34.1 152 20 AAW81028 38 44 34.1 152 20 AAW81028 39 44 34.1 152 20 AAW81028 39 44 34.1 152 20 AAW81028 30 44 34.1 152 20 AAW81028 31 33.3 254 20 AAW81028 32 44 33.3 32 34 44 34.1 152 20 AAW81028 34 44 34.1 1630 22 AAR95962 44 33.3 3.3 254 20 AAW81028 45 43 33.3 418 20 AAW8118  ALIGNMENTS  SULT 1 F71038 FAY71038 Standard; Peptide; 28 AA.  AAY71038 FXEEPLOCOCCUS PYOGENES STRAIN SF370 GRAB PROTEIN FRAGME GRAB PROTEIN; PROTEIN GRAB DEOTEIN FRAGME                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 16       | 45         | 34.9         | 502          | 21   | AAY54580              |                                          |
| 18 45 34.9 1447 20 AAM81029 19 45 34.9 1637 22 ABB60342 20 44 34.1 274 21 AAG58293 22 44 34.1 274 21 AAG58292 23 44 34.1 284 22 AAM85122 24 44 34.1 296 21 AAG58292 25 44 34.1 296 21 AAG58292 26 44 34.1 358 21 AAG58292 27 44 34.1 358 21 AAG58292 28 44 34.1 358 21 AAG58293 29 44 34.1 358 21 AAG58293 30 44 34.1 358 21 AAG58292 30 44 34.1 358 22 AAG92957 31 44 34.1 421 22 AAB59208 33 34.1 1420 22 AAG92957 34 34.1 1420 22 AAG92957 34 34.3 33.3 22 AAB59208 36 44 34.1 1420 22 AAG92957 37 44 34.1 1420 22 AAG92957 38 44 34.1 1420 22 AAG92957 39 43 33.3 254 22 AAG92957 44 34.1 1420 22 AAG92957 44 34.1 1420 22 AAG92957 37 44 34.1 1420 22 AAG92957 38 43 33.3 254 22 AAG92957 44 34.1 1622 20 AAV85962 45 33.3 3 254 22 AAG5502 47 44 3 33.3 254 22 AAG5502 48 33.3 3 418 20 AAV55012 47 43 33.3 418 20 AAV55012 48 AAY11038 standard; peptide; 28 AA.  AAY71038 AAY71038;  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 17       | 45         | 34.9         | 1362         | 20   | AAW99481              |                                          |
| 19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 18       | 45         | 34.9         | 1447         | 20   | AAW81029              | Murine pCIP prote                        |
| 22 44 34.1 274 21 AAGS8293<br>22 44 34.1 274 21 AAGS8293<br>24 43 4.1 296 21 AAGS8293<br>25 44 34.1 296 21 AAGS8292<br>26 44 34.1 296 21 AAGS8291<br>27 44 34.1 296 21 AAGS8291<br>28 44 34.1 358 21 AAGS8291<br>29 44 34.1 358 21 AAGS8291<br>31 44 34.1 358 21 AAGS8291<br>31 44 34.1 358 21 AAGS8291<br>32 44 34.1 358 22 AAGS9262<br>34 34.1 42.2 AAGS9257<br>34 34.1 142.2 AAGS9257<br>35 44 34.1 142.2 AAGS9257<br>36 44 34.1 142.2 AAGS9257<br>37 44 34.1 142.2 AAGS9257<br>38 44 34.1 142.2 AAGS9257<br>44 33.3 256 21 AAY4712<br>45 43 33.3 256 22 AAY35145<br>46 43 33.3 256 22 AAY35145<br>47 43 33.3 256 20 AAY35145<br>48 43 33.3 418 20 AAY6572<br>49 43 33.3 418 20 AAY6572<br>40 43 33.3 418 20 AAY6572<br>41 43 33.3 418 20 AAY6577<br>42 43 33.3 418 20 AAY6571<br>44 43 33.3 418 20 AAY6571<br>45 43 33.3 418 20 AAY6571<br>46 43 33.3 56 20 AAY6571<br>47 43 33.3 418 20 AAY6571<br>48 471038<br>AAY71038 standard; peptide; 28 AA.<br>AAY71038;<br>5treptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein fragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | o (      | 4.5        | 9.4          | 1637         | 7 6  | ABB60342              |                                          |
| 23                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0,5      | # <b>*</b> | 34.T         | 7 - 0        | 77   | ABGUIU//              | Novel numan diagno                       |
| 23 44 34.1 284 22 AAM76512 24 44 34.1 296 21 AAG58292 25 44 34.1 296 21 AAG58292 26 44 34.1 34 19 AAW65234 28 44 34.1 358 21 AAG51026 29 44 34.1 371 21 AAG51026 29 44 34.1 371 21 AAG51026 30 44 34.1 371 21 AAG51026 31 44 34.1 12 2 ABB77817 31 44 34.1 142 2 AAG3957 33 44 34.1 142 22 AAG3957 34 44 34.1 142 22 AAG3957 35 44 34.1 142 22 AAG3957 36 44 34.1 1630 22 AAG3957 37 44 34.1 1630 20 AAW81025 38 43 33.3 224 AAR3145 44 33.3 32 22 AAR3145 44 33.3 32 26 21 AAR3145 44 43 33.3 418 20 AAY05071  ALTONO AAY05071  ALTONO AAY05071  AAY11038 standard; peptide; 28 AA.  AAY11038;  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein Graphe                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 22       | 4 4        | 34.1         | 274          | 21   | AAG61028              |                                          |
| 24 44 34.1 296 21 AAGS8292<br>25 44 34.1 296 21 AAGS8292<br>26 44 34.1 358 21 AAGS8291<br>28 44 34.1 358 21 AAGS8291<br>29 44 34.1 358 21 AAGS8291<br>30 44 34.1 358 21 AAGS8291<br>31 44 34.1 32 AABBC996<br>32 44 34.1 421 22 AABBC996<br>33 44 34.1 1422 22 AAG92957<br>34 44 34.1 1420 20 AAWB1028<br>35 44 34.1 1420 20 AAWB1028<br>36 44 34.1 1420 20 AAWB1028<br>37 44 34.1 1420 20 AAWB1028<br>38 3.3 3.3 32 1 AAY29962<br>40 33.3 32 20 AAY21975<br>41 33.3 32 20 AAY3145<br>42 43 33.3 418 20 AAY3145<br>43 33.3 418 20 AAY3145<br>44 3 33.3 418 20 AAY3145<br>45 43 33.3 418 20 AAY3145<br>46 43 33.3 418 20 AAY3145<br>47 43 33.3 418 20 AAY3145<br>48 43 33.3 418 20 AAY3145<br>48 43 33.3 418 20 AAY3145<br>49 43 33.3 418 20 AAY3145<br>40 43 33.3 418 20 AAY3145<br>44 43 33.3 418 20 AAY3145<br>45 AAY11038 standard; peptide; 28 AA.<br>AAY71038;<br>51 CRAP Protein GRAB Protein fragme GRAB Protein fragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 233      | 44         | 34.1         | 284          | 22   | AAM78512              |                                          |
| 25 44 34.1 296 21 AAGG1027 26 44 34.1 34 19 AAWG1234 27 44 34.1 358 21 AAGG1026 28 44 34.1 358 21 AAGG1026 29 44 34.1 37.1 21 AAR91672 30 44 34.1 37.1 21 AAR91672 31 44 34.1 429 22 ABBG5976 33 44 34.1 1412 22 AABB6996 34 43 34.1 142 22 AAR91028 35 44 34.1 142 22 AAR91028 36 44 34.1 142 22 AAR91028 37 44 34.1 1522 20 AAV11075 38 44 34.1 1630 22 AAR91025 39 43 33.3 226 21 AAY95962 40 43 33.3 254 22 AAR91230 41 33.3 254 22 AAR91230 42 43 33.3 254 22 AAR912557 43 33.3 418 20 AAY95072 44 43 33.3 418 20 AAY05071 45 43 33.3 418 20 AAY05071 46 43 33.3 418 20 AAY05071 47 43 33.3 418 20 AAY05071 48 43 33.3 418 20 AAY05071 48 43 33.3 418 20 AAY05071 49 43 33.3 418 20 AAY05071 40 43 33.3 54 22 AAY05071 41 43 33.3 54 22 AAY05071 42 43 33.3 54 22 AAY05071 43 44 44 44 44 44 44 44 44 44 44 44 44 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 24       | 44         | 34.1         | 296          | 21   | AAG58292              | Arabidopsis thalia                       |
| 26 44 34.1 344 19 AAW661234 27 44 34.1 358 21 AAG68291 28 44 34.1 358 21 AAG68291 29 44 34.1 371 21 AAV881672 31 44 34.1 429 22 ABB67976 32 44 34.1 514 19 AAW80400 33 34.1 514 19 AAW80400 34 34.1 1412 22 AAB69277 34 34.1 1412 22 AAW81028 35 44 34.1 1412 22 AAW81028 36 44 34.1 142 22 AAW81028 37 44 34.1 1630 22 AAV899562 39 43 33.3 226 21 AAV44712 41 43 33.3 226 21 AAV44712 42 43 33.3 226 21 AAV44712 43 33.3 448 20 AAV59507 44 43 33.3 418 20 AAV59507 45 43 33.3 418 20 AAV5971 46 43 33.3 418 20 AAV5971 47 43 33.3 418 20 AAV5971 48 43 33.3 418 20 AAY05071 49 43 33.3 418 20 AAY05071 40 43 33.3 418 20 AAY05071 41 43 33.3 418 20 AAY05071 42 43 33.3 418 20 AAY05071 43 44 43 33.3 418 20 AAY05071 44 43 33.3 418 20 AAY05071 45 44 43 33.3 418 20 AAY05071 46 AAY11038; 47 AAY11038; 48 AAY11038; 51 AAY11038; 529-AUG-2000 (first entry) 52 AAY11038; 53 Exeptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein GRAD Protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 25       | 44         | 34.1         | 296          | 21   | AAG61027              | Arabidopsis thalia                       |
| 28 44 34.1 358 21 AAC61026<br>29 44 34.1 371 21 AAR81672<br>31 44 34.1 429 22 ABB67816<br>32 44 34.1 514 19 AAW80400<br>33 44 34.1 514 19 AAW80400<br>34 43 34.1 514 19 AAW80400<br>35 44 34.1 1412 22 AAR81028<br>36 44 34.1 1412 22 AAR81028<br>37 44 34.1 142 22 AAR81028<br>38 44 34.1 1630 22 AAR81028<br>39 43 33.3 22 20 AAY4102<br>41 43 33.3 22 21 AAY44712<br>41 43 33.3 226 21 AAR812830<br>42 43 33.3 226 21 AAR812830<br>43 33.3 407 20 AAY05071<br>44 43 33.3 418 20 AAY05071<br>45 43 33.3 418 20 AAY05071<br>46 43 33.3 418 20 AAY05071<br>47 43 33.3 418 20 AAY05071<br>48 43 33.3 418 20 AAY05071<br>49 43 33.3 418 20 AAY05071<br>40 AAY1038 standard; peptide; 28 AA.<br>AAY71038;<br>51 AAY1038;<br>529-AUG-2000 (first entry)<br>51 Streptococcus pyogenes strain SF370 GRAB protein fragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 26       | 44         | 34.1         | 344          | 91   | AAW61234              | Streptococcus pneu                       |
| 29 44 34.1 371 21 AAY81672 31 44 34.1 421 22 ABB6781817 32 44 34.1 429 22 ABB6781817 33 44 34.1 514 19 AAW80400 34 44 34.1 514 19 AAW80400 34 44 34.1 1912 22 AAG92957 35 44 34.1 1412 22 AAM81028 36 44 34.1 142 22 AAW81028 37 44 34.1 152 20 AAW81028 38 44 34.1 1630 22 AAW81025 39 43 33.3 226 21 AAW81230 42 43 33.3 226 21 AAW81230 42 43 33.3 226 21 AAW81230 42 43 33.3 226 22 AAR812557 44 43 33.3 226 21 AAW81255 45 44 33 33.3 407 20 AAY80712 46 43 33.3 407 20 AAY80702 47 43 33.3 418 20 AAY80702 48 43 33.3 418 20 AAY80701 49 44 43 33.3 418 20 AAY90702 40 AAY1038 standard; peptide; 28 AA.  AAY11038;  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein Graphe                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 28       | 4 4        | 34.1         | 200          | 7 7  | AAG61026              |                                          |
| 30 44 34.1 421 22 ABB71817 31 44 34.1 429 22 ABB55976 32 44 34.1 592 22 AAG9957 34 44 34.1 592 22 AAG9957 34 44 34.1 1951 20 AAM81028 35 44 34.1 142 22 AAB50278 36 44 34.1 142 20 AAM81025 37 44 34.1 1630 20 AAM81025 38 43 33.3 92 21 AAY21975 40 43 33.3 92 21 AAY4712 41 43 33.3 254 22 AAB5962 42 43 33.3 254 22 AAB12597 44 43 33.3 254 22 AAB12557 44 43 33.3 418 20 AAY05071 45 43 33.3 418 20 AAY05071 45 43 33.3 418 20 AAY05071 45 43 33.3 418 20 AAY05071 45 43 33.3 418 20 AAY05071 45 43 33.3 418 20 AAY05071 45 AAY11038 standard; peptide; 28 AA.  AAY11038; 29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 29       | 44         | 34.1         | 371          | 21   | AAY81672              | Streptococcus pneu                       |
| 31 44 34.1 429 22 ABB65976 32 44 34.1 519 12 AAAB6000 33 44 34.1 519 22 AAA629557 34 44 34.1 1412 22 AAA692957 36 44 34.1 1412 22 AAA892025 36 44 34.1 1412 22 AAA892025 37 44 34.1 1420 20 AAA81025 38 44 34.1 1522 20 AAA21975 39 43 33.3 25 20 AAA21975 40 43 33.3 254 22 AAA5112 41 43 33.3 254 22 AAA5112 42 43 33.3 254 22 AAA5112 44 43 33.3 256 20 AAA95145 44 43 33.3 418 20 AAA95071 45 43 33.3 418 20 AAA95071  AAY11038 standard; peptide; 28 AA.  AAY71038;  Streptcocccus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 30       | 44         | 34.1         | 421          | 22   | ABB71817              | Drosophila melanoc                       |
| 32 44 34.1 514 19 AAW80400<br>34 44 34.1 519 22 AAG805057<br>35 44 34.1 1412 22 AAW81028<br>36 44 34.1 1420 20 AAW81025<br>37 44 34.1 1420 20 AAW81025<br>38 44 34.1 1522 20 AAV21975<br>39 43 33.3 22 AAV21975<br>40 43 33.3 256 21 AAV4712<br>41 43 33.3 256 21 AAV4712<br>42 43 33.3 256 20 AAV3145<br>44 43 33.3 256 20 AAV35145<br>44 43 33.3 418 20 AAV35072<br>45 43 33.3 418 20 AAV35072<br>46 43 33.3 418 20 AAV35071<br>47 43 33.3 418 20 AAV35072<br>48 43 33.3 418 20 AAV35072<br>49 43 33.3 418 20 AAV35071<br>40 AAY71038 standard; peptide; 28 AA.<br>AAY71038;<br>51 AAY71038 standard; peptide; 28 AA.<br>AAY71038;<br>529-AUG-2000 (first entry)<br>51 Streptococcus pyogenes strain SF370 GRAB protein fragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 31       | 44         | 34.1         | 429          | 22   | ABB65976              | Drosophila melanoc                       |
| 33 44 34.1 592 AAWB12897 EF 34.1 592 22 AAB592997 EF 35 44 34.1 1412 22 AAB59278 HV 34.1 142 22 AAB59278 HV 34.1 142 22 AAB59278 HV 34.1 1530 22 AAY21975 HV 39 43 33.3 226 21 AAY95962 Ye 41 34.1 1630 22 AB59874 Dr 42 43 33.3 226 21 AAAV95962 Ye 43 33.3 226 21 AAAV95962 CF 44 43 33.3 256 20 AAY95145 CF 44 43 33.3 418 20 AAY05071 S.S. 45 33.3 418 20 AAY05071 S.S. AAY71038 standard; peptide; 28 AA. AAY71038; 29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragment GRAB protein; protein; protein Greated alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 2.5      | 4 4        | 34.1         | 5.14<br>0.00 | ÷ 5  | AAW80400              |                                          |
| 35 44 34.1 1412 22 AABS9278 Hun 36 44 34.1 142 22 AABS9278 AII 36 44 34.1 142 22 AABS9278 37 44 34.1 1520 20 AABS9278 39 43 33.3 22 ABS9874 Pro 40 43 33.3 22 AAYS9562 41 43 33.3 226 21 AAY97562 42 43 33.3 226 21 AAY9712 Sph 43 33.3 226 21 AAY9712 Ch 44 43 33.3 226 21 AAY9712 Ch 45 43 33.3 26 20 AAY35145 Ch 46 43 33.3 418 20 AAY35145 Sch 47 43 33.3 418 20 AAY05071 Sch 48 43 33.3 418 20 AAY05071 Sch 49 AAY1038 standard; peptide; 28 AA.  AAY1038,  29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragment GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 2 to     |            | 34 · I       | 0 y 2        | 77   | AAG9293/<br>AAW81028  | ER interacting don                       |
| 36 44 34.1 1420 20 AAM81025 37 44 34.1 1522 20 AAX21975 38 44 34.1 1530 22 ABB59874 39 43 33.3 32 21 AAX95962 40 43 33.3 226 21 AAX47112 42 43 33.3 226 22 AAX471230 43 33.3 254 22 AAR12557 44 43 33.3 478 20 AAX93145 45 43 33.3 418 20 AAY05071  KULT 1  K71038 AAY71038 standard; peptide; 28 AA.  AAY71038;  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein Gragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 3.5      |            | 34.1         | 1412         | 22   | AAB59278              | Human SRC-3 prote                        |
| 37 44 34.1 1522 20 AAY21975 39 44 34.1 1630 22 ABB59874 39 43 33.3 32 1 AAY99962 40 43 33.3 25 21 AAY94712 42 43 33.3 254 22 AAB12130 44 43 33.3 256 20 AAY3145 44 43 33.3 407 20 AAY05071 45 43 33.3 418 20 AAY05071  ALIGNMENTS  SULT 1  F71038 FAY71038 standard; peptide; 28 AA.  AAY71038;  Streptcocccus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 36       |            | 34.1         | 1420         | 20   | AAW81025              | AIB1 (Amplified in                       |
| 38 44 34.1 1630 22 ABB58874 40 43 33.3 32.2 AAV595962 40 43 33.3 22 AAV44712 41 43 33.3 226 21 AAB1230 44 43 33.3 258 20 AAV3145 44 43 33.3 258 20 AAV35072 45 43 33.3 418 20 AAV35071 ALICNMENTS  SULT 1 F71038 AAY71038 standard; peptide; 28 AA. AAY71038 standard; peptide; 28 AA. AAY71038; 29-AuG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 37       |            | 34.1         | 1522         | 20   | AAY21975              | Human steroid rece                       |
| 39 43 33.3 35 21 AAN495950.2 41 43 33.3 226 21 AAN21230 42 43 33.3 226 21 AAN21230 43 43 33.3 226 21 AAN21230 44 43 33.3 226 20 AAY58145 45 43 33.3 418 20 AAY58071 45 43 33.3 418 20 AAY58071  ALIGNMENTS  SULT 1  Y1038  AAY11038 standard; peptide; 28 AA.  AAY71038;  29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | æ 0      |            | 34.1         | 1630         | 22   | ABB59874              |                                          |
| 40 43 33.3 226 21 AAB21230<br>41 43 33.3 226 22 AAB21230<br>43 43 33.3 226 20 AAY33145<br>44 43 33.3 407 20 AAY05072<br>45 43 33.3 418 20 AAY05072<br>45 43 33.3 418 20 AAY05071<br>ALIGNMENTS  SULT 1  Y1038 AAY11038 standard; peptide; 28 AA.  AAY71038; 29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein fragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | n •      |            | £            | υ c          | 7 5  | AAY95962              | reast GCN4 mutated                       |
| 43 43 33.3 254 22 AAE12257 43 43 33.3 256 20 AAY35145 44 43 33.3 418 20 AAY05072 44 43 33.3 418 20 AAY05072  ALIGNMENTS  SULT 1  F71038 FAY71038 standard; peptide; 28 AA.  AAY71038;  29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein Gragme                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 7 T      |            | 0.00         | 760          | 7 5  | AAI44/12              | SHOT CHOILE SCUIPIN                      |
| 43 43 33.3 258 20 AAY35145 44 43 33.3 407 20 AAY05072 45 43 33.3 418 20 AAY05071  ALIGNMENTS  F1038  AAY71038 standard; peptide; 28 AA.  AAY71038;  29-AUG-2000 (first entry)  Streptococcus pyogenes strain SF370 GRAB protein fragme GRAB protein; protein G related alpha2M binding protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 7 7      |            |              | 254          | 22   | AAB21230<br>AAE12557  | Chlamydia pheumoni                       |
| 44 43 33.3 407 20 AAV05072 S 45 43 33.3 418 20 AAV05071 S  BULT 1 Y11038 AAY71038 standard; peptide; 28 AA.  AAY71038; 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 43       |            |              | 258          | 50   | AAY35145              | Chlamydia pneumon                        |
| ALIGNMENTS  SULT 1 Y71038 AAY71038 standard; peptide; 28 AA. AAY71038; 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 44       |            |              | 407          | 20   | AAY05072              | _                                        |
| ALIGNMENTS SULT 1 Y71038 AAY71038 standard; peptide; 28 AA. AAY71038; 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 45       | 43         |              | -            | 20   | AAY05071              | . pneumoniae                             |
| Y71038 AAY71038 standard; peptide; 28 AA. AAY71038; 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmeni GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |          |            |              |              |      | ALIGNMENTS            |                                          |
| AAY71038 standard; peptide; 28 AA. AAY71038; 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen. GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT 1 |            |              |              |      |                       |                                          |
| AAY71038; 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ID AAY7] |            | andard       |              | de;  |                       |                                          |
| 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |          | 038:       |              |              |      |                       |                                          |
| 29-AUG-2000 (first entry) Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |          |            |              |              |      |                       |                                          |
| Streptococcus pyogenes strain SF370 GRAB protein fragmen GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |          | rG-2000    | (fir         |              | γ)   |                       |                                          |
| GRAB protein; protein G related alpha2M binding protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | -        | τοσοσαι    |              |              | trai | SF370 GRAB            |                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |            | Dr           | tein G       | rela | ted alpha2M binding n | protein; vaccine;                        |
| alpha2-macroglobulin; group A Streptococcus; GAS;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |          | 2-macro    | oglobu       | lin; gr      | dno  | A Streptococcus; GAS; | antiblotic;                              |

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immune response; Streptococcus pyogenes infection. 99WO-GB03631 Streptococcus pyogenes WO200026240-A2 02-NOV-1999; 11-MAY-2000.

98GB-0023975. Bjorck LH, Rasmussen M; (ACTI-) ACTINOVA LTD. 02-NOV-1998;

New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein  $\,$ 

WPI; 2000-365572/31.

Claim 3; Page 56; 67pp; English

Length 141;

DB 21;

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Query Match
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           The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is one of the repeat regions of GRAB protein from S. pyogenes strain SF370 corresponding to residues 92-119. This fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes strain SF370 GRAB protein fragment #4.
                                                                                                                                                                                                                                                                                   Length 28;
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                                                                                                                                                                                                                                                                                 100.0%; Score 129; DB 21;
100.0%; Pred. No. 4.6e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           AAY71040 standard; peptide; 141 AA.
                                                                                                                                                                                                          useful in vaccine composition
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Best Local Similarity 100.4
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. Pyogenes strain API.

The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Thr at position 18 of GRAB protein fragment (AAY71036) from S. pyogenes strain SF370 is replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
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100.0%; Pred. No. 3.3e-11;
tive 0; Mismatches 0;
100.0%; Score 129; DB 21 100.0%; Pred. No. 3e-11;
                                                  Mismatches
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                                                                                                       1 SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                      58 SDALEALADQTDALQSEEAAVVKADNAA 85
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es 28; Conservative
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                           Best Local Similarity
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AAY71041;

RESULT 4

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                                                                                                                                                                                                                                                                                                                          Claim 5; Page 62-63; 67pp; English.
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                                                                                               99WO-GB03631
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Streptococcus pyogenes
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N-PSDB; AAD00564.
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Best Local Similarity
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                              WO200026240-A2
                                                                                              02-NOV-1999;
                                                                                                                              02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             composition.
                                                               11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a fragment of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-192 and devoid of the membrane spanning region. This fragment is useful in vaccine composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses a new family of proteins termed GRAB (protein G related alpha2b binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and poptides derived from it are used in vaccine compositions for generating a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                           GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
;
                                                                                                                                              Streptococcus pyogenes strain SF370 GRAB protein fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes strain KTL3 partial GRAB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 129; DB 21;
100.0%; Pred. No. 3.4e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SDALEALADQTDALQSEEAAVVKADNAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 57-58; 67pp; English.
                                            AAY71041 standard; peptide; 159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71046 standard; Protein; 167 AA
                                                                                                                                                                                                                                                                                                                                          99WO-GB03631
                                                                                                                                                                                                                                                                                                                                                                          98GB-0023975
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                                                                                                           29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasmussen M;
                                                                                                                                                                                                                                          Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                           (ACTI-) ACTINOVA LTD.
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nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 AA;
                                                                                                                                                                                                                                                                         WO200026240-A2.
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Sequence

Query Match Matches

ò g AAY71046;

AAY71046

02-NOV-1999; 02-NOV-1998;

Bjorck LH,

11-MAY-2000.

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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. Pyogenes strain KTL3.

The protein has alpha2M binding region and is useful in vaccine
New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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label= alpha2-macroglobulin_binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes strain SF370 mature GRAB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 129; DB 21; 100.0%; Pred, No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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/note "repeat region"
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a full-length GRAB protein from S. pyogenes strain SF370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217;
                                                                                                          for gram-positive proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes strain KTL9 partial GRAB protein.
                                                                              /label- Cell_wall_spanning_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 129; DB 21; 100.0%; Pred. No. 4.9e-11;
                                                                                                                                                                     /label= Membrane_spanning_region
                                                                                               183..188
/note= "consensus sequence
surface cell wall anchored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
            /label= Repeat_region_1
                                             Repeat_region_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 SDALEALADQTDALQSEEAAVVKADNAA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71043 standard; Protein; 259 AA
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N-PSDB; AAD00559, AAD00560.
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                                                            .192
                           20..147
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                                                                                                                                                                                                                                                                                                                                                                                    Bjorck LH, Rasmussen M;
                                             /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                   (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AA;
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                                                                                                                                                      Region
                                                                Region
                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus, pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a manture GRAB protein from S. pyogenes strain SF370 without the and useful in vaccine composition.
                                                                                                                                                                                                                                                                                                                                               New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 184;
/note= "consensus sequence for gram-positive
surface cell wall anchored proteins"
160..184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , 4e-11;
0;
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                                                            /label- Membrane_spanning_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34..91
/label- alpha2M_binding_site
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/label= Signal_sequence
34..217
/label= Mature_GRAB_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SDALEALADQTDALQSEEAAVVKADNAA 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71042 standard; Protein; 217 AA
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                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 56; 67pp; English.
                                                                                                                                                                      99WO-GB03631
                                                                                                                                                                                                       98GB-0023975
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                                                                                                                                                                                                                                                                             Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
                                                                                                                                                                                                                                          (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 AA;
                                                                                               WO200026240-A2
                                                                                                                                                                                                       02-NOV-1998;
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                                                                                                                                  11-MAY-2000
                                                                                                                                                                                                                                                                           Bjorck LH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain AP49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic, vaccine, prevention, treatment, infection, envelope, identification, binding compound, bacterium; life cycle, activator, bacteria, inhibitor, duodenal ulcer disease, chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
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                                                                                                                                                                                                               Length 271;
                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                               100.0%; Score 129; DB 21;
100.0%; Pred. No. 6.3e-11;
tive 0; Mismatches 0;
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Misc-difference 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWT.
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                                                                                                                                                                                                                                                                                       174 SDALEALADQTDALQSEEAAVVKADNAA 201
                                                                                                                                                                                                                                                                        1 SDALEALADQTDALQSEEAAVVKADNAA 28
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                                                                                                                                                                                                                                                                                                                                                                           AAW20445 standard; Protein; 192 AA.
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                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 18
                                                                                                                                                                                      271 AA;
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07-JUN-1995;
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       AAW20445;
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                           RESULT 10
AAW20445
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                                                                                                                                                                                                           The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is a lso useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain KTL9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                            immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 259;
                                                                                                                                            • alpha2M binding protein for generating a protective ing
group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes strain AP49 partial GRAB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 129; DB 21; 100.0%; Pred. No. 6e-11; wiematches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 SDALEALADQTDALQSEEAAVVKADNAA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY71045 standard; Protein; 271 AA.
                                                                                                                                                                                 Claim 5; Page 59-60; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 61-62; 67pp; English
                                                                                                                                         New alpha2M binding protein for
             98GB-0023975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB03631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
les 28; Conservative
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                                                                      Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACTI-) ACTINOVA LTD.
                                        (ACTI-) ACTINOVA LTD
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N-PSDB; AAD00563.
                                                                                                 WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                        259 AA;
                                                                                                                N-PSDB; AAD00561
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           02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                            composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-2000
                                                                      Bjorck LH,
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71045;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.

222 AA;

Sequence

888888**8** 

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This sequence represents a H. pylori secreted or periplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori Infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori allowing the sequence of the pylori and lyse for of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a H. pylori secreted or periplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ONF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
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0
                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 18; Length 192;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylor1 secreted or periplasmic protein, 02ce10216orf1.
                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW20638 standard; protein; 222 AA
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                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             192 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT67891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1996;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least for treating or proteins are claimed, as are probes containing at least for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of the products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acids and proteins - used to develop products for the detection, prevention and treatment of H. pylori
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 Score 57; DB 18; Length 222; Pred. No. 1.5;
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                              7; Indels
                                                                                                                                                                                                                                                H. pylor1 ORF 09ce10413_35336707_f2_9 secreted protein.
                                                                                                                                                                                                                                                                               Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein; cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claims 27, 31; Page 201-202; 279pp; English.
                              4; Mismatches
                                                                                                                                                              AAY10994 standard; Protein; 412 AA.
                                                                            4 LEALADQTDALQSEEAAVVKADN 26
44.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.2%;
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96US-0739150.
96US-0759739.
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                Best Local Similarity 52,2
Matches 12; Conservative
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Best Local Similarity 52.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                           Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D;
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28-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections
                                                                                                                                                                                          AAY10994;
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    Query Match
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ABG30268;

ABG30268

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of Chiamydia trachomatis (see AA201425). The polypeptides can be used as vecines against chiamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chiamydia trachomatis is responsible for a large number of diseases, e.g. eye plaseases such as conventional trachoma, nonendemic trachoma, end inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, and venerallymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
                                                                                                                                                                                                                                                                                               Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perhiepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
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O
                                                                                                                                                                                                                                                      Chlamydia trachomatis cellular envelope protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 668-669; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG90301 standard; Protein; 705 AA.
                                                                                                               AAY36771 standard; Protein; 258 AA
581 AVIQLTPQTEAVRSEDAPVAPRDN 604
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                                                                                                                                                                                                           (first entry)
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Best Local Similarity 36.47
Best Local Similarity 36.47
                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.
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                                                                                                                                                             AAY36771;
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                                                                                       AAX3677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymetheotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymelectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations crasponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 60627; 103pp; English.
                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #30259
                                                                                                                                                        ABG30268 standard; Protein; 1164 AA
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                     Tang YT;
4 LEALADOTDALQSEEAAVVKADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
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Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS94455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Gaps

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Indels

Sequence

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Location/Qualifiers

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Binding-site
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                                                                                                                                                                                                 09-FEB-2000.
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               Domain
                                                                                                         Domain
                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of nucleotide and protein acquences from the Corynebcerium Corynebcaterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and manyshing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium activity a particular of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, saccharides are useful for producing particularly Llysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium/calmodulin dependent protein kinase; CaMK-VI; CaMK-IV; CaMK-VI related peptide; CARP; neuronal plasticity; epilepsy; kainate-induced selzure; selzure; central nervous system; hippocampus; acute brain insult; stroke; trauma; hypoxia; ischemia; neurodegenerative disease; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A rat calcium/calmodulin dependent protein kinase designated CaMK-IV
                                                                                                                                                                                                                          Yokoi H;
Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                     Claim 17; SEQ ID NO: 4055; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 35.7%; Score 46; DB 22; Length 705; Best Local Similarity 37.5%; Pred. No. 2.3e+02; Matches 9; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                         Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY54580 standard; Protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LEALADQTDALQSEEAAVVKADNA 27
                                                                                                                                           16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                  18-DEC-2000; 2000EP-0127688
                                      Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000 (first entry)
            organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Patent Office.
                                                                                                                                                                                                                                                               WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               705 AA;
                                                                                                                                                                                                                                                                           N-PSDB; AAH65520
                                                                EP1108790-A2
                                                                                        20-JUN-2001
                                                                                                                                                                                                                         Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus sp.
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                                                                                                                                                                                                                                      Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
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the present sequence represents a calcium/calmodulin dependent protein kinase (CaMR-IV). The specification also describes another CaMR.

Kinase (CaMR-IV) and a CaMR-VI related peptide, designated CARP. The designated CARP. The came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of the Came of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian calcium/calmodulin dependent protein kinase related protein useful as a modulator of calcium/calmodulin dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                  //note= "residue thought to be crucial for
activation of the kinase by phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful as a modulator of calcium/calmodulin dependent protein kin
activity, useful for treating seizures and damage to the central
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                                                                                        'note= "residue involved in ATP binding"
/note= "putative catalytic domain"
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Pred. No. 2.1e+02;
3; Mismatches 4,
                                                                                                                                                                                                                                                                                                             "Ser/Thr kinase motif"
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "regulatory domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 34-36; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99481 standard; Protein; 1362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-0202654.
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58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98EP-0202654.
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                                                                                                                                                                                                                                                                                                                  /note= "Si
346..364
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                                                                                                                                                                                                                                                               227..234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-138770/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                 Misc-difference
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The AIBI protein is a member of the steroid receptor coactivator-1 (SCR-1) family of nuclear receptor co-activators that interact with estrogen receptors (FR) to enhance ER-dependent transcription.

The AIBI gene is amplified and over-expressed in certain cancers in particular breast cancer and steroid hormone responsive cancers. The AIBI polypeptide can be used to identify compounds which inhibit ER-dependent transcription. Increased expression of the AIBI gene indicates aberrantly proliferating cells, thus detection of increased expression of the AIBI gene or an increase in the number of copies of the AIBI gene or an increase in the number of copies of the AIBI gene can be used to diagnose cancer or a predisposition towards developing cancer. Compounds which inhibit carpoid receptors or nuclear co-factors can be used for reducing the proliferation of cancer cells. This sequence is of the murine pCIP protein, mouse ortholog of AIBI.
                                                                                                                                                                                                                                                                                                                                                                                    New isolated steroid receptor co-activator, AIB1 - used to develop products for the diagnosis and treatment of steroid-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                            tumours, e.g. breast, lung, prostate or colon cancers or melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                /label- Potential_C_terminus /note- "This position encoded by stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 7818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.9%; Score 45; DB 20; 41.7%; Pred. No. 7.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 39-42; 57pp; English.
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                                                                                                                                                            98WO-US12689
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Matches 10; Conservative
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                                                                                                                                                                                                                                          (USGO ) US GOVERNMENT
                                                                                                                                                                                                                                                                                  Meltzer P, Trent JM;
                                                                                                                                                                                                                                                                                                                       WPI; 1999-080946/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1447 AA;
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV99919
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                                                                             WO9857982-A2
                                                                                                                                                            17-JUN-1998;
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                                                                                                                       23-DEC-1998
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  Region
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ABB60342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the amino acid sequence of the mouse p/CIP (p300/CBP/co-integrator-associated protein) polypeptide. The protein can regulate gene expression so are potentially useful therapeutically, e.g. against (breast) cancer, inflammatory disease (e.g. atherosclerosis)
                                                                                                                                                                         /note= "there appears to be 20 amino acids missing between these positions in the sequence given in the specification"
                                                                                                                                                                                                                                                      "there appears to be 20 amino acids missing
between these positions in the sequence given
in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding p/CIP and NcoA-2 polypeptides - are used to identify agents that regulate gene expression, e.g. for treatment of cancer, inflammatory disease and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 6.8e+02;
4; Mismatches 10; Indels
                                                                                                                       /note= "defined in specification as O" Misc-difference 44..45 /note= "there appears to be 20 amino --
                                                                                              note- "defined in specification as ?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine pCIP protein (ortholog of human AIB1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torchia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.9%; Score 45; DB 3
Best Local Similarity 41.7%; Pred. No. 6.8e*
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glass CK, Rose DW, Rosenfield MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81029 standard; Protein; 1447 AA.
                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Fig 1; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US12263
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0049452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX26000
                                                                         Misc-difference
                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1998;
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                Mus sp.
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10; Indels

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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclocide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity amino acid sequences of data and products dependent on DNA and amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.1%; Score 44; DB 22; Length 42; 36.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                               The invention relates to isolated polynucleotide (1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana protein fragment SEQ ID NO: 75231.
                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                  Claim 20; SEQ ID No 31436; 103pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG58293 standard; Protein; 274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DALEALADQTDALQSEEAAVVK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0121825.
99US-0123180.
99US-0123548.
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99US-0126264
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99US-0130891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 36.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     42 AA;
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   biodiversity
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23-APR-1999;
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23-MAR-1999;
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08-APR-1999
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                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 7818; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 45; DB 22; Length 1637; 47.8%; Pred. No. 8.4e+02; tive 4; Mismatches 8; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wlpo.int/pub/published_pct_sequences
                                                                                  Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #1068.
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23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                Adams M,
                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL04445.
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es 11; Conserv
                                               (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1637 AA;
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                                                                                Venter JC,
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| PR 21-JUL-1999; 99US-0144814. PR 21-JUL-1999; 99US-0145086. PR 22-JUL-1999; 99US-0145086. PR 22-JUL-1999; 99US-0145081. PR 22-JUL-1999; 99US-0145081. PR 22-JUL-1999; 99US-0145087. PR 23-JUL-1999; 99US-0145192. PR 23-JUL-1999; 99US-0145145. PR 23-JUL-1999; 99US-0145214. PR 27-JUL-1999; 99US-0145214. PR 27-JUL-1999; 99US-0145218. PR 27-JUL-1999; 99US-0145919. PR 27-JUL-1999; 99US-0145919. PR 02-AUG-1999; 99US-0145919. PR 02-AUG-1999; 99US-0146388. PR 03-AUG-1999; 99US-0146389. PR 04-AUG-1999; 99US-0147204. PR 04-AUG-1999; 99US-0147204. PR 05-AUG-1999; 99US-0147302. PR 05-AUG-1999; 99US-0147303. PR 06-AUG-1999; 99US-0147303. PR 06-AUG-1999; 99US-0147303. PR 06-AUG-1999; 99US-0147416. | 10-Aug-1999; 9908; 11-Aug-1999; 9908; 13-Aug-1999; 9908; 13-Aug-1999; 9908; 13-Aug-1999; 9908; 13-Aug-1999; 9908; 14-Aug-1999; 9908; 20-Aug-1999; 9908; 22-Aug-1999; 9908; 25-Aug-1999; 9908; 27-Aug-1999; 9908; 27-Aug-1999; 9908; 31-Aug-1999; 9908; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 9008; 900 | 13. SEP - 1999; 9908; 15. SEP - 1999; 9908; 26. SEP - 1999; 9908; 22. SEP - 1999; 9908; 23. SEP - 1999; 9908; 24. SEP - 1999; 9908; 24. SEP - 1999; 9908; 06. OCT - 1999; 9908; 07. OCT - 1999; 9908; 13. OCT - 1999; 9908; 13. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; 14. OCT - 1999; 9908; |
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| PR 28-APR-1999; PR 30-APR-1999; PR 04-MAY-1999; PR 05-MAY-1999; PR 06-MAY-1999; PR 11-MAY-1999; PR 11-MAY-1999; PR 14-MAY-1999; PR 14-MAY-1999; PR 19-MAY-1999; PR 21-MAY-1999; PR 22-MAY-1999; PR 22-MAY-1999; PR 22-MAY-1999; PR 22-MAY-1999; PR 22-MAY-1999; PR 27-MAY-1999; PR 28-MAY-1999; PR 29-MAY-1999; PR 29-MAY-1999; PR 01-JUN-1999; PR 01-JUN-1999; PR 01-JUN-1999;                                                                                                                   | 10-50N-1999<br>16-50N-1999<br>16-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>18-50N-1999<br>23-50N-1999<br>23-50N-1999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 20 JUN 1993<br>30 JUN 1993<br>30 JUN 1993<br>00 JUL 1993<br>00 JUL 1993<br>13 JUL 1993<br>14 JUL 1993<br>16 JUL 1993<br>19 JUL 1993<br>19 JUL 1993<br>19 JUL 1993<br>19 JUL 1993<br>19 JUL 1993<br>19 JUL 1993<br>19 JUL 1993<br>20 JUL 1993                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

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990S-0144005
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990S-0144325
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990S-0144333
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99US-0139899.
99US-0140353.
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990S-0141287.
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Pred. No. 1.5e+02;
5; Mismatches 9; Indels
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39.1%;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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2hao QA, Wang D, Wang J, 2hang J, Ren F, Chen R, Wang
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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Pred. No. 1.5e+02;
5; Mismatches 9; Indels
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15-SEP-2000; 2000US-0654936.
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Best Local Similarity 39.1%;
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polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemacopoiesis regulating activity, immunomodulatory activity and activity, inmunomodulatory activity and activity, inthe diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                            inilammation. Mote: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                        Length 296;
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Pred. No. 1.6e+02;
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                                                                                                                     5; Mismatches
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99075-0132049
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990S-0161993.
                                                                                        Query Match
Best Local Similarity 39.1%;
Matches 9; Conservative
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99US-0135124.
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| 99US - 0137528<br>99US - 0137528<br>99US - 0137754<br>99US - 0137754<br>99US - 0138540<br>99US - 0139452<br>99US - 0139452<br>99US - 0139452<br>99US - 0139455<br>99US - 0139455<br>99US - 0139456<br>99US - 0139459<br>99US - 0139459<br>99US - 0139463<br>99US - 0139463<br>99US - 0139463<br>99US - 0139463<br>99US - 0140991<br>99US - 0140991<br>99US - 014236<br>99US - 014236<br>99US - 0144334<br>99US - 0144334<br>99US - 0144336<br>99US - 0145086<br>99US - 0145086<br>99US - 0145087<br>99US - 0145192                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5066<br>5066<br>5066<br>5066<br>5066<br>5066<br>5066<br>5066                                                         | is of                       |
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 75229.
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99US-0135124.
99US-0135353.
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   The present sequence represents a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein
can be useful in vaccines for inducing protective antibodies against
Streptococcus pneumoniae, for treatment or prevention of infection e.g.
care used to detect Streptococcus infection (by usual hybridisation or
amplification methods), also for isolating Streptococcus genes or their
calelic variants. The protein can be used similarly to detect specific
allelic variants and immunoassays, especially for diagnosing or
monitoring infections. Antibodies which bind the protein are used to
detect corresponding antigens, to purify the protein and for passive
immunisation (optionally coupled to a toxin). Vaccines are administered,
e.g. by injection, orally or through the skin, typically at 0.01-1000
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Pred. No. 1.9e+02;
2; Mismatches 7; Indels
               Indels
Best Local Similarity 39.1%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 9;
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                                                                                                                                          AAW61234 standard; Protein; 344 AA.
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                                                            75 EALQQRDKALSERDKALIERDNA 97
                                          5 EALADQTDALQSEEAAVVKADNA 27
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55.0%;
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3 AGQTDASQIEKAAVSQGGKA 22
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Best Local Similarity 55.0°
Matches 11; Conservative
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N-PSDB; AAV27419.
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Pred. No. 2e+02;
5; Mismatches 9; Indels
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EALQQRDKALSERDKALIERDNA 159
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Best Local Similarity 39.1
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21-0CT-19
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   990S-0145085.
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990S-0145089.
990S-0145192.
990S-0145145.
990S-0145218.
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990S-0145913.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                               99US-0121825.
99US-0123548.
99US-0125788.
99US-01257826.
99US-0126785.
99US-0127462.
99US-0128714.
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9905-0131449
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990x-0139462.
990x-0139750.
990x-0139750.
990x-0139817.
990x-0139899.
                                                                                                                                                                               25-FEB-2000; 2000EP-0301439
                                                                         Arabidopsis thaliana
                                                                                                                                                                                                               25 - FEB - 1999; 05 - MAR - 1999; 06 - MAR - 1999; 23 - MAR - 1999; 25 - MAR - 1999; 25 - MAR - 1999; 26 - MAR - 1999; 26 - MAR - 1999; 27 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 29 - MAR - 1999; 28 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - M
                                                                                                           EP1033405-A2
                                                                                                                                           06-SEP-2000
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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antilifammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and/or antigens. The nucleotide sequences can be useful for the detection and diagnostis of S. pneumoniae. The protein sequences and interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA055614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                     New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.1%; Score 44; DB 21; Length 371; 55.0%; Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                              Claim 6; Page 91; 108pp; English.
                                                                                                        (MICR-) MICROBIAL TECHNICS LTD.
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                                    99WO-GB02451.
                                                                              99US-0125164.
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11-JUL-2000; 2000US-0614150.
                                                                 98GB-0016337
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                                                                                                                                     Hansbro PM;
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                                                                                                                                                             WPI; 2000-195300/17.
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                                      27-JUL-1999;
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19-MAR-1999;
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Pred. No. 2e+02;
5; Mismatches 9; Indels
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39.18;
                                                                 99US-0154039.
99US-0154779.
99US-0155139.
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99us-0161993.
99us-0162142.
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99US-0159293
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Matches 9; Conservative
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insecticides, therapeutics and pharmaceutical drugs. The invention
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                                                                                                                                                                                                                                            RESULT 32
                                                                                                                                                                                                                                                        AAW80400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                             13
                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
                                       1000 or more
and cell-cell
                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                     New isolated nucleic acid detection reagent for detecting 1000 genes from Drosophila and for elucidating cell signalling and c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 24720; 21pp + Sequence Listing; English.
                                                                                      Disclosure; SEQ ID NO 42243; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                              Length 421;
                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 24720.
                                                                                                                                                                                                                                                                                           Score 44; DB 22;
Pred. No. 2.4e+02;
3; Mismatches 11;
                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                                                                                              3 ALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB65976 standard; Protein; 429
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M
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                                                                                                                                                                                                                                                                                             34.1%;
46.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                         sequences (ABL01840-A
(ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                       Local Similarity
nes 12; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
N-PSDB; ABL10079.
WPI; 2001-656860/75.
N-PSDB; ABL15920.
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                                                                                                                                                                                                                                                                  421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W0200171042-A2
                                                               interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB65976;
                                                                                                                                                                                                                                                                                           Query Match
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                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haematopoiesis regulating activity, tissue growth activity, activin, inhibin activity, chemotactic; chemokinetic activity, haemostatic; thrombolytic activity; anti-inflammatory activity; cadherin: tumour invasion suppressor activity; tumour inhibition activity.
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human poly:nucleotide(s) and secreted proteins obtained from e.g. human foetal kidney, placenta, foetal brain, adult testes, adult brain or adult uterus cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg D;
                                                                                                                                                                                                                                                                                        2.5e+02;
ches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; immune stimulating; suppressing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCoy JM,
                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A secreted protein encoded by clone dd71_2.
                                                                                                                                                                                                                                                                        Score 44;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lavallie ER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 NAAEVLAAGNAADESVSAAVAPAONAA 208
                                                                                                                                                                                                                                                                                                                                                                                             2 DALEALADQTDALQSEEAAVVKADNAA 28
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                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW80400 standard; Protein; 514
                                                                                                                                                                                                                                                                     34.1%;
ilarity 48.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US04977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Racie LA, Spaulding V,
                                                           (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-520812/44.
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                429 AA;
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Length 514;

DB 19;

34.18; Score 44;

receptor; transcription;

RESULT 33

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(SCR-1) family of nuclear receptor co-activators that interact with estrogen receptors (ER) to enhance ER-dependent transcription.

The AIBI gane is amplified and over-expressed in certain cancers in particular breast cancer and steroid hormone responsive cancers in particular breast cancer and steroid hormone responsive cancers in particular breast cancer and steroid hormone responsive cancers.

The AIBI polypeptide can be used to identify compounds which inhibit ER-dependent transcription. Increased expression of the AIBI gene or an increase in the number of copies of the AIBI gene or an increase in the number of copies of the AIBI gene can be used to diagnose cancer or a predisposition towards developing cancer. Compounds which inhibit interaction of AIBI cancer calls. The PAS domain of the AIBI cancer cells. The PAS domain of the AIBI protein is a highly conserved domain among the SC-1 family of proteins. The ER-interacting domain of AIBI mediates binding of AIBI with a steroid hormone receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated steroid receptor co-activator, AIB1 - used to develop products for the diagnosis and treatment of steroid-responsive tumours, e.g. breast, lung, prostate or colon cancers or melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The AIB1 protein is a member of the steroid receptor coactivator-1
                                                                                                                                                                                                                                    AIB1; amplified in breast cancer; cancer; steroid; receptor coctivator; SCR; estrogen; ER; estrogen dependent transcribreast cancer; lung cancer; colon cancer; prostate cancer; melanoma; PAS region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                              ER interacting domain of AIB1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB59278 standard; protein; 1412 AA.
                                                                AAW81028 standard; Protein; 951 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 34-35; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USGO ) US GOVERNMENT.
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                    12-MAY-1999
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                                       AAW81028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of nucleotide and protein are queences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Caryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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Pred. No. 3.6e+02;
3; Mismatches 9; Indels
                                            Indels
. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                             C glutamicum protein fragment SEQ ID NO: 6711.
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ozaki A;
                      Pred.
                                                                                                                                                                                                                                 AAG92957 standard; Protein; 592 AA
                                                                                                              240 SIKAOROATOLLKEEEARLVESNNA 264
                                                                                 3 ALEALADQTDALQSEEAAVVKADNA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SDALEALADQTDALQSEEAAVV 22
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.18;
                   36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                   26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S, Mizoguchi H,
Tateishi N, Senoh A, Ike
           Best Local Similarity 36.09
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-376931/40.
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2001.
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Gaps

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Indels

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Length 951;

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Steroid receptor coactivator-3; SRC-3; transcription enhancement; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The AIB1 protein is a member of the steroid receptor coactivator-1 (SCR-1) family of nuclear receptor co-activators that interact with estrogen receptors (ER) to enhance ER dependent transcription. The AIB1 gene is amplified and over-expressed in certain cancers. The AIB1 polypeptide can be used to identify compounds which inhibit ER-dependent transcription. Increased expression of the AIB1 gene indicates aberrantly proliferating cells, thus detection of increased expression of the AIB1 gene or an increase in the number of copies of the AIB1 gene can be used to diagnose cancer or a predisposition towards developing cancer. Compounds which inhibit with steroid receptors or nuclear co-factors can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone response element; estrogen receptor alpha; neoplastic state.
                                                                                                                                                                                                                                                                                                                                                                                                  New isolated steroid receptor co-activator, AIB1 - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                     tumours, e.g. breast, lung, prostate or colon cancers or melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                   products for the diagnosis and treatment of steroid-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 20; Length 1420;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
         /label- Serine/Threonine_rich_region
1129..1244
/label- Glutamine_rich_region
1244..1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human steroid receptor coactivator-3 (SRC-3).
                                                                                  /label- Polyglutamine_tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reducing the proliferation of cancer cells.
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Misc-difference 1432
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Misc-difference 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 31-33; 57pp; English.
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1086 QALEPKQDAFQGQEAAVMMDQKA 1108
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                                                                                                                                                                                                98WO-US12689
                                                                                                                                                                                                                                97US-0049728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                     (USGO ) US GOVERNMENT.
                                                                                                                                                                                                                                                                                                                                           WPI; 1999-080946/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1420 AA;
                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV99915
                                                                                                                      WO9857982-A2.
                                                                                                                                                                                                                                17-JUN-1997;
                                                                                                                                                                                              17-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-1999
                                                                                                                                                                                                                                                                                                         Meltzer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY21975:
Region
                                 Region
                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY21975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an antisense oligonucleotide, targeted to a nucleic acid molecule encoding human steroid receptor coactivator-3 (SRC-3). The invention is useful for inhibiting the expression of SRC-3 in human cells or tissues in vitro. It is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is useful prophylactically, to prevent or delay infection, inflammation or tumor formation.
                                                                                                                                                                                                                                                                                                                                                                                              Novel antisense compound useful to prevent or delay infection, inflammation or tumor formation, specifically hybridizes with and inhibits the expression of human steroid receptor coactivator-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coactivator; SCR; estrogen; ER; estrogen dependent transcription; breast cancer; lung cancer; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.1%; Score 44; DB 22; Length 1412; 43.5%; Pred. No. 9.9e+02; Live 4; Mismatches 9; Indels
                                               Steroid receptor coactivator-3; SRC-3; antisense; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIB1; amplified in breast cancer; cancer; steroid; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16..88
/label-_Basic_helix_loop_helix_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263..302
/label- PAS_domain
396..715
/label- Serine/Threonine_rich_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIB1 (Amplified in breast cancer-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Column 43-54; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW81025 standard; Protein; 1420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- PAS_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 EALADOTDALQSEEAAVVKADNA 27
                                                                   inflammation; tumour; cancer
                                                                                                                                                                                                           99US-0440612.
                                                                                                                                                                                                                                                 99US-0440612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                        Bennett CF, Cowsert LM;
                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
             Human SRC-3 protein.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-079549/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                           .S-NOV-1999;
                                                                                                                                                                                                                                                 15-NOV-1999;
                                                                                                   Homo sapiens
                                                                                                                                                                         05-DEC-2000
                                                                                                                                     US6156571-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW81025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Gaps

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01019, expressed DNA sequences (ABL01019, expressed DNA sequences (ABL01019, O-ABL16175) and the encoded proteins
                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labeled polypeptide binding partner compositions useful for monitoring protease activity by detecting signal modulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled-coil; yeast; GCN4; general control of nitrogen; protease; caspase; assay; signal modulation.
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                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6414; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "caspase protease cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast GCN4 mutated coiled-coil peptide used in caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.1%; Score 44; DB 22;
40.0%; Pred. No. 1.2e+03;
tive 4; Mismatches 11;
                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
17..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LEALADOTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY95962 standard; Peptide; 33
                                                      PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2000; 2000WO-GB00601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FLUO-) FLUORESCIENCE LTD.
                                                      H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae
                                                      Adams M,
                                                                                        2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-565459/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserv
                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1630 AA;
                                                                                          WPI; 2001-656860
N-PSDB; ABL03977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200050635-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-2000
                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coyler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY95962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY95962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This represents a human steroid receptor coactivator-3 (SRC-3). Host cells transformed with vectors comprising the SRC-3 gene can be used for the recombinant production of the SRC-3 protein. SRC-3 can be used to enhance the transcription of genes, which are regulated by hormone response elements, e.g. estrogen receptor alpha. SRC-3 can be used in methods to screen for compounds that bind to SRC-3 or which modulate formation of SRC-3 transcription complexes. Determining the amount of SRC-3 in a sample is also useful in a method to detect overexpression of SRC-3 and therefore determining the neoplastic states of cells in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding a steroid receptor co-activator-3, useful determining the neoplastic states of cells in humans or animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 20; Length 1522;
Pred. No. 1.1e+03;
; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 6414.
/note= "encoded by TAA"
                                                                       TAG"
                                                                                                            TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB59874 standard; Protein; 1630 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 61-68; 75pp; English.
                                                                     note- "encoded by
                                                                                                          /note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| : || | : ||||:
1086 QALEPKQDAFQGQEAAVMMDQKA 1108
                                  'note- "encoded
                                                                                                                                                                                                                                                                                              (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 EALADQTDALQSEEAAVVKADNA 27
                                                                                                                                                                                                                                                                                                                                   Suen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.18;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                           97US-0068511
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                                                                                                                                                                                                                        98WO-US25478
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Best Local Similarity 43.59
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                   Frail DE, Lyttle CR,
                                                      Misc-difference 1510
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-405171/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1522 AA;
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX80992
                 Misc-difference
                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                 WO9932621-A2
                                                                                                                                                                                                                        01-DEC-1998;
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                                                                                                                                                                                   01-JUL-1999
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                                The present sequence is that of a homomeric coiled-coil domain derived from amino acids 249-281 of Sarcharomyces cerevisiae GCN4 (general control of nitrogen). The native GCN4 sequence was modified to include a caspase site. A polypeptide useful in the present invention is capable of multimerising with similar or different polypeptides. The polypeptide requires a binding domain, such as a coiled-coil domain, which allows multimerisation. The nultimer preferably comprises a first polypeptide associated with a label and a second polypeptide, where (a) at least 1 of the polypeptides to form a multimer is detectable via a signal emitted by the signal, and (c) digestion of at least 1 polypeptides results in dissociation of the multimer and modulation of the signal emitted by the label. The multimer is used to monitor the activity of a protease. In an example of the method, the polypeptide caspase assay, with the signal analysed by fluorescence resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides used to make cells palatability of cold foods and
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone s3-2; shorthorn sculpin skin-type antifreeze protein; sssAFP; antibacterial; cold tolerance; ice recrystallisation; refrigerated food; antifreeze.
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                                                                                                                                                                                                                                                                                                               Score 43; DB 21; Length 33; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shorthorn sculpin skin-type antifreeze protein.
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antifreeze polypeptides and cold resistant and to improve the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY44712 standard; Protein; 92 AA.
            Example 5; Page 59; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                               98US-0090794.
98US-0095713.
99US-0344529.
                                                                                                                                                                                                                                                                                                               33.3%;
                                                                                                                                                                                                                                                                                                                                                                   DALEALADQTDALQSEEAAVVK
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                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            & DEV LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myoxocephalus scorpius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-170905/15
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ49960
                                                                                                                                                                                                                                                             energy transfer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200000512-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1998;
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24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JAN-2000
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY44712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liquids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hew CL;
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY44712
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The present sequence is shorthorn sculpin skin-type antifreeze protein

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(sssAFP-2) encoded by cDNA clone s3-2. The AFPs are alanine-rich polypeptides that are synthesised in the peripheral tissues, such as skin and gills, and serve to depress the freezing temperature of intracellular fluids. The AFPs are used to make aqueous compositions resistant to freezing, to improve the cold tolerance, for inhibiting ice recrystallisation, and for stabilising biological membranes. They are also used to improve the shelf life and food quality of many refrigerated foods and have antibacterial properties. This has many useful applications in medicine, agriculture and aquaculture.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                           ; DB 21; Length 92; 59;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                           Pred. No. 59;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                   33.3%; Score 43; 39.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 39.37
Watches 11; Conservative
                                                                                                                                                                                                                                                                  92 AA;
                                                                                                                                                                                                                                                                     Sequence
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GenCore version 5.1.3
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OM protein - protein search, using sw model

October 13, 2002, 02:06:51; Search time 24.6578 Seconds Run on:

(without alignments) 157.503 Million cell updates/sec

Perfect score:

US-09-847-539A-6 777 1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP Sequence:

BLOSUM62 Gapop 60.0 , Gapext 60.0 Scoring table:

Total number of hits satisfying chosen parameters: 231628 seqs, 24425594 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

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/cgn2\_6/ptodata/2/laa/PCTUS.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |        | :               | Appl     | Appli          | Appl            | Appli          | Appli          | Appli           | Appl            | Appl        | Appl              | Appl             | Appl              | Appl              | Appl             | Appl             | Appl             | Appl             | Appli           | Appl           | Appl            | Appl       | Appl     | Appl      | Appl     | Appl         | Appl         | Appl           | Appl        |
|-----------|--------|-----------------|----------|----------------|-----------------|----------------|----------------|-----------------|-----------------|-------------|-------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-----------------|----------------|-----------------|------------|----------|-----------|----------|--------------|--------------|----------------|-------------|
|           |        | . :             | 10,      | 2,             | 14,             | ř              | ,<br>,         | 9               | 25,             | 25,         | 25,               | 25,              | 25,               | 25,               | 25,              | 25,              | 25,              | 25,              | 6               | 10,            | 10,             | 26,        | 26,      | 26,       | 26,      | 26,          | 26,          | 26,            | 26,         |
|           |        | tio<br>::       | ce       | ë              | ce              | See            | ce             | ce              | ce              | ce          | oce               | ce               | o                 | oce               | ce               | ce               | oce              | oce              | oce             | ce             | ce              | ce         | ce       | ce        | ce       | ce           | ce           | ce             | ce          |
|           |        | Description     | Seguence | Sequence       | Sequence        | Sequence       | Sequence       | Sequence        | Sequence        | ednence     | Sequence          | Sequence         | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Sequence         | Sequence        | Sequence       | Sequence        | Sequence   | Sequence | Sequence  | Sequence | Sequence     | Sequence     | Sequence       | Sequence    |
|           |        | Des             | Se       | Se             | Se              | Se             | Se             | Se              | Se              | Se          | Se                | Se               | Se                | Se                | Se               | Se               | Se               | Se               | Se              | Se             | Se              | Se         | Se       | Se        | Se       | Se           | Se           | Se             | Se          |
|           |        | į               |          |                |                 |                |                |                 |                 |             |                   |                  |                   |                   |                  |                  |                  |                  |                 |                |                 |            |          |           |          |              |              |                |             |
|           |        |                 |          |                |                 |                |                |                 |                 |             |                   |                  |                   |                   |                  |                  |                  |                  |                 |                |                 |            |          |           |          |              |              |                |             |
|           |        |                 | -10      | ?              | 14              | _              | -              | S               | 52              | -25         | -25               | 52               | -25               | -25               | 25               | 52               | A-25             | -25              | <b>~</b>        |                | 10              | 56         | -26      | -26       | 56       | -26          | -26          | 56             | 56          |
| S         |        | į               | -408B    | 08B            | 68              | 00             | 216            | 54-(            | ::              | -463-288A-2 | 45A               | 79-              | 10A               | 47A               | 14-              | 06               | 506              | 206              | 62-1            | - 76           | -94             | -363-311-2 | 288A-    | 0-445A-26 | 2-619-26 | -466-210A-26 | -467-147A-26 | -08-469-014-26 | -346-290-26 |
| SUMMARIES |        | 1               | 59-4     | 9-4            | 34-1            | 33-7           | 5-16           | 28-2            | 53-3            | 53-2        | 70-4              | 52-6             | 56-2              | 57-1              | 9-69             | 16-2             | 3-10             | 3-10             | 73-4            | 16-8           | 15-7            | 53-3       | -463-2   | 70-4      | 9-29     | 2-99         | 57-1         | 9-69           | 16-2        |
| UMM/      |        |                 | 699-80   | 9-8            | 8-26            | 8-3            | us9            | 8-33            | 8-3             | 8-4(        | 8-4               | 8-4(             | 8-4(              | 8-4               | 8-4              | 8-3              | us9              | us9              | 8-9             | 8-2            | -6              | 8-3        | 8-4      | 8-47      | 8-46     | 8-4          | 8-4          | 8-4            | 6-3         |
| S         |        | a :<br>:        | OS-0     | US-08-669-408B | US-08-294-189-1 | US-08-353-700- | PCT-US95-16216 | US-08-328-254-6 | US-08-363-311-2 | ns-08       | US-08-470-445A-25 | US-08-462-679-25 | US-08-466-210A-25 | US-08-467-147A-25 | US-08-469-014-25 | US-09-346-290-25 | PCT-US93-10506A- | PCT-US93-10506-2 | US-08-973-462-8 | US-08-216-894- | US-09-115-746-1 | us-08      | ns-08    | us-08     | 0S-08    | us-08        | ns-08        | us-0           | 0S-09       |
|           |        | m :             | ٣        | ٣              | Н               | -              | ഗ              | -               | 1               | 7           | 7                 | 7                | 7                 | ~                 | ď                | 4                | Ŋ                | ņ                | 4               | ~              | ₹               | Н          | 7        | 7         | 7        | 7            | 7            | ~              | 4           |
|           |        | Match Length DB | 413      | 664            | 20              | 3248           | 3248           | 2482            | 46              | 46          | 46                | 46               | 46                | 46                | 46               | 46               | 46               | 46               | 1786            | 472            | 472             | 46         | 46       | 46        | 46       | 46           | 46           | 46             | 46          |
|           | , حج   | ٦ ;<br>إ        | 7        | Φ              | <b>&amp;</b>    | <b>&amp;</b>   | æ              | ~               | o,              | 6           | 6                 | 6                | 6                 | 6                 | 6                | 6                | σ                | 6                | 80              | ø              | ڡ               | 'n         | D.       | 'n        | S.       | so.          | 'n           | 'n             | 'n          |
| ø         | Query  | Matc            | 11.      | 10.            | o,              | ď              | ö              | 9               | 80              | æ           | æ                 | ω.               | æ                 | æ                 | ω.               | œ                | œ                | œ                | æ               | æ              | œ               | œ          | æ        | œ         | ထ        | æ            | œ            | αċ             | σ.          |
|           |        | Score           | 91       | 82             | 92              | 92             | 16             | 75              | 69              | 69          | 69                | 69               | 69                | 69                | 69               | 69               | 69               | 69               | 68              | 29             | 67              | 99         | 99       | 99        | 99       | 99           | 99           | 99             | 99          |
|           | 1      | SS              |          |                |                 |                |                |                 |                 |             |                   |                  |                   |                   |                  |                  |                  |                  |                 |                |                 |            |          |           |          |              |              |                |             |
|           | Result | Ş               | 7        | 7              | m               | ₹              | ស              | vo              | 7               | 89          | 6                 | 10               | 11                | 12                | 13               | 14               | 15               | 16               | 17              | 18             | 19              | 20         | 21       | 22        | 23       |              | 25           | 56             | 27          |
|           |        |                 |          |                |                 |                |                |                 |                 |             |                   |                  |                   |                   |                  |                  |                  |                  |                 |                |                 |            |          |           |          |              |              |                |             |

| Appl               | Appl              | 8, Appli        | Appl             | Appli            | Appli           | Appli           | Appli           | Appli           | Appl              |                  |                   | Appl             |                 | Appli           | App1i           | Appl1           | Appli            |   |
|--------------------|-------------------|-----------------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|-------------------|------------------|-------------------|------------------|-----------------|-----------------|-----------------|-----------------|------------------|---|
| 26,                | 26,               | 8               | 10,              | 'n               | 'n              | 6               | æ               | œ               | 15,               | 15,              | 13,               | 13,              | ģ               | ģ               | 4               | æ               | 'n               |   |
| Seguence           | Sequence          | Sequence        | Sequence         | Sequence         | Sequence        | Sequence        | Sequence        | Sequence        | Sequence          | Sequence         | Sequence          | Sequence         | Sequence        | Sequence        | Sequence        | Sequence        | Sequence         |   |
|                    |                   |                 |                  |                  |                 |                 |                 |                 |                   |                  |                   |                  |                 |                 |                 |                 |                  |   |
| PCT-US93-10506A-26 | PCT-US93-10506-26 | US-08-591-079-8 | US-08-591-079-10 | US-08-728-323A-2 | US-08-216-894-2 | US-09-115-746-2 | US-08-216-894-8 | US-09-115-746-8 | US-08-317-450B-15 | US-08-800-593-15 | US-08-317-450B-13 | US-08-800-593-13 | US-08-961-858-6 | 08-09-089-593-6 | US-08-950-925-4 | US-09-346-408-8 | US-08-770-301A-3 |   |
| 'n                 | S                 | N               | ~                | N                | 7               | 4               | N               | 4               | -                 | 4                | Н                 | 4                | 7               | ٣               | ٣٠              | 4               | 7                |   |
| 46                 | 46                | 593             | 593              | 1162             | 564             | 564             | 643             | 643             | 1111              | 1111             | 1193              | 1193             | 288             | 288             | 288             | 461             | 666              |   |
| 8.5                | 8.5               | 8.5             | 8.5              | 8.4              | 8.2             | 8.5             | 8.5             | 8.5             | 8.2               | 8.2              | 8.2               | 8.3              | 8.1             | 8.1             | 8.1             | 8.0             | 8.0              |   |
| 99                 | 99                | 99              | 99               | 65               | 64              | 64              | 64              | 64              | 64                | 64               | 64                | 64               | 63              | 63              | 63              | 62              | 62               |   |
| 28                 | 29                | 30              | 31               | 32               | 33              | 34              | 35              | 36              | 37                | 38               | 39                | 40               | 41              | 42              | 43              | 44              | 45               |   |
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APPLICANT: GUSS, Bengt
APPLICANT: GUSS, Hengt
APPLICANT: JONDSENG, MATTIN
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RAITAMAKI, Lilsa K.
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
TOWBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PID PPY disk
COMPUTER: PID PPY disk
COMPUTER: PID PPY disk
COMPUTER: PACHOLIAN
COMPUTER: PACHOLIAN
COMPUTER: PACHOLIAN
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COMPUTER: PACHOLIAN
APPLICATION NUMBER: US/08/669,408B
FILING DATE: 03-JUL-1996
CLASSIFICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1993
ATTONEY/AGENT INPORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERRACE/DOCKET NUMBER: 29,768
                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
               Sequence 10, Application US/08669408B Patent No. 6100055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 413 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-408B-10
US-08-669-408B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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GENERAL INFORMATION:
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MOLECULE TYPE:
Patent No. 5707822
                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM:
US-08-294-189-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUSS, Bengt
APPLICANT: GUSSON, Hans
APPLICANT: JUNDBERG, Martin
APPLICANT: LINDBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RAITAMARI, Lilsa K.
APPLICANT: RAITAMARI, Lilsa K.
APPLICANT: RAITAMARI, LILSA K.
ATTLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: 3000 K Street, N.W., Sulte 500
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Pred. No. 0.021;
2; Mismatches 12; Indels
                              Length 413;
                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,408B
TITING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                           Score 91; DB 3;
Pred. No. 0.0021;
1; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIETCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BETY, Stephen A.
REGISTRATION NUMBER: 61743/102
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5300
TELEFAX: (202)672-5300
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TELEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-294-189-14
; Sequence 14, Application US/08294189
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08669408B Patent No. 6100055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%;
                        Query Match 11.7%;
Best Local Similarity 59.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.24
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Sequence 1, Application US/08353700

Patent No. 5599919

GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RAITHEN, JEROME B.
TITLE OF INVENTION: TRANSTENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720

CITY: PHILADELPHIA
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                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TILLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 9.8%; Score 76; DB 1;
Best Local Similarity 58.3%; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: JOSKSON ESQ., David A.
REGISTRATION NUMBER: 26, 72
REFERENCE/DOCKET NUMBER: 600-1-118
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO FRAGMENT TYPE: C-terminal ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 KPVVKKEERQNVNTLPTTGEESNP 159
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                                                                                                                                     E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEFUNE: 201 497-5800
TELEAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LEUGHH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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46 EDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Zhu, Xuellang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3248;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carbryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: RECOMMENTATION: REGISTRATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 9.8%; Score 76; DB 5
Best Local Similarity 21.0%; Pred. No. 2.2;
Matches 21; Conservative 28; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-328-254-6
Squence 6, Application US/08328254
; Patent No. 5710022
    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                           SS: not relevant
not relevant
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PCT-US95-16216-1
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GENERAL INFORMATION:
APPLICANT: Ten, Timothy J.
APPLICANT: Ratiner, Jerome B.
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use NUMBER OF SEQUENCES:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 EDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
SUSPERMING PATENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION NUMBER: 36,254
TELECOMMUNICATION NUMBER: 36,254
TELECOMMUNICATION NUMBER: 36,252
TELECOMMUNICATION NUMBER: 36,252
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQ 145
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOCY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103-2307
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NA ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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GENERAL INFORMATION:
APPLICANT: Machel, James L.
APPLICANT: Masper, Dennis L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
TITLE OF INVENTION: Streptococcus
TITLE OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: D.C.
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                                 E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                             SOFTWARE STATEM STATEM SOFTWARE SOFTWARE STATEM SOFTWARE STATEM SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.9%; Score 69; DB 2;
65.0%; Pred. No. 0.075;
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                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 25, Application US/08470445A
; Patent No. 584344
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TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH 46 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bugaisky, Lawrence B. REGISTRATION NUMBER: 35,086 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 KKEERQNVNTLPTTGEESNP 159
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Best Local Similarity 65.0°
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-463-288A-25
   CORRESPONDENCE ADDRESS:
                                                     STREET: 1100 New CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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1792 EKEQEKVQMKEKSSTAMEMLQTQLKELNERVAALHNDQEACKAKEQNLSSQVECLELEKA 1851
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                                                                                                                                                                                                                                                                          Sequence 25, Application US/08363311
Patent No. 6548241
GENERAL INFORMATION:
APPLICANT: MACHEL, James L.
APPLICANT: Ausubel, Frederick M.
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08463288A
Patent No. 5820860
GENERAL INFORMATION:
APPLICANT: Michel, James L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Michel Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine For Group B
TITLE OF INVENTION: Streptococcus
                                                                                                     1852 QLLQGLDEAKNNYIVLQSSVNGLIQEVEDGKQKLEKKDEE 1891
                                                                106 EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/968,866
FILING DATE: 02-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CIMDALA, Michele A.
REGISTRATION NUMBER: 0609.3740004
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 833-8716
TELEFAX: (202) 833-8716
TELEFAX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPELST AMINO acids
TYPELST AMINO ACIDS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20036-2678
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9
Best Local Similarity 65.0
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,210A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/363,311
APPLICATION NUMBER: US 08/363,311
APPLICATION NUMBER: US 07/968,866
FILING DATE: 22-DEC 1994
PRIOR APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION NUMBER: US 07/408,036
FILING DATE: 15-SEP-1989
ATTONERY/AGENT INFORMATION:
NUMBER: 15-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Michel, James L.
APPLICANT: Kasper, Dennis L.
APPLICANT: Adsubel, Frederick M.
APPLICANT: Adsubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine For Group VITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 8.9%; Score 69; DB 2; Best Local Similarity 65.0%; Pred. No. 0.075; Matches 13; Conservative 2; Mismatches
                             FILING DATE: 15-SEP-1989
FILING DATE: 15-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: BUGAISTY, LAWRENCE B.
REGISTRATION NUMBER: 35,086
REPERENCE/DOCKET NUMBER: 0609.2370008
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202) 371-2540
TELEFAX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.237000B
TELECOMMUTCATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEFAX: 248636 SSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08466210A Patent No. 5858362 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
FINGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-462-679-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: USA
20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US' ZIP
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Sequence 25, Application US/08462679

Sequence 25, Application US/08462679

Patent No. 5847081

GENERAL INFORMATION:

APPLICANT: Michel, James L.

APPLICANT: Ausubel, Frederick M.

APPLICANT: Madoff, Lawrence C.

APPLICANT: Madoff, Lawrence C.

TITLE OF INVENTION: Conjugate Vaccine For Group B.

TITLE OF INVENTION: Streptococcus

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.C.

STREET: 1100 New York Avenue, NW, Suite 600

STATE: N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.9%; Score 69; DB 2; Length 46; Best Local Similarity 65.0%; Pred. No. 0.075; Matches 13; Conservative 2; Mismatches 5; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,445A
FILING DATE: 06-JUN 1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363,311
FILING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
FILING DATE: 07-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,036
FILING DATE: 15-SEP-1989
ATORNEY/AGENT INFORMATION:
NAME: BUGAISKY, LAWTENCE B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET UNBER: 35,086
REFERENCE/DOCKET UNBER: 0609.237000A
TELECOMMUNICATION INFORMATION:
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ZIP: 2006-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Rolease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,679
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/33,311
FILING DATE: 22-DEC-1994
PILOR APPLICATION DATA:
PRICK APPLICATION DATE: 02-DEC-1994
FILING DATE: 02-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 aming acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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GENERAL INCOMMATION:
APPLICANT: Masper, Dennis L.
APPLICANT: Ausubel, Trederick M.
APPLICANT: Ausubel, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine Against Group B TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STRATE: 10.C.
COUNTRY: USA
INCOMPTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFFWANDED
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Pred. No. 0.075;
2; Mismatches
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REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.2370006
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEX: 248636 SST
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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US-09-346-290-25
Sequence 25, Application US/09346290
Patent No. 6342223
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Sequence 25, Application US/08469014 Patent No. 5968521
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                                   140 KKEERQNVNTLPTTGEESNP 159
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65.08;
                                                                              2 KKEDAKKAETLPTTGEGSNP 21
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Best Local Similarity 65.0
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                          RESULT 13
US-08-469-014-25
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                                                                                                                                                                                                                                                 8.9%; Score 69; DB 2; Length 46; 65.0%; Pred. No. 0.075; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%; Score 69; DB 2; Length 46; 65.0%; Pred. No. 0.075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-467-147A-25
Sequence 25, Application US/08467147A
Patent No. 5908629
GENERAL INFORMATION:
APPLICANT: Michel, James L.
APPLICANT: Assper, Dennis L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Erederick M.
TITLE OF INVENTION: Conjugate Vaccine For Group B
TITLE OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION UNMBER: US/08/467,147A
FILING DATE: 06-UNN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/363,311
FILING DATE: 22-DEC-1994
PRIOR APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION NUMBER: US 07/408,036
PRIOR APPLICATION NUMBER: US 07/408,036
PRIOR APPLICATION NUMBER: US 07/408,036
PRIOR APPLICATION NUMBER: 15-SEP-1989
ATPORNEY/AGENT INFORMATION:
NAME: BUGA18KY, LAWTENCE B.
REGISTRATION NUMBER: 35,060
                                                                                                                                                                                                                                                                                                                                                                             140 KKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                     2 KKEDAKKAETLPTTGEGSNP 21
                                                    LENGTH: 46 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-466-210A-25
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.09
Matches 13; Conservative
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INFORMATION FOR SEQ ID NO:
                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
SY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10506A
FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10506
FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.; Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%; Score 69; DB 5;
65.0%; Pred. No. 0.075;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
AFILING DATE: 02-NOV-1992
AFILING DATE: 02-NOV-1992
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33 861
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-260
TELEFAX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
                                                                                1100 New York Ave., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
ATTORNEY/AGENT INFORMATION:
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COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 46 amino acids
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Best Local Similarity 65.03
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide
PCT-US93-10506A-25
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                                                                                                        CITY: Washington
                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                               FILING DATE: 0 CLASSIFICATION:
                                                                                                                             D.O.
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                                                                                                                                              COUNTRY:
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0
APPLICANT: Michel, James L.
APPLICANT: Kasper, Dennis L.
APPLICANT: Ausbel, Frederick M.
APPLICANT: Ausbel, Erederick M.
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kesel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Full Street
APPLICANT: Full Street
APPLICANT: United States of America
APPLICANT: United States of America
APPLICANT: To Francis Street
APPLICANT: Boston, Massachusetts 02115
APPLICANT: United States of America
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%; Score 69; DB 4; Length 46; 65.0%; Pred. No. 0.075; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/346,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE GENERAL HOSPITAL CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.2370006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,036
FILING DATE: 15-SEP-1989
ATTORNEY/AGENT INFORMATION:
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PCT-US93-10506A-25
Sequence 25, Application PC/TUS9310506A
Sequence 15, Application PC/TUS9310506A
SHERAL INFORMATION:
APPLICANT: THE GENERAL HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/469,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
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Best Local Similarity 65.09
Watches 13; Conservative
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LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
MOLECULE TYPE: peptide
US-09-346-290-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                           STATE:
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Gaps

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Length 46;

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Query Match
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Sequence 8, Application US/08973462B

Patent No. 6191210.

GENERAL INFORMATION:

APPLICANT: DAUBERSIES, PIERRE

APPLICANT: DAUBERSIES, PIERRE

TITLE OF INVENTION: HALARIAL PRE-ERTTHROCYTIC STAGE POLYPEPTIDE MOLECULES

FILE REFERENCE: 0660-0125-0 PCT

CURRENT APPLICATION NUMBER: US/08/973,462B

CURRENT FILING DATE: 1998-02-06

EARLIER APPLICATION NUMBER: FCT/FR96/00894

EARLIER FILING DATE: 1996-06-12

EARLIER FILING DATE: 1995-06-13

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATCHIN VOR: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8%; Score 68; DB 4; Length 1786;
15.9%; Pred. No. 10;
tive 28; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08216894
Patent No. 5876734
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                             Length 46;
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                                                                                                                                                                                                                                                                                                                           Score 69; DB 5;
Pred. No. 0.075;
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.237PC01
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: 248636 SSK
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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65.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KKEDAKKAETLPTTGEGSNP 21
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 65.0
Matches 13; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                       ; TOPOLOGY: both
; MOLECULE TYPE: peptide
PCT-US93-10506-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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LENGTH: 1786
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US-08-216-894-10
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255 EKQRAAEATKVAEAEKQKAAEATKVAEAEKQRAAEATKVAEAEKQKAAEATKVAGDEKQK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Kelko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSS:
ADDRESSEE: FOLLY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.6%; Score 67; DB 2; Length 472;
20.0%; Pred. No. 2.6;
tive 20; Mismatches 52; Indels
                                                                                                                                                                                    CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/216,894

FILING DATE: 24-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REFERENCE/DOCKET NUMBER: 85326/102/DRLO

TELEPHONE: (202)672-5300

TELEPHONE: (202)672-5309

TELEX: 904136

INFORMATION FOR SEQ ID NO: 10:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
     3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 LADQTDALQSEEAEVVQSDNAASDAWEKAA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 472 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 20.0%
Matches 18; Conservative
STREET: 3000 n CTTY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000 n crry: CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
            CITY: WALL
COUNTRY: USA
COUNTRY: USA
20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-216-894-10
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSBE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, NW, Suite 600 CITY: Washington STATE: D.C. STATE: D.C. COUNTRY: USA ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,288A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/363,311
APPLICATION NUMBER: US 08/363,311
FILING DATE: 22-DEC-1994
PRIOR APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION NUMBER: US 07/408,036
FILING DATE: 13-SEP-1989
ATPONENTY/AGENT INFORMATION:
AMARIE: 15-SEP-1989
ATPONENTY/AGENT INFORMATION:
AMARIE: 15-SEP-1989
ATMONENTY/AGENT INFORMATION:
                                                                                                                                                                                                                                      APPLICANT: Machel, James L.
APPLICANT: Rasper, Dennis L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine For Group
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESSONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 2, Pred. No. 0.18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.2370007
TELECOMMULCATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-470-445A-26; Sequence 26, Application US/08470445A; Patent No. 5843444; GENERAL INFORMATION:
                                                                                                                                                                         Sequence 26, Application US/08463288A Patent No. 5820860 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                       140 KKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 KKEERQNVNTLPTTGEESNP 159
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                                                                 2 KKDDAKKAETLPTTGEGSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-463-288A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                  RESULT 21
US-08-463-288A-26
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                                                                                                                                                                                                                                                                  DB 4; Length 472;
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                                                                                                                                                                                                                                                                                                              52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Michel, James L.
APPLICANT: Michel, James L.
APPLICANT: Ausubel, Frederick M.
TITLE OF INVENTION: Conjugate Vaccine Against Group II
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS.
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,311
                                                                                                                                                                                                                                                               8.6%; Score 67; DB 20.0%; Pred. No. 2.6; tive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/07/968,866
FILING DATE: 02-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CIMBAIA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3740004
TELECOMMUTICATION INFORMATION:
TELEFAX: (202) 466-0800
TELEFAX: (202) 833-8716
TELEFAX: 424656 SSK
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.5%; Score 66; DB
60.0%; Pred. No. 0.18
Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 AAEATKVAEAEKQKAAEATKVAEAEKQKAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                93 LADQTDALQSEEAEVVQSDNAASDAWEKAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-363-311-26
; Sequence 26, Application US/08363311
; Settent No. 6548241
; GENERAL INFORMATION:
                                  TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                             EENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-115-746-10
                    TELEPHONE: (202)672-530
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 20.09
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 amino acids
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Best Local Similarity 60.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20036-2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-363-311-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Gaps
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Sequence 26, Application US/08466210A

Patent No. 5858362

GENERAL INFORMATION:
APPLICANT: Machel, James L.
APPLICANT: Rasper, Dennis L.
APPLICANT: Asubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine For Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIF: 20005-3934

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5%; Score 66; DB 2; Length 46; 60.0%; Pred. No. 0.18; Live 3; Mismatches 5; Indels
                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: BACENTIN Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,679
FILING DATE: US-08/10-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363,311
FILING DATE: US 2-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
FILING DATE: US 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,036
FILING DATE: US-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,210A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bugaisky, Lawrence B.
REGISTRATION VUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.2370008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2600
TELEXX: (202) 371-2540
TELEX: 246636 SSK
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 KKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KKDDAKKAETLPTTGEGSNP 21
                                  ZIP: Z.0005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.5
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-462-679-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: PatentI
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                   APPLICANT: Kasper, Dennis L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Michel, James L.
APPLICANT: Rasper, Dennis L.
APPLICANT: Assubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine For Group ITILE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 66; DB 2; 60.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.237000A
TELEPAN: (202) 371-2600
TELEPAN: (202) 371-2540
TELEPAN: (202) 371-2540
TELEPAN: (202) 371-2540
TELEPAN: 248636 SSK
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08462679 Patent No. 5847081
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Michel, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KKDDAKKAETLPTTGEGSNP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
MOLECULE TYPE: peptide
                                                                                                                                                                                   STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-470-445A-26
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US-08-462-679-26
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0; Gaps

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Sequence 26, Application US/08469014

Patent No. 5966521

GENERAL INFORMATION:
APPLICANT: Michel, James L.
APPLICANT: Asper, Dennis L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Madoff Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 66; DB 2; Length 46; 60.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,014
FILING DATE: 05-JUN-1995
CLASSIFICATION: 4.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.2370006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SED ID NO: 26:
SEQUENCE CHARACTERISTICS:
     NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.2370009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: 248636 SSK
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICR APPLICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/363,311
FILING DATE: 22-DEC-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,036
FILING DATE: 15-SEP-1999
ATTORNEY/AGENT INFORMATION:
NAME: BUGAISKY, LAWIENCE B.
REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 KKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKDDAKKAETLPTTGEGSNP 21
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 amino acids
                                                                                                                                                                                                                                                                             TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-467-147A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
US-08-469-014-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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Sequence 26, Application US/08467147A

Patent No. 5908629

GENERAL INFORMATION:
APPLICANT: Michel, James L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Angudel, Eawrence C.
TITLE OF INVENTION: Conjugate Vaccine For Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.5%; Score 66; DB 2; Length 46; 60.0%; Pred. No. 0.18; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/467,147A
FILING DATE: 06-JUN 1995
CLASSIFICATION NUMBER: US 08/363,311
FILING DATE: 22-DEC-1994
FILING DATE: 22-DEC-1994
FILING DATE: 02-NOV-1992
PRIOR APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION NUMBER: US 07/968,866
FILING DATE: US 02-NOV-1992
PRIOR APPLICATION NUMBER: US 07/408,036
APPLICATION NUMBER: US 07/408,036
ATITING DATE: US 07/408,036
                                                                                                                                                                                                                                                                ATTOKNEZ/ADEAL INFORMATION.

NAME: BUGAISKY, LAWTENCE B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609.237000B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2640

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 46 amino acids

TYPE: amino acid
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363,311
FILING DATE: 22-DEC-1994
PRIOR APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,036
FILING DATE: 15-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: BUGAISKY, LAWFENCE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 KKEERONVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKDDAKKAETLPTTGEGSNP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 8.5%
Best Local Similarity 60.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-466-210A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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CT-US93-10506A-26
Sequence 26, Application PC/TUS9310506A
GENERAL INFORMATION:
APPLICANT: THE GENERAL HOSPITAL CORPORATION
APPLICANT: Fruit Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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MOLECULE TYPE: Pe
PCT-US93-10506A-26
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                                                                                                                              Gaps
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                                                                                      Length 46;
                                                                                                                              5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Michel, James L.
APPLICANT: Kasper, Dennis L.
APPLICANT: Rasper, Dennis L.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine Against Group
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/346,290
                                                                                      DB 2;
                                                                                8.5%; Score 66; DB 2;
60.0%; Pred. No. 0.18;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,014
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02 07/968,866
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
FILING DATE: 15-SEP-1989
ATTORNEY AGENT INFORMATION:
NAME: BUGAISKY, LAWIENCE B.
REGISTRATION NUMBER: 05,066
RECFERENCE/DOCKET NUMBER: 0609.2370006
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09346290 Patent No. 6342223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2600
TELEX: 246636 SSK
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino
                                                                                                                                                                  140 KKEERQNVNTLPTTGEESNP 159
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                                                                                                                                                                                         2 KKDDAKKAETLPTTGEGSNP 21
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                                                                              Query Match
Best Local Similarity 60.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 46 amino acids
amino acid
; TOPOLOGY: both
; MOLECULE TYPE: Peptide
US-08-469-014-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-09-346-290-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rY: USA
20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                      US-09-346-290-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                     RESULT 27
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APPLICANT: Boston, Massachusetts 02114
APPLICANT: United States of America
APPLICANT: United States of America
APPLICANT: Boston, Massachusetts 02115
APPLICANT: United States of America
ITILE OF INVENTION: Conjugate Vaccine Against Group B
ITILE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 29
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Michel, James L.
APPLICANT: Kasper, Dennis
APPLICANT: Rasper, Dennis
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Madoff, Lawrence C.
TITLE OF INVENTION: Conjugate Vaccine Against Group B
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 29
ANDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: PCT/US93/10506A
FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.5%; Score 66; DB 5; Best Local Similarity 60.0%; Pred. No. 0.18; Matches 12; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-NOV-1993
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REPERENCE/DOCKET NUMBER: 0609,237PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-260
TELEPAX: 248636 SSK
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application PC/TUS9310506 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 KKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KKDDAKKAETLPTTGEGSNP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pept1de
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58 SSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDA 117
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                                                                                                                                                                                                                      Length 593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08591079
Patent No. 5972899
GENERAL INFORMATION:
APPLICANT: Zychlinksky, Arturo
APPLICANT: Zychlinksky, Arturo
APPLICANT: Apollons Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE SISSMERS ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
ADBRESSE: ADRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,079
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVIDAT, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET UNDABER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-076
TELEPAN: (202) 887-076
TELEFAN: (202) 887-076
TELEFAN: (202) 887-076
TELEFAN: (202) 887-076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                   Query Match 8.5%; Score 66; DB 3
Best Local Similarity 26.7%; Pred. No. 4.6;
Matches 23; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
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26.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         118 WEKAATPIALDVKKTKDTKPVVKKEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                 199 KEALDKATDATVKAGTDAKAKAEKAD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 WEKAATPIALDVKKTKDTKPVVKKEE 143
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNPOERSWSH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENCYTH: 593 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20006-1812
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                  , MOLECULE TYPE: protein US-08-591-079-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                   amino acid
                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-591-079-10
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Pred. No. 0.18;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Avenue, NW
                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10506
FILING DATE: 02-NOV-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
          : 1100 New York Avenue, N.W.; Suite 600 Washington
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,866
FILING DATE: 02-NOV-1992
ATTORNEY AGENT INFORMATION:
NAME: Cimbala, Michele A,
RECISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.237PC01
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELER: 248636 SSK
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/591,079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08591079 Patent No. 5972899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 KKEERQNVNTLPTTGEESNP 159
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Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: both
MOLECULE TYPE: peptide
PCT-US93-10506-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-591-079-8
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COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMEUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/216,894
                         3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 564 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 20.28
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 h CTTY: Washington, D.C.
                    STREET: 3000 A CTTY: Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                       20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bohenarky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Belman, Isldore S.
APPLICANT: Moore, Partick S.
ITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma Associated Herpesylus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
8.4%; Score 65; DB 2; Length 1162;
Best Local Similarity 15.5%; Pred. No. 14;
Matches 18; Conservative 35; Mismatches 63; Indels
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Patent No. 5876734
GENERAL INFORMATION:
APPLICAMT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFUTEN: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
| : : : : 199 KEALDKATDATVKAGTDAKAKAEKAD 224
                                                                                                                              Sequence 2, Application US/08728323A
Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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: U.S.A.
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STATE: New York
COUNTRY: U.S.A.
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367 AVETEKORAAEATKVAEAEKOKAAEAAKAVETEKORAAEATKVAEAEKORAAEAMKVAEA 426
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Patent No. 6228601
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Score 64; DB 2; Length 564; 20.2%; Pred. No. 7.6; Live 20; Mismatches 55; Indels
                                                                                                                                                                                                                     CURRENTING SISTEM: FC-LUDZ, ID-LUDZ
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELEFHONE: (202)672-5300
TELEFHONE: (202)672-5300
TELEFAX: (202)672-5300
TELEFAX: (202)672-5300
TELEEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 ALEALADQTDALQSEEAEVVQSDNAASDAWEKAA 122
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NAME: BENT, Stephen A.
RELIGHATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
., Sulte 500
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3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                             367 AVETEKORAAEATKVAEAEKOKAAEAAKAVETEKORAAEATKVAEAEKORAAEAMKVAEA 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.2%; Score 64; DB 2; Length 643; Best Local Similarity 20.2%; Pred. No. 9; Matches 19; Conservative 20; Mismatches 55; Indels
                                                                                                                                                                                                            DB 4; Length 564;
                                                                                                                                                                                                                                              55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
SOFTWARE: PPELICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24 *MRR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 427 EKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAA 460
                                                                                                                                                                                                                                             20; Mismatches
                                                                                                                                                                                                                                                                                                                                                 89 ALEALADQTDALQSEEAEVVQSDNAASDAWEKAA 122
                                                                                                                                                                                                            8.2%; Score 64;
20.2%; Pred. No. 7
          TELEFAX: (ZOL,
TELEFAX: 9(4136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
mvPE: amino acid
mvPE: amino acid
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acids
                                                                                                                                                                                                     Query Match 8.2%
Best Local Similarity 20.2%
Matches 19; Conservative
                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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367 AVETEKORAAEATKVAEAEKOKAAEAAKAVETEKORAAEATKVAEAEKORAAEAMKVAEA 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                 APPLICANT: Kitchhoff, Louis V.
APPLICANT: Ctsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
COMBRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 9; 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 EKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAA 460
89 ALEALADQTDALQSEEAEVVQSDNAASDAWEKAA 122
                                          427 EKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 64; 20.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08317450B
Patent No. 5660982
GENERAL INFORMATION:
APPLICANT: Trygyvason, Karl
APPLICANT: Kallunki, Pekka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
                                                                                                                                                       Sequence 8, Application US/09115746 Patent No. 6228601
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELES: 904136
INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-115-746-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 XY: USA
20007-5109
                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                           RESULT 36
US-09-115-746-8
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30 LRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDA 89
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC Compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,450B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Chao, Mark
RESTERNCE/DOCKET NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778
TELECOMMUTCATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tryggvason, Karl
APPLICANT: Fryggvason, Karl
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BANNER & ALLEGRETTI, LTD. STREET: Ten South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08317450B Patent No. 5660982 GENERAL INFORMATION:
                                                                               REFERENCE/DOCKET NUMBER: 94,77;
RELECHNUICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Amino acid
TYPE: Amino acid
US-08-800-593-15
                ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-317-4508-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1015 LE 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 8.2%; Score 64; DB 1; Length 1111; Best Local Similarity 32.3%; Pred. No. 18; Matches 20; Conservative 8; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRIES

ZIP: 60606
COMPUTER: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFFWATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,593
****TING DATE: 18 FEB-1997
                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin RC-DOS/MS-DOS
CURRENT APPLICATION UNBARE: US/08/317,450B
FILING DATE: O4-OCT-1994
FILING DATE: O4-OCT-1994
ATTONNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET UNBER: 94,778
TELEPHONE: 312-15-1000
TELEPHONE: 312-15-1000
TELEPHONE: 312-15-1134
INFORMATION FOR SEO ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 amino acids
TTYPE: Annion acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Tryggvason, Karl
APPLICANT: Tryggvason, Karl
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chlosgo
STATE: 111inois
COUNTRY: USA
3: BANNER & ALLEGRETTI, LTD.
Ten South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,450
FILING DATE: 04-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08800593 Patent No. 6143505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: protein
    Abb...
STREET: 1c..
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-317-450B-15
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US-08-800-593-15
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  0; Gaps
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8; Mismatches 34; Indels
                                                                                                                                                                                                                               RESULT 40
US-08-800-593-13
Sequence 13, Application US/08800593
Sequence 13, Application US/08800593
Fatent No. 6143505
GENERAL INFORMATION:
APPLICANT: TY999vason, Karl
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIREET: 300 SOULD WACKER DRIVE
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60606
COMPUTE: FADABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,593
FILING DATE: 18-FEB 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,450
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 13, 2002, 02:12:49 Job time : 27.6578 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-593-13
20; Conservative
                                                                                                                                                                    1015 LE 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1015 LE 1016
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Matches
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| 104 13.4 548 9 AU177381<br>99 12.7 344 9 AU180137<br>99 12.7 615 9 AI057981<br>98 12.6 475 10 BM029212<br>97 12.5 517 9 AU179732<br>96 12.4 380 9 AU179899<br>88 11.3 567 12 AZ895651<br>87 11.2 895 12 AZ895651<br>86 11.1 394 9 AU179547<br>86 11.1 333 12 CNS06072 | 13 85 10.9 1097 12 CNSO6NL1<br>14 84 10.8 577 12 BH363565<br>15 84 10.8 775 12 BH363566<br>16 83 10.7 994 12 CNSO6OVL<br>17 81 10.4 453 9 AUT79269<br>18 80 10.3 308 9 AUT79269<br>20 80 10.3 308 9 AUT69406<br>21 80 10.3 1123 11 AK005846<br>22 80 10.3 1158 11 AK01987 | 79 10.2 556 12 TA249H11Q<br>79 10.2 850 12 A0875889<br>79 10.2 850 12 A2168111<br>79 10.2 928 12 CNS03T32<br>79 10.2 1076 12 CNS0400G<br>78 10.0 494 12 A0875428<br>78 10.0 498 10 B1863069<br>78 10.0 653 12 A0504321<br>78 10.0 753 9 A0103803<br>78 10.0 755 9 AJ395963 | C 34 78 10.0 968 12 CNSO7CXJ AL439757 T7 end of AL439757 T7 end of AL439757 T7 end of AL439757 T7 end of AL439757 T7 end of AL429760 T7 end of AL429760 T7 end of AL429760 T7 end of AL429760 End end of AL429760 End end of AL429760 End end of AL429760 End end of AL429760 End end of AL429760 End end of AL429760 End end of AL429760 End end of AL429760 End end end end end end end end end end e                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESULT 1  AU180004/c LOCUS  DEFINITION AU180004 Medaka liver cDNA library (OLE) from HNI Oryzias latipes CDNA clone OLe18.01d similar to glol/B0259671 Oryzias latipes CDNA clone OLe18.01d similar to glol/B0259671 Oryzias latipes CDNA clone OLe18.01d similar to glo/B0259671 Oryzias latipes ACCESSION AU180004  AU180004.1 GI:13428841  KEYWORDS SOURCE SOURCE ORGANISM CAPACIACIA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopherygli; Neopterygli; Teleostei; Euteleostei; Actinopherygli; Neopterygli; Teleostei; Euteleostei; Actinopherygli; Neopterygli; Teleostei; Euteleostei;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | REFERENCE 1 (bases 1 to 442) Addingtones; Adrianichthyldae; Oryzinae; Deloniformes; Adrianichthyldae; Oryzinae; Oryzinas.  Addrons; Naruse, K., Mitani, H. and Tanaka, M.  TITLE Medaka EST Project in University of Tokyo (2001) CONMENT Contact: Kiyoshi Naruse Department of Biological Sciences Graduate School of Science, University of Tokyo Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan Tel: 81-3-5841-4443 Fax: 81-3-5841-4443 Fax: 81-3-5841-4440 |
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| GenCore version 5.1.3  Copyright (c) 1993 - 2002 Compugen Ltd.  OM protein - nucleic search, using frame_plus_p2n model  Run on: October 13, 2002, 02:12:56; Search time 1886.74 Seconds  (*without alignments)  137.418 Million cell updates/sec                     | RONVNTLPTTGEESNP 1                                                                                                                                                                                                                                                        | Searched: 13736207 segs, 6748477542 residues  Total number of hits satisfying chosen parameters: 27472414  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%  Maximum Match 100%  Listing.first 45 summaries                  | Command line parameters: -WODEL-frame+_D2n.model -DEV-xlh -Q-/cgn2_1/USPTO_spool/US09847539/runat_10102002_092548_3435/app_query.fasta_1.526 -Q-/cgn2_1/USPTO_spool/US09847539/runat_10102002_092548_3435/app_query.fasta_1.526 -Q-/cgn2_1/USPTO_spool/US09847539/runat_1010202_092548_3435/app_query.fasta_1.526 -UNITS-bits -STARR=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -UNITS-bits -STARR=1 -END=-1 -MATRIX=100 -THR_MIN=0 -ALIN=0  Database : EST:*  1: em_estba:* 2: em_estlum:* 3: em_estlum:* 4: em_estlu:* 5: em_estlu:* 6: em_estlo:* 7: em_estlo:* 8: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estlo:* 1: em_estl | th<br>S.93                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neoptorygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthomotperygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
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AU179963.1 GI:13428800
                                   1. 442
/organism="Oryzias latipes"
/stain="HNI"
/db.xref="taxon:8090"
/clone="OLe18.01d"
/clone="lole-medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
/dev_stage="adult"
a 169 c 52 g 94 t
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clone was isolated from Medaka liver cDNA library (OLe). Location/Qualifiers
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Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
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Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tal: 81-3-5841-4443
Fax: 81-3-5841-4410
Email: naruse@biol.s.u-tokyo.ac.jp
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Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Acherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
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5' end enriched cDNA library (OLB) from
clone OLa30.05b similar to gb|AB025967|
chorlogenin Hminor, complete cds, mRNA
                                                                   /crganism="Oryzias latipes"
/strain="NNI"
/db.zref="taxon:8090"
/clone="local7.07a"
/clone=lib="Medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
/dev_stage="addlt"
203 c 84 g 126 t
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This clone was isolated from Medaka liver cDNA library (OLe). Location/Qualifiers
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Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
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Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
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AU177381 Sugano-Kawakami
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Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Sugano-Kawakami 5'
library (OLa).
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Department of Blotogical Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                    548
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'Organism-"Oryzias latipes"
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/db_xref-"taxon:8090"
/clone-"Jib-"Sugano-Kawakami 5' er
(OLa) from HNI"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                     /tissue_type="whole body"
/dev_stage="adult"
189 c 81 q 126
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                                                                                                                                                                                                                                                                                                                                                                               (1-548)
                                               Location/Qualifiers
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104.00
40.00%
26.67%
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                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
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ORGANISM
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AU180137/c
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TITLE
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COMMENT
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EST 20-JUL-1998
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( passes 1 to 615)

Williams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J.

Genes expressed in infective third stage larvae of Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWOVL3CAN21G06SK Onchocerca volvulus infective larva cDNA (SAW94WL-OvL3) Onchocerca volvulus cDNA clone SWOvL3CAN21G06 5', AND57981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         volvulus
Unpublished (1995)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
Tel: 4135853826
Fax: 4135853786
                                                                                                                                                         /db.xref='taxon:8090"
/db.xref='taxon:8090"
/clone='lote19.11e'
/clone=lib="Medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
/dev_stage="adult" 74 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 AsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 GCTGAGGATTNTGAGGTTTTGAAGGGTACTGAGGCTGCTGAGGATTCTGAGGATGTTGAG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GAGGCTGCTGAGGATTCTGAGGTTTTGAAGGATACTGAGGCTGCTGAGGATTCTGAGGAT 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp
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11
53
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Matches:
Conservative:
Mismatches:
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                                                                                                                                     /organism-"Oryzias latipes"
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Seq primer: pBluescript SK
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99.00
43.01%
31.18%
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/db_xref="taxon:7998"
/clone_lib="Skin cDNA library"
/note="Organ: Skin; Vector: pSport1; Site_1: Not1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU179732 Mcdaka liver cDNA library (OLe) from HNI Oryzias latipes cDNA clone OLe13.10d similar to gb|AB025967| Oryzias latipes mRNA for choriogenin Hminor, complete cds, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Setinopeterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyddae; Oryzlinae; Oryzlas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
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Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4410
Email: naruse@bilol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 Swingle Hall, Auburn University, Auburn, AL 36849, USA Tel: 334 844 4054 arx: 334 844 9208 Email: zlu@acsag.auburn.edu Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 517)
Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                             475
27
18
48
0
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Mismatches:
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Matches:
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                                                                                                                                                      /organism="Ictalurus
                                                                                                       Location/Qualifiers
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48.39%
29.03%
12.61%
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Oryzias latipes
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Best Local Similarity:
                                                                                                                                                                                                                                                              229
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VERSION
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TITLE
JOURNAL
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                                                                                                              FEATURES
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E 1 (bases 1 to 475)

S Karsi, A., Cao, D., Li, P., Ju, Z., Kocabas, A., Feng, J., Patterson, A., Mickett, K.D. and Liu, Z.

Transcriptome analysis of channel catfish (Ictalurus punctatus):
Initial analysis of gene expression and microsatellite-containing cDNAs in the skin
Unpublished (2001)

Contact: Liu ZJ

The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
                                                                                                                                                                                       Anote—"Vector: Inmode Unizap XR; Site_1: EcoR I; Site_2:
Xho I; Cutaneous filarial nemacode parasite of humans.
MRNA was prepared from third stage infective larvae of
Onchocerca volvulus isolated from mosquitoes 10 days after
infection and converted to double stranded cDNA using
reverse transcriptase and oligo(df) followed by Rhase H
and DNApol I: The library had I: 8 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Wenhong Lu. The library is
available from Br. S.A. Williams, email genome@smith.edu.
186 c 176 g 173 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM029212 475 bp mRNA linear EST 05-NOV IpSkn00051 Skin cDNA library Ictalurus punctatus cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AspalaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla 89
                                                                                                          /clone="SWOvL3CAN21G06"
/clone_l1b="Onchocerca volvulus infective larva cDNA
(SAW94WL-OvL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 SerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAsp 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 GAAACGAACGCATCATCAAGTGCCGGTCGTGCAGCGCACGGCACGGCAGGAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
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26
16
37
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Matches:
Conservative:
Mismatches:
Indels:
                                          /organism="Onchocerca volvulus"
/strain="Sierra Leone"
/db_xref="taxon:6282"
                                                                                                                                                                          /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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  Location/Qualifiers
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BM029212.1 GI:16742782
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Query Match:
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BM029212
    FEATURES
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12.36%
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Query Match:
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                                                                                                                 107
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source
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AUTHORS
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AZ895651
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Annianichthyidae; Oryziinae; Oryzias.
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AU179899 Medaka liver cDNA library (OLG) from HNI Oryzias latipos. cDNA clone OLG16.08a similar to gb[AB025967] Oryzias latipos mRNA for choriogenin Hminor, complete cds, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
       /organism="Oryzias latipes"
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/db_xref="taxon:8090"
/clone="Ote13.10d"
/clone=lib="Medaka liver cDNA library (OLe) from HNI"
/tssue_type="liver"
/dev_stage="adult"
/ 181 c 74 g 114 t 3 others
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Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Locatton/Qualifiers
                                                                                                                                                                                                                                                                                                           GluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThr
                                                                                                                                                                                                                                                                                                                             73 GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 AAGGATACTGAGGCTGCTGAGGATTCTGAGGATGTTGAGGCTGCTGAGGATTNTGAGGTT
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Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
                                                                                                                                                                          517
29
17
65
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Matches:
Conservative:
Mismatches:
Indels:
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EST.
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41.44%
26.13%
12.48%
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Best Local Similarity:
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AU179899/c
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AZBYDDS 11120.TJ RPCI-24 Mus musculus genomic clone RPCI-24-211J20.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 567)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Outbullshed (1999)
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejongémail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 211 row: J column: 20
                                                                                               /clone_lib="Medaka liver cDNA library (OLe) from HNI"
/tesue_type="liver"
/dev_stage="adult"
144 c 47 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 AsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLySAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 ACTGAGGCTGATGAGGCTGCTGAGGTTTTGAAGGATACTGAGGCTGCTGAGGATTCTGAG
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Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
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28
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                  Length:
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                         /strain="HNI"
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DNA library
Seg primer: Ml3-Reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 764.
Location/Qualiflers
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                                                                                                       /strain-"HM1: IMSS
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43.41%
22.48%
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Best Local Similarity:
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                                                              Email: bjloftus@tlgr.org Clones are derived from the Entamoeba histolytica \mbox{HM}\xspace:
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Entamoeba histolytica.

Enkaryota; Entamoebidae; Entamoeba.

1 (bases) to 895)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba lancing sheared DNA library

Unpublished (2000)

Contact: Breadan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9208
                                                                                                                                                                                                                                                           267
200
443
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                                                                                                                                                                                                                                                                                    Conservative:
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Indels:
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Matches:
                          Location/Qualifiers
1. .567
/organism="Mus musculus"
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                                                                                                                                                                                                        254 g
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AZ534176
AZ534176.1 GI:11090551
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29.21%
11.33%
 Seq primer: SP6
Class: BAC ends
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DB:
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AZ534176
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TITLE
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/db.xref—"haranosba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
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/clone_lib="betataon:5759"
/clone_weetor: pHOS1: Site_l: BST !: Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica:
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + imethod used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 GAAGCTAAACAAAAGCAGAGGAAGAGGCTAAACAGAAAGGAGAAGAAGCTAAAAAGAAA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GCTAAACAGAAAGCAGAAGAAGAAGCTAAACAAAAAGCAGAGGAAGAGGGTAAACAGAAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGln 43
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Mismatches:
Indels:
/organism="Entamoeba histolytica"
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Matches:
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Direct Submission

L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:

seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyverowyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae ORF YOR009w [
                                                                                                                                                                     Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Dujon, B., Durens, P., Lepingle, M., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Welssenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <31. >>25
/note="similar to Saccharomyces cerevisiae ORF YER011w
TIR1; cold-shock induced protein of the Tirlp,Tiplp
family ]*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to Saccharomyces cerevisiae ORF YOR010c TIR2 ; cold shock induced protein ]"
           Bon, E., Neuveglise, C., Lepingle, A., Wincker, P., Artiguenave, F., Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts: 6. Saccharomyces exiguus
FEBS Lett. 487 (1), 42-46 (2000)
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/organism="Saccharomyces exiguus"
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/evidence=not_experimental
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/db_xref="taxon:34358"
/clone="Av0AA004C03"
/clone=lib="Av0AA"
/note="end : T7"
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48.81%
25.00%
  (bases 1 to 833)
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T7 end of clone AV0AA004C03 of library AV0AA from strain CBS 379 of
Saccharomyces exiguus, genomic survey sequence.
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neoperygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Saccharomyces exiguus
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib-"Medaka liver cDNA library (OLe) from HNI"
/tissue_type-"liver"
/dev_stage="adult" 79 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 GGTACTGAGGCTGCTGAGGATTCTNAGGATGNTGAGNCTGCTGAGGATTCTGAGGTTTTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 GATGAGGCTGCTTAGGATTCTGAGGATACTGAGGCTGAGGGTTCTGAGGTTTTGAAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AAGGATACTGAGGCTGCTGAGGATTCTGAGGATGTTGAGGCTGCTGAGGATTCTGAGGTT 73
                                                                                                                                                                                                                                                                                                                                                                         Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsn
                                                                                                                                                              Naruse, K., Mitani, H. and Tanaka, M. Medaka EST Project in University of Tokyo (2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                      of Tokyo
                                                                                                                                                                                                                                                        Department of Biological Sciences
Graduate School of Science, University of Toky
Hongo 73-1, Bunkyo-ku, Tokyo 113-0033, Japan
Fal: 81-3-5841-4443
Fax: 81-3-5841-4410
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25
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryzias latipes"
/strain="HNI"
/db_xref="taxon:8090"
/clone="OLe11.02b"
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                                                                                                                                                                                                                                          Contact: Kiyoshi Naruse
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86.00
42.86%
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                      Japanese medaka
                                           latipes
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CNS0607Z/c
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Email: szhaoétigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq prime: 73 row: J column: 24
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus novreglcus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                           77 AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 ThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAla 113
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/clone="CH230-203J24"
/clone_11b="CH0RI-230 Segment 1"
/sex="Female"
                                                                                   Length:
Matches:
Conservative:
Mismatches:
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BH363656
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L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux. CP 5706, 91057 EWRY cedex, FRANCE. (E-mail:
2 rue Gaston Cremieux. CP 5706, 91057 EWRY cedex, FRANCE. (E-mail:
3 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii. Zygosaccharomyces rouxii,
Saccharomyces Kluyveri, Kluyveromyces thermocolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 17-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           1097 bp DNA linear GSS 17-JUN-200 of Saccharomyces kluyveri, genomic survey sequence.
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Casaregola, S.,
de-Montigny, J., Dujon, B., Bortlar, P., Casaregola, S.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Surti, W., Tekata, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
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Neuveglise, C., Bon, E., Lepingle, A., Wincker, P., Artiguenave, F.,
                                                                                                                                                                                                                                   93 LeualaaspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsn 112
  AlaileGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 72
                                                                                                                                             73 GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galllardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
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/organism="Saccharomyces kluyveri"
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FEBS Lett. 487 (1), 56-60 (2000)
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/db_xref="taxon:4934"
/clone="AU0AA015A11"
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/note="end : T3"
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3 (bases 1 to 994)
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremeleux, CP 5706, 91057 EWRY cedeax, FRANCE. (E-mail :

seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angusta Debaryomyces hansenli var. hansenli, Pitchia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSOGOVL 745 bp DNA linear GSS 05-JUL-2001 T7 end of clone AVOAA009E03 of library AVOAA from strain CBS 379 of Saccharomyces exiguus, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces exiguus.
Saccharomyces exiguus
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bon, E., Neuveglise, C., Lepingle, A., Wincker, P., Artiguenave, F., Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts: 6. Saccharomyces exiguus FEBS Lett. 487 (1), 42-46 (2000)
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FEBS Lett. 487 (1), 3-12 (2000)
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Soudete,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Soudete,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvegilse,C., Ozier-Kalogeropoulos,O., Potier,S.
Saurin,W., Tekala,F., Toffano-Nloche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
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352 GAGGCAGAGGCAGAGGCAGAGGCAGAGGCAGAGGCAGAGGCAGAGGCAGAGGCA 411
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Mismatches:
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                                           Length:
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TITLE

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COMMENT

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CNSO7EBO 994 bp DNA linear GSS 08-JUL-2001 T7 end of clone XBDOAA002G03 of library XBDOAA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
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Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z. (bases 1 to 994)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.;
Souciet, J.L., Aigle, M., Artiguenave, F., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potter, S.,
Saurin, W., Tekaia, F., Toffano Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
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Candida tropicalis
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Matches:
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the other extremity of this insert.
Location/Qualifiers
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    organism="Saccharomyces"

                                                                                         /strain="CBS 379"
/db_xref="taxon:34358"
/clone="AvOaA009E03"
/clone_lib="AVOAA"
/note="end : T7"
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           Direct Submission

L Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
3 seqref@genoscope.cns.fr - Web :
    This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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Oryzias latipes

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsn 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AlaileGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           812 GAAGAAGAAGAAAAGAGTCAAGAAAGAAAGCTCATCTAGCTCTGATAGTGATTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                           others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2202
                                                                                                                                                                                                                                                                                                1. 994
/organism="Candida tropicalis"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="xBb0AA012633"
/clone_lib="xBb0AA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
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AU179269.1 GI:13428106
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10.68%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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AU179269/c
LOCUS
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Barfish.L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Quellet,T., Robert,L.S., Singh,J.A, Sprott,D. and Tinker,N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zm08_10h09_A
Zm08_10h09_A
Zm08_AAFC_ECORC_Fusarium_graminearum_inoculated_corn_ear Zee mays
ZMA clone Zm08_10h09, mRNA sequence.
BG837033.1 GI:14203356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags from Developing Maize Kernels Six Days after Slik Channel Inoculation with Fusarium graminearum Unpublished (2001)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bidg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:8090"
/clone="OLe06.03e"
/clone_lib="Medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 GluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThr 52
                                                                                                                                                            Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GGTACTGAGGCTGCTGAGGATTCTGAGGATGTTGAGGCTGCTGAGGATTCTGAGGTTTTG
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                 Contact: Klyoshi Naruse
Department of Biological Sciences
Graduate School of Science, University of Toky
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Fax: 81-3-5841-4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 LeualaaspGlnThraspAlaLeuGlnSerGluGluAlaGlu 106
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Matches:
Conservative:
Mismatches:
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|TIGAAGGATACTGAGGCTGCTGAGGATTCTGAGGATACTGAG
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                                                                                                                                                                                                                                                         /organism="Oryzias latipes"
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                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
159 c 59 ¤
                                                                                                                                                                                                                                                                                       /strain-"HNI
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81.00
44.59%
32.43%
Unpublished (2001)
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Pred. No.:
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                                                                                                                                          /db_xref="taxon:4577"
/clone="xm08_10h09"
/clone_lib="zm08_AAFC_ECORC_Fusarium_graminearum_inoculate
d_corn_ear"
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/dev_stage="10-11 days post-silk emergence"
/dev_stage="10-11 days post-silk emergence"
/note="Vector: Bluescript SA+/AhoI-EcoRI; Site_1: EcoRI;
Site_2: XhoI; Fleid-grown maize ears were silk
channel-inoculated in the morning (-10 am) with 1 ml of a
Fusarium graminearum macrocondial suspension (500,000
spores/ml) and whole ears were collected and immediately
frozen in liquid nitrogen 6 days later:"
220 c 217 g 146 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Research Group
National Institute of Radiological Sciences
Matdonal Institute of Chiba 263-8555, Japan
Emall: Kmita@nirs.go.jp
method:uni-directional sequence direction:sequenced from T3 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 IleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAla 64
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Mida, K. 15hlkawa. Y. and Yamauchi, M.
Establishment of CDNA database of medaka, Oryzias latipes
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 ACAGCAACAGATGCAGCATCAACAGCAACAGATGCAAATGCA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAla 99
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-857)
                                                                                                     /organism="Zea mays"/cultivar="CO430"
           Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-847-539A-6 (1-159) x BG837033
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28.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryzias latipes
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Best Local Similarity:
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AU169406 AU169406 744 bp mRNA linear EST 29-JAN-2001 AU169406 Ol-br-ad cDNA Oryzias latipes cDNA clone br4594, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Acanthomorpha; Adanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1 (bases 1 to 744)
Mita, K. Ishikawa, Y. and Yamauchi, M.
Establishment of cDNA database of medaka, Oryzias latipes
Unpublished (2001)
Contact: Mita K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Research Group
National Institute of Radiological Sciences
National Institute of Chiba 263-8555, Japan
Email: Kmita@nirs.go.jp
method:uni-directional sequence direction:sequenced from T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GCAACCAGCGCAGTCAGAGCTGCAGCCAGCACAGTCTCAGTTAGAGCAGATGCAGCC 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
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Mismatches:
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Matches:
                1. .308 /organism="Oryzias latipes" /strain="HNI"
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Location/Qualifiers
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89 c 98 g
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AU169406.1 GI:12591475
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Best Local Similarity:
Query Match:
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FANTOM Consortium.

Functional annotation of a full-length mouse CDNA collection

Nature 409, 685-690 (2001)

5 (bases 1 to 1123)

Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,

Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Hanagaki, T.,

Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,

Hume, D., Imotani, K., 1811, D., Hiramoto, K., Hiraoka, T., Hori, F.,

Kato, H., Kawai, J., Kojima, Y., Konno, H., Koya, S.,

Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,

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160. 984
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233 c 295
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AKO05846.1 GI:12838633
HTC: CAP trapper.

Mus musculus (strain:C57BL/6J) adult male testis CDNA to mRNA, clone_110:RIKEN full-length enriched mouse cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibeta, N. Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Shibeta, K., Itoh, M., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunnoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunrai, M., Noneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunrai, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sakiki Integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mismatches:
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                              Length:
Matches:
                                            212
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178 c 238 g
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukuda, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishli, Y., Itoh, M., Zawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konoo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, T., Okido, T., Owa, C., Quackenbush, J., Salto, H., Salto, R., Sakai, C., Yanaaka, T., Toya, T., Yananaka, T., Tagwa, A., Tagwa, A., Tagwa, T., Yananaka, T., Yananaka, T., Yananaka, T., Yananaka, T., Yananaka, T., Yananaka, T., Direct chhimin.
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nkalrebhgalodeevaloeeakiloewnullogkitnnilpgktonddpkkcgprm
                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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Mismatches:
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1158
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239 c 302
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishli,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
KIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK014987 linear HTC 19-JAN-2002 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921530L21:hypothetical protein, full insert
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                              703 ATGAGGGATGGAGTGGCGGCGGAGCTGGCCGAGGCCCTGACCAAGGAGGGGGGCTGCTCTG 762
                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_llb:RIKEN full-length enriched mouse cDNA library clone:4931530L21.
Mus musculus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                        Conservative:
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Indels:
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CTGAGAGAGGCATGGGGCTCTCCAAGATGAAGAA 858
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Daker's yeast.

Baker's yeast.

Baccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Baccharomycetales; Saccharomycetaceae; Saccharomyces.

I (bases 1 to 797)

Saccharomycetales; Saccharomycetaceae; Saccharomyces.

I (bases 1 to 797)

Soss-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption

Lupublished (1999)

Contact: Kumar A

Michael Snyder, Dept. of Mol. Cell. and Dev. Biology

Yale University

P.O. Box 2008103, New Haven, CT 06520-8103, USA

Tel: 203 432 9949

Fax: 203 432 1916
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/db_xref="taxon:4932"
/clone_lib="mTn-3xHA/lacz Insertion Library, strain Y2278"
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                                              504 GAACAATCAGGCGCTCTATTCAAAATGAGCGACAGGCAGTGAGACAAGCGGAGCAAGGG 445
                                                                                                                   98 AspalaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAla 117
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te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTCTTTGGAAGTAC
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREUS27/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
misort libraries for whole genome shotgun sequencing projects. In
Barrell, Oxford University Press, 1999).
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                                                                                                                                                      674 GAGGAGACCAAGGCTCTGCAACACCAGGAGGGCTCTCAGAATGGAAGAAAGCTCTG 733
                                                                                                                                                                                                                                                                                                                  734 ATGAGGGATGGAGTGGCGGCGGAGCTGGCCGAGGCCCTGACCAAGGAGGGGGCTGCTCTG 793
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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Mel Ville, S.E., Rajandream, M.A. and Barrell, B.G.
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/strain="TREU927"
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High quality sequence stop: 850.
Location/Qualifiers
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/organism="Strongylocentrotus purpuratus"
/dLore="Plate=103 Col=20
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/clone="Plate=103 Col=20
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/clone="Organ: sperm: Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SP_0103_B2_C10_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate*103 Col=20 Row=F, DNA sequence.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinodea; Euchinodea; Echinodea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 850)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray,
G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
                                                                                                                                                  283
                                                                                                                                                                                                                                                                                             223
                                                                                                                                                                                                                                                                                                                                                             163
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                                                                                                                               GluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIle 45
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                                                                                                                                                                                                                                                           66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
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additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
2040256.
Contact: Cameron, RA, Davidson, EH, Hood, L.
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 393-3047
   17
333
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                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                           106 GluValValGlnSerAspAsnAlaAlaSerAspAla 117
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   Matches:
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                                                                                             (1-797)
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Plate: 103 row: F column: 20
Seg primer: SP6
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                                                                                            US-09-847-539A-6 (1-159) x AQ875889
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AZ168111.1 GI:8338479
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                Percent Similarity:
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 928)

1 (bases 1 to 928)

1 (bases 1, Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="054N14"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzil, Zygosaccharomyces rouxil, Saccharomyces rouxil, Saccharomyces rouxil, Saccharomyces rouxil, Luyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
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AL405734
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Saccharomyces Kluyveri.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 1076)
Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,
Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S., Belotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S. Sautin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                          590 CAACGGTCTGTGAAGAGGTTTGAGGAGGTGGCGAGCAGCTTTCAGGTCTGCAGGCTGAG 531
                                                                                                                                                                                                                                                                                                                      37 IleAspGluLeuLysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAla 56
                                                                                                                                                                                                                                                                                                                                                                                                  57 AlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGlu 76
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/clone_lib="G"
/note="Genoscope sequence ID
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FEBS Lett. 487 (1), 56-60 (2000)
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GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodonidae; Takifugu.

SE Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K.,
Unrania, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR0042547 338 bp DNA 11near GSS 22-OCT-1999
Fugu rubripes GSS sequence, clone 152F05bE3, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ThrLeuThrAsnLeuLeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArg 35
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/organism="Saccharomyces kluyver1"
/strain="CBS 3082"
/db_xref="taxon:4934"
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/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
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/organism="Takifugu rubripes"
/db_xref="taxon:31033"
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biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
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S Ross-Wacdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R.,
Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,
Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
L Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4932"
/clone_lib="mfn-3xHA/lacZ Insertion Library, strain Y2278"
/lab_host="E. coli"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi, Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                          235 TGGGTCAAAGAGTCCAGCAGAGCCGAGGCAGAAATGGCTGCGCTCCGATCCAGTATGGAG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                         91 GlualaLeualaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSer 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
                                                                                                                                                                                                                                                                  71 AlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAsp
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                                    5 others
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/organism="Saccharomyces cerevisiae
/strain="Y2278 - S288C background,
                                                                                                                               Conservative:
Mismatches:
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                                                                                                  Length:
Matches:
/clone_lib="cosmid 152F05"
/clone="152F05bE3"
122 c 72 g 84
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te of mTn-3xHA/lacz insertion.
Seq primer: GGCCTTCTTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                               Indels:
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78.00
48.78%
25.61%
10.04%
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                                                                                                                               Percent Similarity:
                                                                                   Alignment Scores:
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DB:
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AUTHORS
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rmi6b06.y1 Meloidogyne arenaria egg pAMPl vl Chiapelli McCarter Meloidogyne arenaria egg pAMPl vl Chiapelli McCarter B1863069.
B1863069 arenaria cDNA 5', mRNA sequence.
B1863069.1 G1:16004859
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without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lac2 minitransposon containing lac2, URA3, and tet resistance.
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Tylenchoidea, Heteroderidae, Meloidogyninae, Meloidogyne.
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Mrhe library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
Washington University, St. Louis. DNA Sequencing by: Washington
Washington Griversity, St. Louis. DNA Sequencing by: Washington
Driversity Genome Sequencing Center St. Louis. Nematodes were
provided by Dr. David Bird and Daniel Snyder of North Carolina
State University.
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/clone_lib="Meloidogyne arenaria egg pAMP1 vl Chiapelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AAAGCTGAAACTGCCGCCCAAGATGTCCAACAAAAGTTGGAAGAAACCAAAGAATCTTTG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLys 120
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Unpublished (1999)
Contact: McCarter JP
Mashington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysalaaspasnalaalaSeraspalaLeuGlualaLeuAlaaspGlnThraspalaLeu
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Matches:
Conservative:
Mismatches:
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High quality sequence stop: 415.
Location/Qualifiers
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Meloidogyne arenaria
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us-09-847-539a-6.rst

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McCarrea.
/dev_stage="egg"
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/note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1;
/note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1;
The library was constructed by Brandi Chiapelli and Dr.
James McCarrer at Washington University, St. Louis. The
CDNA was made by using Dynabead oligo-dT priming (Dynal).
PCR based library using a modified protocol from the
SMART PCR cDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nematodes were
provided by Dr. David Bird and Daniel Snyder of North
Carolina State University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPCI-11-282A24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-282A24, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (lnfo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished (1997)
Other_GSSS: RPCI-11-282A24.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAAAATGTCGAAACATGGGTCTTTAACTGACAGATAATTCAATTGGAAGACGAAGTA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                       58 SerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 AlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThr 97
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Matches:
Conservative:
Mismatches:
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1..623
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Best Local Similarity:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla; Bombycoldea; Bombycidae; Bombyx.

1 (bases 1 to 753)

Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Establishment of cDNA database of Bombyx mori
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                                                                                                                                             /sex-
/sex-
/sell_type="Lymphocytes"
/note="Vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 CATGACATGGGATATGAAAGGAAATTCTTCAGTGAAACAGATAGCATAAATAGCAAACA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 ATTAACCCAATCTGTCAAACACAAAAAAAAAAATTTTGAAAAATGAACAAAGCCTCCA 306
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National Institute of Radiological Sciences
National Institute of Radiological Sciences
Anagawa 4.9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
PROJECT - 'CREST project by JST'.
1.053ion/Qualifiers
1.753
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Indels:
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/organism="Homo sapiens"
/db_xref="GDB:7607927"
/db_xref="taxon:9606"
/clone="RPCI-11-282A24"
/clone_lb="RPCI-11"
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Contact: Mita K
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DEFINITION
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Archosauria: Aves: Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

| (bases 1 to 755)
| Abdrakhamov, I., Lodygin, D., Geroth, P., Arakawa, H., Law, A., Plachy, J., Korn, B. and Buerstedde, J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                            ### 11 GAGGAGAGCATCACCGAGGAGCTGGTCGCCGCCAGTGACAAGGCGAAGGAG 530
                                                                                                                                                                                                                                                                                                                                 351 GCCGCAAATGAGATTTACAAGACTTTAAAAGAGTTCAGTGATCAAGTGACCGAGTCGCAC 410
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                                                                                                                                                                                                                                                                                                                                                                                                                         97 ThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsnAlaAlaSerAsp 116
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                                                                                                                                                                                                                                          57 AlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGlu 76
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Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: NRL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                        291 CTGGATGAGCTGCAGGCGCAAGCTAAAAACGATGTGGAACTCACGAAAGCCACGTTGACA
                                                                                                                                                                                                                                                                                                                                                                 77 AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln
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234
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/db_xref="taxon:7091"
/clone="ws00597"
/clone_lib="Bombyx mori p50(Daizo)"
177 c 220 g 113 t
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124 c 185 g 131 t
                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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/organism="Gallus gallus"
/strain="CES"
/db_ref="texn:9031"
/clone="24m17r1"
/clone=lib="dkf2426"
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1 (bases 1 to 968)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
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T7 end of clone BDOAA007F08 of library BDOAA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottler,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvegilse,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida tropicalis
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGln 101
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Mismatches:
Indels:
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20584726
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Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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AMATVALI-InO7b12.yl Leishmania major FVI random genomic Library Leishmania major genomic Clone LRANFVI_LNO7b12 5, similar to contains element VI-chi_type_II.5 leishmania repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kisinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., T., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Glbbons, M., Harvey, M., McCann, R., Tsagareishyrli, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shotgun sequencing: a resource for DNA microarrays and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTTATCAGTTTCAGATGAATCAGCATCAGTTTCACTTGACTCAGCGTCAGAACCAGAT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 SerAsp...AsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAsp 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 CCAGATTTGTTGTCAGTTTCGGATGCATCAGTTTCAGAAGCACTGGCATTAGAGTTAGAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AspalaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
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Leishmania major
Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases 1 to 394)
                                                                                                                                                                                                                                                      others
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Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
Contact: Akopyants, NS / Beverley, SM
                                                                                                                                                                                                                                                                                                                         968
29
18
46
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 TCGGAACCAGAAAAGAATCGGCACCAGAAGTAGAAGCAGAA 48
                                                                                                    Location/Qualifiers
1. 968
1. 968
/organism="Candida tropicalis"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0AA07F08"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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48.96%
30.21%
10.04%
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Best Local Similarity:
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/organism="Leishmania major"
/organism="Leishmania strain V1"
/db_xref="taxon:5664"
/clone="LMAJYL_In07b12"
/clone="LMAJYL_In07b12"
/clone="the="Leishmania major FV1 random genomic library"
/lab_host="ToP10 (Invitrogen)"
/lab_host="Vector: pZero-2 (Invitrogen);
/notc="Vector: pZero-2 (Invitrogen);
Genomic DNA was isolated from strationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline Phosphatase and ligated into pZero-2 vector's EcoRV site."
50 a 115 c 179 g 50 t
                                                                                                                       Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin Strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For Information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 29-JUL-1998
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AA784607.1 GI:2844775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emericella nidulans.
Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 CATGCCCGCGTGGTTGCTGCGCTGGAGGCGAGGCGTGTGCTGCCGAGCGTGAGGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
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118
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Mismatches:
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77.00
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28.57%
9.91%
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21

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Unpublished (2000)
Contact: Olin Anderson
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77.00
49.38%
28.40%
9.91%
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Best Local Similarity:
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                                                       An Aspergillus nidulans EST Database

In Dupublished (1998)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Partington Oval, Norman, OK 73019, USA
Tel: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: SK
High quality sequence stop: 394.
                                                                                                                                                                                                                                                                                                                                                  /close_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycella, asexual structures"
/note="Vector: pBlueScript SK-: Site_l: BcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BJ039902 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL038n24 5', mRNA sequence.
BJ039902.1 GI:17375674
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1 (bases 1 to 588)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GlnSerGluGluAlaAlaValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla
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21
20
37
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Mismatches:
                                                                                                                                                                                                                                                                                         /organism="Emericella nidulans"
/strain="FCSC A26"
//db_xref="taxon:162425"
/clone="f2f10a1"
Eurotiales; Trichocomaceae; Emericella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
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                 (bases 1 to 425)
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77.00
52.56%
26.92%
9.91%
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Best Local Similarity:
Query Match:
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                              AUTHORS
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Triticum destivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
Triticeae; Triticum.
1 (bases I to 663)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes Pre-anthesis spike cDNA library
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                                                                                                                                                                                                                                                                                                              70 AspAlaLeuGinSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
Expressed genes in X. laevis embryo (2001). Unpublished (2001). Contact: Tadasu Shin-i Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Pata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                          /organism="Xenopus laevis"/db_xref="taxon:8355"
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112 c 144 g
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BF483682.1 GI:11566983
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/organism="Bombyx mori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws00687"
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77.00
44.34%
22.64%
9.91%
                           domestic silkworm.
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Best Local Similarity:
Query Match:
DB:
                                                      Bombyx mor1
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KEYWORDS
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                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="texon: 4565"
/clone="Inb="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Spike before anthesis"
/dev_stage="Adult plant"
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tal: 5105595773
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AU003869 Bombyx mori p50(Dalzo) Bombyx mori cDNA clone ws00687,
mRNA sequence.
AU003869.1 GI:4161240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 GCCACCAAGGATGGCGCCGGAAACTGCTGCTGCCGCCGCCGCAGAAGCCGGTACCAAGACT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThr 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp 83
                                                                                                                          Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 uArgGlnAsnValAsnThrLeuProThrThrGlyGluGluSerAsnPro 159
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Matches:
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Best Local Similarity:
Query Match:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Ptersygota; Neoptera; Bndopterygota; Lepidoptera; Glossata; Ditrysia; Bombycidea; Bombyc
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 723)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 GAGGAGGATCAACAGCATCACCGAGGAGCTGGTCGCCGCCAGTGACAAGGCGAAGGAG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AlaTrpGluLysAlaAlaThrProIleAlaLeuAspValLysLysThrLysAspThrLys 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 GCCAGGGACTTTGCCCAGCAAGCGCAAAAGGAATATGCCGACAAAGCTTCTGAGGCCGCC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGlu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 IleAspGluLeuLyaLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAla 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGln
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                                                                                                                                                                                                                                                                Mith.K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Establishment of cDNA database of Bombyx mori Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             675
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164 c 193 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmitafalirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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/Strain="C57BL/64"
/Gb_xref="taxon:10090"
/Glone_11b="Mouse 10kb plasmid UUGC2M library"
/Glone_11b="Mouse 10kb plasmid UUGC2M library"
/Glone_11b="Mouse 10kb plasmid UUGC2M library"
/Gra="UGC2MU21018"
/Jab host="E. coli strain XL10-Gold, T1-resistant, F-"
/Jab host="E. coli strain XL10-Gold, T1-resistant, F-"
/Jab host="E. coli strain XL10-Gold, T1-resistant, F-"
/Jab host="Jax.org/resources/documents/dnares/). The DNA
was blydrodynamically sheared by repeated from the Jackson
[Ahttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by a polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb]AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly i.M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse Whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                           Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah 84.112, USA Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ArgAsnGluGluArgAlalleAspGluLeuLysLysGlnAlaIleGluAspLysGluAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAsp 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 AlaLeuGlnSerGluGluAlaAlaValLysAlaAspAsnAlaAlaSerAspAlaLeu 90
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0211 row: 0 column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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Location/Qualifiers
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77.00
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27.478
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Best Local Similarity:
Query Match:
DB:
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ORIGIN
  AUTHORS
                                                                                                                                                          JOURNAL
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91 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSer 110
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111 AspAsnAlaAlaSerAspAlaTrpGluLysAla 121 ŏ

Search completed: October 13, 2002, 03:33:06 Job time : 1894.74 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 13, 2002, 01:12:51; Search time 22.9572 Seconds (without alignments) 268.169 Million cell updates/sec Run on:

US-09-847-539A-6 777 1 VDSPIEQPRIIPNGGTLTNL.......KKEERQNVNTLPTTGEESNP 159 Title: Perfect score: Sequence:

Scoring table:

105224 segs, 38719550 residues BLOSUM62 Gapop 60.0 , Gapext 60.0 Searched: 105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            | Description | P06654 streptococc | P19909 streptococc |           | Q01042 herpesvirus | P76072 escherichia | P40552 saccharomyc | P50600 pseudomonas | Q04951 saccharomyc | -         | P12957 gallus gall | _          | Q47125 escherichia | P50532 xenopus lae | P32583 saccharomyc |            | -          | _          | P13390 bacteriopha | P24587 rattus norv | Q28092 bos taurus | Q13439 homo sapien | Q9hry0 halobacteri | Q15320 homo sapien | 068032 rhodobacter | _          |            | _          |            |           | Q08696 drosophila | _          | 391        | Q06068 strongyloce |
|------------|-------------|--------------------|--------------------|-----------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------|--------------------|------------|--------------------|--------------------|--------------------|------------|------------|------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|------------|------------|------------|------------|-----------|-------------------|------------|------------|--------------------|
|            | ΙΟ          | SPG1_STRSP         | SPG2_STRSP         | STF_LAMBD | IE68_HSVSA         | STFR_ECOLI         | TIR3_YEAST         | TOLA_PSEAE         | YM8Z_YEAST         | PS4_ENTFC | CALD_CHICK         | CE05_ECOLI | CE10_ECOLI         | XCPC_XENLA         | SR40_YEAST         | CENF_HUMAN | SCII_CHICK | DYNA_HUMAN | VLTF_BPT5          | AK15_RAT           | CYL2_BOVIN        | GOG4_HUMAN         | GRPE_HALN1         | DDX7_HUMAN         | SBCC_RHOCA         | T2D9_HUMAN | TUB8_SOLTU | TOLA_ECOLI | HTR2_HALVA | NFM_CHICK | MST2_DROHY        | HBHA_MYCTU | GAR2_SCHPO | HS97_STRPU         |
|            | 80          | -                  | -                  | -         | Н                  | -                  | Н                  | Н                  | Н                  | -         |                    | -          | П                  | -                  | -                  | Н          | Н          |            |                    | -                  | -                 | -                  | -                  | -                  | -                  | -          | -          | Н          | Н          | -1        | Н                 | Н          | -          | -                  |
|            | Length      | 448                | 593                | 774       | 407                | 1120               | 569                | 347                | 389                | 516       | 771                | 490        | 490                | 1290               | 406                | 3210       | 1189       | 1278       | 1396               | 464                | 488               | 2230               | 217                | 439                | 1238               | 211        | 211        | 421        | 433        | 857       | 1391              | 198        | 200        | 688                |
| &<br>Ouery |             | 19.9               | 19.9               |           | 11.3               | 10.9               | 10.3               | 10.3               | 10.2               | 10.2      | 10.0               | 8.6        | 8.6                | 9.8                | 7.6                | 9.7        | 9.4        | 9.4        |                    |                    | 9.3               | •                  | ٠                  | •                  | 9.1                | 0.6        | 0.6        | 0.6        |            |           | ٠                 | 8.9        | ٠          | 6.8                |
|            | Score       | 155                | 155                | 66        | 88                 | 82                 | 80                 | 80                 | 79                 | 79        | 78                 | 97         | 92                 | 92                 | 75                 | 75         | 73         | 73         | 73                 | 72                 | 72                | 72                 | 71                 | 71                 | 71                 | 70         | 70         | 70         | 7.0        | 70        | 7.0               | 69         | 69         | 69                 |
| Result     | No.         | 1                  | 7                  | e         | 4                  | 'n                 | 9                  | 7                  | ဆ                  | σ         | 10                 | 11         | 12                 | 13                 | 14                 | 15         | 16         | 17         | 18                 | 19                 | 20                | 21                 | 22                 | 23                 | 24                 | 25         | 56         | 27         | 28         | 53        | 30                | 31         | 32         | 33                 |

| p35601 mus musculu 00878 mus musculu Q03174 streptococc P39292 escherichia P06710 escherichia P56836 chlamydia m Q49419 mycoplasma Q9hp81 halobacteri P71410 halobacteri P71410 blobacteri Q9hwc9 pseudomonas P57145 buchnera ap |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AC15_MOUSE<br>DYNA_MOUSE<br>FRUA_STRMU<br>SPAA_STRMU<br>SPAA_STRMU<br>YJFU_ECOLI<br>DNAK_CHLMU<br>Y328_MYGE<br>HTR2_HALNI<br>HTR2_HALNI<br>RPCC_PSEAE<br>RPOC_BUCAI                                                              |
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| 1131<br>1281<br>1423<br>1528<br>232<br>643<br>654<br>756<br>763<br>1399                                                                                                                                                          |
| $ \begin{array}{cccccccccccccccccccccccccccccccccccc$                                                                                                                                                                            |
| 69<br>69<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60                                                                                                                                           |
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## ALIGNMENTS

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Streptococcus.
NCBI_TaxID=1306;
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REPEAT
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 X 5 AA REPEATS OF [DE]-D-A-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Immunoglobulin G binding protein G precursor (IGG binding protein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sp. (strain G148).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
SUBCELLULAR LOCATION: Type I membrane protein. Cell wall. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR01899; Gram_pos_anchor.
InterPro: IPR00724; IgG_bind_B.
Pfam; PF0146; GA, 2.
Pfam; PF00146; GA, 2.
Pfam; PF00178; IgG_binding_B; 2.
PRINTS: PR0015; GPOSANCHOR.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN G BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.9%; Score 155; DB 1; Length 448; 56.1%; Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEINS.
A0759060C8F9E6CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALA-RICH.
2 X 37 AA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 55 AA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47567 MW;
                                                                                                                                                                                                                  EMBL; M13825; AAA03664.1; -.
                                                                                                                                                                                                                                                                                                                           PDB; 11GD; 01-NOV-94.
PDB; 21GD; 29-JUL-98.
PDB; 1FCC; 20-JUL-95.
PDB; 1GB1; 15-APR-93.
InterPro; 1PR002988; GA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 56.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                  1 PGA; 30-APR-94.
1 PGB; 30-APR-94.
1 PGX; 15-JUL-92.
1 IGC; 03-JUN-95.
1 IGD; 01-NOV-94.
                                                                                                                                                                                                                                       A24496; A24496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 AWEAAA 99
                 -!- SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPG2_STRSP
P19909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SPG2_STRSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Filpula D., Alexander P., Fahnestock S.R.; "NucleoLide sequence of the protein G gene from Streptococcus GX7805, and comparison to previously reported sequences."; Nucleic Acids Res. 15:7210-7210(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-G148;
MEDLINE-8630657; PubMed-3017704;
MEDLINE-8630657; PubMed-3017704;
Guss B., Eliasson M., Olsson A., Uhlen M., Frej A.-K., Joernvall H., Flock J.-I., Lindberg M.;
Flock J.-I., Lindberg M.;
"Structure of the IgG-binding regions of streptococcal protein G.";
EMBO J. 5:1567-1575(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: TYPE I membrane protein, Cell wall, -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R WELL; X06173; CAA.29540.1; -
R EMBL; X06173; CAA.27640.1; -
R EMBL; X060128; CAA.27638.1; -
R PIR; X060128; S00128.
R PDB; 1634; 22-012.9
R PDB; 1634; 22-012.9
R InterPro; IPR0012989; Gram_pos_anchor.
R InterPro; IPR001899; Gram_pos_anchor.
R InterPro; IPR001899; Gram_pos_anchor.
R Pfam; PF01468; Gram_pos_anchor; 1.
R Pfam; PF0178; IgG_binding_B; 3.
R Pfam; PF0378; IgG_binding_B; 3.
R Pfam; PF0378; Gram_pos_anchor; 1.
R Pfam; PF0378; Gram_pos_anchor; 1.
R Pfam; PF0378; IgG_binding_B; 3.
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                                                                                                                        Olsson A., Eliasson M., Guss B., Nilsson B., Hellman U.,
Lindberg M., Uhlen M.;
                                                                                                                                                                                                                              Structure and evolution of the repetitive gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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3 X 37 AA REPEATS.
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                                                                                                                                                                                                                                                                          streptococcal protein G.";
Eur. J. Biochem. 168:319-324(1987).
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                                                                                           MEDLINE-88029445; Pubmed-3665928;
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DOMAIN
TRANSMEM
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Gaps

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DB 1; Length 774; 0.0033; ches 37; Indels

12.7%; Score 99; DB 1 32.9%; Pred. No. 0.003 ive 16; Mismatches

CDD1DF85E919123B CRC64;

774 AA; 77527 MW;

Chemotaxis\_transducer.

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EMBL; J02459; AAA96557.1; ALT_FRAME.
PIR; A04389; QXBP1L.
PIR; A04370; QXBP2L.
                                                                                                             26; Conservative
                                    InterPro; IPR004089;
                                                                                                Similarity
                                                 Fiber protein.
SEQUENCE 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda PaPa:
Hendrix B.W., Duda R.L.;
Handa PaPa:
Hambda PaPa:
Hambda PaPa:
Hambda PaPa:
Hambda Inambda PaPa:
Hambda Inambda Hambda Hambda Virions Have thin,
Johnted tail fibers (side tail fibers) that are absent from lambda
Wild type. Relative to lambda PaPa, Ur-lambda has expanded
receptor specificity and adsorbs to E.coli cells more rapidly.
HER SILL FIBER FAMILY
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
CORRECTED IN POSITION TO 396 TO RECREATE THE ORIGINAL STF PRIDEIN.
                     2-2.
5 x 5 AA REPEATS OF [DE]-D-A-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION AS STF.
MEDLINE-29165720; Pubmed-1531648;
Haggaard-Ljungquist E., Halling C., Calendar R.;
"DNA sequences of the tall fiber genes of bacteriophage P2: evidence for horizontal transfer of tall fiber genes among unrelated
                                                                                                                        Gaps
                                                                                                                                            1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                            VIruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petersen G.B.;
                                                                                             Score 155; DB 1; Length 593;
Pred. No. 1.7e-09;
Mismatches 25; Indels
                                                                       048BAA760D5B2920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-83189071; PubMed-6221115; Sanger F., Coulson A.R., Hong G.F., Hill D.F., Pet "Nucleotide sequence of bacteriophage lambda DNA." J. Mol. Biol. 162:729-773(1982).
 55 AA REPEATS
                                                                                                                                                                                                                                                                                                    21.JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Side tail fiber protein.
                                                                                                                                                                                                                                                                               774 AA
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                                                                                                                                                                                                                                                                                 PRT;
2 x 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 174:1462-1477(1992)
                                                                       63291 MW;
                                                                                               19.9%;
                                                                                                          56.1%;
                                                                                                         t_Local Similarity 56.1
ches 37; Conservative
                                                                                                                                                                                                                                                                                 STANDARD;
427
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                                                                       593 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              STF_LAMBD : P03745;
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AWEAAA 99
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                                                                       SEQUENCE
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           REPEAT
REPEAT
DOMAIN
                                              DOMAIN
                                                                                                                                                                                             61
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                                                                                                                    Matches
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"Analysis of nucleotide sequence of the rightmost 43 kbp of
herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
organization between HVS and Epstein-Barr virus.";
virology 188:296-310(1992).
-- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 AND
HSV-2 IE-68 (US1), EHV-1 65, EHV-4 (ORF4), PRV RSP40, AND VZV 63.
50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
                                                            190 AESSKNAAATSAGAAKTSETNAAASQOSAATSASTAATKASEAATSARDAVASKEAAKSS 249
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Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Blesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
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407 AA; 46617 MW; FFD399CA82CE136C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   407 AA
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MEDLINE-92230228; PubMed-1314457;
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                                                                                                                                                                    250 ETNASSSAGRASSATAAE 268
                                                                                                                            110 SDNAASDAWEKAATPIALD 128
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Matches 25; Conservative
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PIR; S20244; S20244.
HSSP; P53041; 1A17.
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DOMAIN 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 OR ECLF1.
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50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
                                                                                                                                                  TIR3_YEAST
P40552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGULATION.
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SEQUENCE
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                           LADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makinoto K., Mizobuchi K., Mori T., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; Saito N., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
           EERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEA
                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004089; Chemotaxis transducer.
Hypothetical protein; Fiber protein; Repeat; Complete proteome.
SEQUENCE 1120 AA; 113779 MW; 542E59D71EE795B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%; Score 85; DB 1; Length 1120; 32.5%; Pred. No. 0.17; ive 13; Mismatches 39; Indels
                                                                                                                                                                                                                  FIFR_ECOLI STANDARD; PRT; 1120 AA.
757672; P77560;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Side tail fiber protein homolog from lambdoid prophage Rac.
STFR OR B1372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000234; AAC74454.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12;
MEDLINE-97251357; PubMed-9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90774; BAA14966.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG13370; stfR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PO4002; 1WFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shao Y.;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                        153 TGEES 157
                                                                                                                                                217 EAEEA 221
                                                                                                                                                                                                                                                                                                                                            Escherichia
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Abramova N., Sertil O., Mehta S., Lowry C.V.;
Abramova N., Sertil O., Mehta S., Lowry C.V.;
"Reciprocal regulation of anaerobic and aerobic cell wall mannoprotein gene expression in Saccharomyces cerevisiae.";
J. Bacteriol. 183:2881-2887(2001).
--- FUNCTION: COMPONENT OF THE CELL WALL.
--- FUNCTION: COMPONENT OF THE STEL WALL.
--- SIMILARITY: BELONGS TO THE SRPI / TIPI FAMILY.
49 EATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

Barrell B.G., Badcock K., Copsey T., Dear S., Devlin K., Fraser A.,

Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,

Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

Walsh S.V., Whitchead S.,

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 CELL WALL PROTEIN TIR3.
269 ALA/SER-RICH.
26308 MW; 48AF914D8C149124 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
01-MR-2002 (Rel. 41) rast annotation update)
TIR3 OR YIL011W.
                                                                                                                                                                                                                                                                                                                                    269 AA.
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Pfam; PF00660; SRP1_TIP1; 1.
PROSITE; PS00724; SRP1_TIP1; 1.
CC11 wall; Glycoprotein; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z38113; CAA86238.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 QSDNAASDAWEKAATPIA 126
                                                                                           110 SDNAASDAWEKAATPIA 126
                                                                                                                                                              250 ETNASSSASSAASSATA 266
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SGD; S0001273; TIR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 AA;
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les 22; Conserv
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389 AA

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TOLA\_PSEAE P50600;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: STRONG, TO YEAST YGR279C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecium (Streptococcus faecium).
Bacteria: Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
Enterococcus.
NCBI_TaxID=1352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-89385998; PubMed-2780297;
Fuerst P., Mosch H.-U., Solioz M.;
Fuerst p., Mosch H.-D., Solioz M.;
A protein of unusual composition from Enterococcus faecium.";
Nucleic Acids Res. 17:6724-6724(1989).
                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 40.5 kDa protein in UBP15-GAS1 intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%; Score 79; DB 1; Length 389; 23.6%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN YMR305C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces
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01-NOV-1991 (Rel. 20, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.2%; Score 79; DB 18est Local Similarity 23.6%; Pred. No. 0.26; Matches 21; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                       PRT;
   84 NAASDALEALADQTDALQSEEAEV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 120
389 AA; 40469 MW;
                                             223 KKARALAELLSDTTERQQALADEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Signal. SIGNAL 1 18 CHAIN 19 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMR305C OR YM9952.07C
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STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                   YM82_YEAST
Q04951;
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STRAIN-ATCC 15692 / PAO1;

STRAIN-20437337; pubmed-10984043;

SLOVER C.K., Pham X.-O.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larblyg K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P04002; 1WFA.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 APEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKAD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:959-964(2000),
-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 80; DB 1; Length 347; 29.8%; Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEDD4B04AA095945 CRC64;
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PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY - ALA.
                                                                                                                                                                    PRT;
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191 KSSSSAKSSGSSAASSAA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa."
                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 516;
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muscle caldesmon.";
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. 402ECAA439846D26 CRC64;
SUBCELLULAR LOCATION: ATTACHED TO THE CELL-WALL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 164:503-511(1989).
                   -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 79; DB 1;
16.9%; Pred. No. 0.35;
tive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         P54 PROTEIN.
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Hayashi K., Fujio Y., Kato I., Sobue K.;
                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                       EMBL; X16421; CAA34442.1; ALT_INIT.
PIR; S05542; S05542.
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MEDLINE-89340480; PubMed-2760048;
                                                                                                                                                                                                                                                                               InterPro; IPR000064; NLPC_P60. Pfam; PF00877; NLPC_P60; 1. Signal; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                             54596 MW;
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516
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429 4
516 AA;
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NCBI_TaxID=9031;
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phosphorylation sites."

1. Biol. Chem. 266:19971-19975(1991).

2. Biol. Chem. 266:19971-19975(1991).

3. Biol. Chem. 266:19971-19975(1991).

4. Biol. Chem. 266:19971-19975(1991).

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8. Chem. 266:19971-19975(1997).

8. Chem. 266:1997
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PTM: IN NON-WUSCLE CELLS, PHOSPHORYLATION BY CDC2 DURING MITOSIS CAUSES CALDESMON TO DISSOCIATE FROM MICROFILAMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K., Yamada S., Kanda K., Kimizuka F., Kato I., Sobue K.; "35 kDa fragment of h-caldesmon conserves two consensus sequences of the tropomyosin-binding domain in troponin T."; Biochem. Biophys. Res. Commun. 161:38-45(1989).
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MEDLINE-88293484; PubMed-3401222;
Mornet D., Audemard E., Derancourt J.;
Identification of a 15 kilodalton actin binding region on gizzard caldesmon probed by chemical cross-linking.";
Biochem. Blophys. Res. Commun. 154:564-571(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yano H., Hayashi K., Haruna M., Sobue K.;
"Identification of two distinct promoters in the chicken caldesmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ō
                                                                                                                           BRAIN L-CAD AND GIZZARD L-CAD).
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Mak A.S., Carpenter M., Smillie L.B., Wang J.H.;
"Phosphorylation of caldesmon by p34cdc2 kinase. Identification
                                                                                                                                                                               MEDLINE-94071934; PubMed-8250919;
Haruna M., Hayashi K., Yano H., Takeuchi O., Sobue K.;
"Common structural and expressional properties of vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 451-756 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 201:618-626(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bryan J., Lee R.;
"Sequence of an avian non-muscle caldesmon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muscle Res. Cell Motil. 12:372-375(1991).
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                                                                                                                                 SEQUENCE FROM N.A. (GIZZARD H-CAD;
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MEDLINE-92042686; PubMed-1939602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
MEDLINE-94271210; Pubmed-8002994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89273666; PubMed-2730665;
Biol. Chem. 266:355-361(1991).
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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24
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nes 24; Conserv
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Plasmid.
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NCBI_TaxID=562;
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Q47500;
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYOSIN AND CALMODULIN-BINDING.
10 X 13 AA APPROXIMATE TANDEM REPEATS.
1.
2.
3.
PHOSPHORYLATION REDUCES CALDESMON BINDING TO ACTIN, MYOSIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01076; CALDESMON.
Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
                                     REORGANIZATION (BY SIMILARITY).
SIMILARITY: TO A TROPOMYOSIN BINDING SITE DOMAIN OF TROPONIN
       CALMODULIN AS WELL AS ITS INHIBITION OF ACTOMYOSIN ATPASE
ACTIVITY. PHOSPHORYLATION ALSO OCCURS IN BOTH QUIESCENT AND
DIVIDING SMOOTH WUSCLE CELLS WITH SIMILAR EFFECTS ON THE
INTERACTION WITH ACTIN AND CALMODULIN AND ON MICROFILAMENTS
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BAA04539.1; JOINED.
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InterPro; IPR000075; Caldesmon.
Pfam; PF02029; Caldesmon; 1.
                                                                                                                             EMBL; J04968; AAA49067.1; -. EMBL; D17648; BAA04539.1; -.
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DOMAIN 26 199
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EMBL; D17552; BAA04490.1;
EMBL; M26684; AAA48811.1;
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BAA04538.1;
BAA04538.1;
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BAA04538.1;
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BAA04539.1
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251
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D176421;
D17643;
D17644;
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D17646;
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D17636;
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D17638;
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D17640;
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D17647;
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D17634;
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D17639;
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"Evidence that the immunity protein inactivates colicin 5 immediately prior to the formation of the transmembrane channel.";

J. Bacteriol. 177:6966-6972(1995).

-! FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING TO DISSIPATION OF CELLULAR ENERGY.

-! FUNCTION: COLICINA ARE POLYEPPIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.

-! SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
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TROPOMYOSIN-BINDING (POTENTIAL).
TROPOMYOSIN-BINDING (POTENTIAL).
STRONG ACTIN-BINDING.
CALMODULIN-BINDING.
WEAK ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 1; Length 771;
Pred. No. 0.69;
                                                                                                                                                                                                                                              (POTENTIAL).
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Last annotation update)
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PHOSPHORYLATION
PHOSPHORYLATION
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POLY-GLU.
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MEDLINE-96074329; PubMed-7592492;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1 - FUNCTION: REQUIRED FOR BOTH ASSEMBLY AND STRUCTURAL MAINTENANCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
-1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-1- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                    SEQUENCE FROM N.A.
MEDINE-99042742; Pubmed-7954811;
Hirano T., Mitchison T.J.;
"A heterodimeric colled-coll protein required for mitotic chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 LRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDA 89
                                ELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTD 98
                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOTIC CHROMOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1290;
32; Indels
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W; 2931249924FE90F6 CRC64;
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COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
POLY-CLY.
POLY-ALA.
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21.3%; Pred. No. 2;
*ive 24; Mismatches 35;
                                                                                                                                                                                                                                          01-077-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                              1290 AA
 22; Conservative 15; Mismatches
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InterPro; IPR003405; SMC_C.
                                                                                                                                                                                                                                                                                               Chromosome assembly protein XCAP-C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          condensation in vitro.";
Cell 79:449-458(1994).
                                                                                                                                                                                                               STANDARD;
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1129
1290
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NCBI_TaxID=8355;
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                                                                                                ALOSEEAEV 107
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P50532;
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DOMAIN
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Matches
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-!- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF TRANSMEMBRANE TOXING DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING TO DISSIPATION OF CELLULAR ENERGY.
-!- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.
-!- SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                               39 ELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pilsl H., Braun V.; "Novel colicin 10: assignment of four domains to TonB- and TolC-dependent uptake via the Tsx receptor and to pore formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 76; DB 1; Length 490;
Pred. No. 0.72;
                                                                                                                                                                                                Indels
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                                                                                                                             187614D103B953E2 CRC64;
                                                                                                                                                                                              32;
                                           PRINTS; PR00280; CHANICOLICIN.
PRODOM; PD002657; Channel_colicin; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
Antibiotic; Bacteriocin; Plasmid; Transmembrane.
TRANSEM 447 467
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                             490 AA.
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                                                                                                                                                                Score 76;
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Pfam; PF01024; Colicin; 1.
PRINTS; PR00280; CHANLCOLICIN.
ProDom; P0002657; Channel_colicin; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
             InterPro; IPR000293; Channel_colicin.
Pfam; PF01024; Colicin; 1.
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                                                                                                                              490 AA; 53137 MW;
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Local Similarity 31.9%;
les 22; Conservative 15
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EMBL; X87835; CAA61102.1; -.
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(Rel. 37, I
(Rel. 40, I
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          DVQSKQAIV 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
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15-DEC-1998 (
15-DEC-1998 (
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Colicin 10.
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ID CE10_ECOLI
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REDUCE, ESTEDAN P.F., Baladron V., Gonzalez G.A., Cantalejo J.G., Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.;
"The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPLI genes and three new open reading frames.";
rew open reading frames.";
-!- FUNCTION: NOT KNONN; WEAK SUPPRESSOR OF A MUTANT OF THE SUBUNIT AC40 OF DNA DEPENDANT RNA POLYMERASE I AND III.
                                                                                                                      01-007-1993 (Rel. 27, Created)
01-007-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Suppressor protein SRP40.
SRP40 OR YKR092C OR YKR412A.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Kungl: Ascomycota: Saccharomycotina: Saccharomycetaies; Saccharomycetaies;
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 28583 / FL100;
Lalo D., Carles C., Sentenac A., Thuriaux P.;
Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> N (IN REF. 1).
8EA007695AF4BAID CRC64;
                                                                                                     406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASP/SER-RICH.
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01-FEB-1996 (Rel. 33, Created)
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nes 15; Conservative
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                             90 LEALADQTDALQSEE 104
                                                458 MDSLKKETQGLQEEK 472
                                                                                                     STANDARD;
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                                                                                                     SR40_YEAST
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MEDLINE=98437347; PubMed=9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";
J. Cell Biol. 14:49-63(1998).
-!-FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROFIEIN (RB), CENP-E AND BUBRI.
-!- SUBUNIT: HOMO- OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.
-:- DEVELOPMENTAL STAGE: GRADDALLY ACCUMULATES DURING THE CELL CYCLE.
-:- DEVELOPMENTAL STAGE: GRADDALLY ACCUMULATES DURING THE CELL CYCLE.
-:- PIM: HYPERPHOSPHORYLATED DURING MITOSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95379846; PubMed-7651420; Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Zhons D., Yang-Feng T.L., Lee W.-H. Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression.";
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MEDLINE-95336446; PubMed=7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;
"A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Breast carcinoma;
MEDILINE-95348175: Pubmed-7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
KICENP-F: sa a protein of the nuclear matrix that assembles onto
Kinetochores at late G2 and is rapidly degraded after mitosis.";
J. Cell Biol. 130:507-518(1995).
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CENP-F kinetochore protein (Centromere protein F) (Mitosin) (AH
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DOMAIN 14 197 COILED COIL (POTENTIAL).

DOMAIN 273 769 COILED COIL (POTENTIAL).
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MEDLINE-95370296; Pubmed-7642639;
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Best Local Similarity 24.7%;
Matches 21; Conservative 1
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                                                                                                                                                                                                                                                                                                                        STANDARD;
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G -> D (IN REF. 2).

MISSING (IN REF. 2).

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V -> A (IN REF. 2).

ER -> DG (IN REF. 3).

ER -> DG (IN REF. 3).

D -> N (IN REF. 3).

D -> N (IN REF. 3).

ER -> DG (IN REF. 3).

ER -> DG (IN REF. 3).
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-1- FUNCTION: MITOSIS-SPECIFIC CHROMOSOME SCAFFOLD PROTEIN THAT
COLOCALLIZES WITH TOPOISOMERASE II. MAY FUNCTION IN CHROMOSOME
CONDENSATION OR SISTER CHROMATID DISJUNCTION.
-1- SUBCELLULAR LOCATION: NUCLEAR. LOCATED ALONG THE ENTIRE LENGTH OF
THE CHROMATID ARM AXIS.
-1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COLLED-COLL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-1- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                    EDKEATTAIEAASSDALEALADOTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                       9.7%; Score 75; DB 1; Length 3210; 21.0%; Pred. No. 6.4;
                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                        (IN REF. 3).
W; 11D83324960E4334 CRC64;
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
2 x 177 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                               2580 QLLQGLDEAKNNYIVLQSSVNGLIQEVEDGKQKLEKKDEE 2619
                                                                                                                                                                                                                                                                                                                                106 EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Chromosome scaffold protein ScII.
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Matches 21; Conserv
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Q90988;
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Blochim. Blophys. Acta 1442:432-436(1998),
-1- FUNCTION: REQUIRED FOR THE CYTOPLASMIC DYNEIN-DRIVEN RETROGRADE
MOVEMBRY OF VESICLES AND ORGANELLES ALONG MICROTUBULES, DYNEIN-
DYNACTIN INTERACTION IS A KEY COMPONENT OF THE MECHANISM OF AXONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holzbaur E.L.F., Tokito M.K.; "Localization of the DCTNI gene encoding p150Glued to human chromosome 2pl3 by fluorescence in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           014203; 095296; 09U102; 01-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Dynactin 1 (150 kDa dynein-associated polypeptide) (DP-150) (DAP-150) DCTN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          819 VEALVLELEQLKQEQASYKQQSEAAQQAIASLKEQVSALEAEAVKTRESLKNAENELSSE 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=99017972; Pubmed=9799602; Collin G.B., Nishina P.M., Marshall J.D., Naggert J.K.; "Human DCTN1: genomic structure and evaluation as a candidate for
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SPEQUENCE OF 18-1278 PROMED-199055007;
TOKITO M.K., HOlzbaur E.L.F.;
"The genomic structure of DCTN1, a candidate gene for limb-girdle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                                                                                                                                                                                                                                                                                                       9.4%; Score 73; DB 1; Length 1189;
                                                                                                                                                                 ed coll; Nuclear protein.
ATP (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
AMM; 9055BC895C45AD5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 9-1278 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 ATPIALDVKKTKDTKPVVKKEERQN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            879 KGLMEERTKDIKAKSAKIEKYREON 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96435441; PubMed-8838327;
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                                                                                                                                                                                                                                                                                                                                            1189 AA; 134940 MW;
EMBL; X80792; CAA56767.1; -.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
Pfam; PP02483; SMC_C; 1.
Pfam; PP02463; SMC_N; 1.
Mitosis; ATP-binding; Coiled oc
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11

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Late protein.
CONFLICT 9
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                                                         86
                                                                                              1024
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                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGSKRHVYSKTÞSGSRMSABAŚARPLRVGSRVBVJGKGHR
QVARVGATLEATGKWGVILDBAKGKNDGTVGGRKYFTCD
EGHGIFVVDVEDGADTTSPETPDSASKVLKREGTD
TTAKTSKL -> MMRQ (IN ISOFORM P135).
                SUBUNIT: LARGE MACROMOLECULAR COMPLEX OF AT LEAST 10 COMPONENTS. P150(GLUED) BINDS DIRECTLY TO MICROTUBULES AND TO CYTOPLASMIC
                                                                   -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; P150 (SHOWN HERE) AND P135;
-:- TISSUE SPECIFICITY: BRAIN.
-:- PTW: PHOSPHORYLATED.
-:- SIMILARITY: BELONGS THE DYNACTIN 150 KDA SUBUNIT FAMILY.
-:- SIMILARITY: CONTAINS 1 CAP-GIY DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01302; CAP_GLY; 1.

PROSITE; PS00845; CAP_GLY_1; 1.

PROSITE; PS50245; CAP_GLY_2; 1.

Motor protein; Microtubules; Dynein; Coiled coil; Cytoskeleton; Alternative splicing; Phosphorylation.

DOMAIN 48 90 CAP-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB 1; Length 1278; Pred. No. 4.1;
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S -> N (IN REF. 2 AND 3).
MISSING (IN REF. 2 AND 3).
D -> V (IN REF. 2 AND 3).
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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24.4%; Pred. No. 4...
10. Mismatches
10. Mismatches
TRANSPORT OF VESICLES AND ORGANELLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SER-RICH,
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JOINED.
JOINED.
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JOINED.
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EMBL; AF064204; AAD55811.1; JOINED.
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JOINED.
JOINED.
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BMBL; AF086928; AAD03694.1; JOINED.
EMBL; AF086929; AAD03694.1; JOINED.
EMBL; AF086930; AAD03694.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF086945; AAD03694.1; JOINED. AF086946; AAD03694.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF064205; AAD55811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interPro; IPR000938; CAP-Gly.
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132 138
712 712
1278 AA; 141694 M
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EMBL; AF086942; AAD03694.1;
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AAD03694.1;
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AAD03694.1
AAD03694.1
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EMBL; AF086938; AAD03694.1
EMBL; AF086939; AAD03694.1
EMBL; AF086940; AAD03694.1
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=10726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88289370; PubMed-3267228; Kaliman A.V., Kryukov V.M., Bayev A.A.; The uncleotide sequence of bacteriophage T5 DNA at the region between early and late genes."; Nucleic Acids Res. 16:6230-6230(1988).
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Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kryukov V.M.;
"The nucleotide sequence of the bacteriophage T5 ltf gene.";
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9.4%; Score 73; DB 1; Length 1396;
Best Local Similarity 29.5%; Pred. No. 4.5;
Matches 23; Conservative 13; Mismatches 42; Indels
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WW; 18CD2192F65FFFC1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTE_BPT5 STANDARD; PRT; 1396 AA. P1330; 048502; 01-JAN-1990 (Rel. 13, Created) 01-JEB-1996 (Rel. 33, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) L-shaped tail fiber protein (LFF protein).
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                                                                                                                                                                                                                                                   ; AJ001191; CAA04591.1;
S01982; S01982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 366:46-48(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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P24587;
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ID AK15
AC P245
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19; Conservative

Matches

Local Similarity

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Gaps

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39; Indels

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25
189
189
2189
226
324
3324
380
488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                          Cytoskeleton;
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DOMAIN
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REPEAT
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REPEAT
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01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
A-kinase anchor protein 150 (AKAP 150) (CAMP-dependent protein kinase regulatory subunit II high affinity binding protein) (P150)
                                                                                                                                                   TISSUE-Brain;
MEDLINE-89174725; PubMed-2538452;
MEDLINE-89174725; PubMed-2538452;
MEDLINE-89174725; PubMed-2538452;
MEDLINE-8917475; PubMed-2538452;
Migh affinity binding protein for the regulatory subunit of CAMP-dependent protein kinase II-B. Cloning, characterization, and expression of CDNas for rat brain p150.";
J. Biol. Chem. 264.4648-46561989).
I-FUNCTION: MAY ANCHOR THE KINASE TO CYTOSKELETAL AND/OR ORGANELLE-ASSOCIATED PROPERING, TARGETING THE SIGNAL CARRIED BY CAMP TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 KKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 KTAAEEKKSGETALGQAEEASSVSQADKSVLSQAEEATVGHTEEATVIQAQSQAKEGKLS 101
                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                   SPECIFIC INTRACELLULAR EFFECTORS.
SUBUNIT: BINDS DIMER OF THE RII-BETA REGULATORY SUBUNIT OF CAMP-
DEPENDENT PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3%; Score 72; DB 1; Length 464;
11.4%; Pred. No. 1.9;
(ve. 12; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 X 8 AA REPEATS.
BDD21CF95CCBAC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Testis;
MEDLINE-95255491; PubMed-7737358;
Hess H., Held H., Zimbelmann R., Franke W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYlicin II (Multiple-band polypeptide II).
CYLC2 OR CYL2.
                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO OTHER AKAP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 1
59 349 3
464 AA; 48335 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 31.48
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 OSEEAEVVOS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 QAEEATVAQA 111
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYL2_BOVIN
Q28092;
                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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DOMAIN
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CYL2_BOVIN
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"The protein complexity of the cytoskeleton of bovine and human sperm heads: the identification and characterization of cylicin II."; Exp. Cell Res. 218:174-182(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 KKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 KKGSKKGKESATESEGEKKDSKKDKAGKKDPTKAGEKGDESKDKKDAKKKDSKKEKKDEK 447
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MEDLINE-96215236; PubMed-8626529;
MEDLINE-96215236; PubMed-8626529;
Erlich R., Gleeson P.A., Campbell P., Dietzsch E., Toh B.-H.;
"Molecular characterization of trans-Golgi p230: a human peripheral membrane protein encoded by a gene on chromosome 6p12-22 contains extensive coiled-coil alpha-helical domains and a granin motif.";
J. Biol. Chem. 271:8328-8337(1996).
                                                                                                                                                                                                                            Hess H., Held H., Franke W.W.;
"Molecular characterization of mammalian cylicin, a basic protein of the sperm head cytoskeleton.";
-1. Cell Blol. 12:1043-1052(1993).
-1. FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS. MABE INVOLVD IN SPERMATIO DIFFERENTIATION.
-1. SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE.
-1. TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOG4_HUMAN STANDARD; PRT; 2230 AA.
013439; 014436; 013270; 013654;
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last sequence update)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural protein; Repeat; Sperm; Spermatogenesis. 5 487 49 x 3 AA REPEATS OF K-K-X. 9 407 8 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Indels
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                                                                                                                                                                                             MEDLINE-93359502; Pubmed-8354692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z46789; CAA86753.1; -.
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Conservative 1
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2012
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2012
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RESULT 22
GRPE_HALN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                  GOLGI MEMBRANE.
-!- ALTERNATIVE PRODUCTS: DIFFERENTS ISOFORMS MAY ARISE BY ALTERNATIVE
                                                                                                                                                                                                                                                  DISEASE: ANTIGEN IN THE AUTOIMMUNE DISEASE SJOEGREN'S SYNDROME AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC FACE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
                                                                                                                                                                    Thesis (1994), Instituto municipal de investigacion medica, Spain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPYKGGNLYHTDVSLFGEPTEFEYLRKVLFEY -> HLT
AICTIRMSHSLENLPNLSICEKCFLSI (IN ISOFORM
                                                                            Fritzler M.J., Lung C.-C., Hamel J.C., Griffith K.J., Chan E.K.L.;
Molecular characterization of golgin-245, a novel Golgi complex
Protein containing a granin signature.";
J. Biol. Chem. 270:31262-31268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWLRSSS (IN ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Y -> H (IN REF. 3).

T -> A (IN REF. 3).

T -> A (IN REF. 3).

T -> A (IN REF. 3).

K -> E (IN REF. 3).

K -> E (IN REF. 3).

K -> N (IN REF. 3).

W, 3BB733DB1EA86134 CRC64;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                     Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
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MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
FTSPRSGIF -> SWLRSSS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Mismatches
                                                                 MEDLINE-96125112; PubMed-8537393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261139 MW;
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                                            SEQUENCE OF 131-2230 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000237; GRIP.
Pfam; PF01465; GRIP; 1.
Golgi stack; Antigen; Coiled
                                                                                                                                  SEQUENCE OF 524-672 FROM N.A. TISSUE-Gastric fundus;
                                                                                                                                                                                                                                                                                                                                                                           EMBL; U41740; AAC50434.1; -. EMBL; X82834; CAA58041.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U31906; AAC51791.1; -. EMBL; X76942; CAA54261.1; -.
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                                                                                                                                                                                                                                                               IN HEPATITIS B.
SEQUENCE FROM N.A.
                                                       TISSUE-Placenta;
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                                                                                                                                                           Balaque C.;
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MEDLINE-2000448.7.

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MARTIZELL S., Wair D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Renbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Rehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.";

"Genome sequence of SINILARITY MITH DNAJ, THE APPASE ACTIVITY OF

"T. FUNCTION: STIMULAPES, JOINTLY WITH DNAJ, THE APPASE ACTIVITY OF

"MORE EFFICIENTLY (BY SIMILARITY).

"SIMILARITY: BELONGS TO THE GRPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                         Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP-dependent helicase DDX7 (DEAD-box protein 7) (NP-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 AA; 23863 MW; DIEBED19AA7471F8 CRC64;
                                           439 AA
217 AA.
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InterPro; IPR00740; GrpE.
Pfam; PF01025; GrpE; 1.
PRINTS; PR00773; GRPEPROTEIN.
PROSTIE; PS01071; GRPE; FALSE_NEG.
Chaperone; Heat shock; Complete proteome.
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=64091;
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                                                                                                                                                                                                                                                                       Halobacterium
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Q15320;
GRPE_HALN1
Q9HRY0;
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                                                                                                                                            EMBL; AF010496; AAC16118.1; -.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Hydrolase; Nuclease; Exonuclease; Endonuclease; DNA replication;
DNA recombination; ATP-binding; Coiled coil.
                                                                                                                                                                                                                              434 COLLEG COLL.
438 COLLED COLL (POTENTIAL).
487 COLLED COLL (POTENTIAL).
600 COLLED COLL (POTENTIAL).
770 COLLED COLL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Pharm. Bull. 19:122-126(1996).
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4395
466
466
521
724
77
901
1019
1238 AA;
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-! FUNCTION: SbcCD cleaves DNA hairpin structures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3'-5' double strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity (By similarity).
-! SUBUNIT: Heterodimer of sbcC and sbcD (By similarity).
-! SIMILARITY: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                             MEDLINE-94183253; Pubmed-8135819; Kitajima Y., Yatsuki H., Zhang R., Matsuhashi S., Hori K.; "A novel human homologue of a dead-box RNA helicase family."; Blochem. Blophys. Res. Commun. 199.748-754(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EA9E81631D5D0B47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PROGRESS FALSE_NEG.
Hydrolase; PS00039; DEAD_ATP_HELICASE; FALSE_NEG.
Hydrolase; ATP_binding; Helicase; RNA-binding.
NP_BIND 39 46 ATP (POTENTIAL).
SITE 148 DEAD BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.1%; Score 71; DB 1; 26.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nuclease sbcCD subunit C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
                                                                                                                                                                                                                                                                                                                    InterPro; IPR001410; DEAD.
InterPro; IPR000629; DEAD_ATP_helicase.
InterPro; IPR001650; Hellcase_C.
Pfam; PF00270; DEAD; 1.
Ffam; PF00271; hellcase_C; 1.
SMART; SM00487; DEXDC; 1.
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STRAIN-SB1003 / St Louis;
MEDLINE-97404404; PubMed-9256491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 AA; 47405 MW;
                                                                                                                                                                                                                                                                                    EMBL; D26528; BAA05534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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409 TVPVVEKPKKK 419
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nes 19; Conserv
                  SEQUENCE FROM N.A.
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068032;
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42 KQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQ 101
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MEDLINE-56418138; Pubmed-8820923;
Kuzuhara T., Horikoshi M.;
"Isolation and characterization of a cDNA encoding a human TFIID subunit containing a variety of putative structural motifs including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CORE TAFII PRESENT IN BOTH OF THE PREVIOUSLY DESCRIBED TRIID SPECTES WHICH EITHER LACK OR CONTAIN TAFIIJO (TFIID ALPHA AND TFIID BETA RESPECTIVELY).
-!- SUBJUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS). INTERACTS WITH TAFIIIB BOTH IN VITRO AND INTRACELLULARLY; ALSO INTERACTS DIRECTLY WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of hTAFII18, hTAFI120 and hTAFI128: three subunits of the human transcription factor TFIID."; EMBO J. 14:1520-1531(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Transcription initiation factor TFIID 28 kDa subunit (TAFII-28)
(TAFII28) (FIID subunit p30-beta).
9.1%; Score 71; DB 1; Length 1238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95246745; PubMed-7729427;
Mengus G., May M., Jacq X., Staub A., Tora L., Chambon P.,
                                                                        31; Indels
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X 6-7 AA REPEATS OF E-E-P-A-A.

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PIR; S28046; S28046.
                                                                                                                                                                                                                                                                                      Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                          211 AA;
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P19934;
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Burnformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                               55 EAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAA 114
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               14 ETGESDETAAVPGDPGATDTDGIPEETDGDADVDLKEAAAEEGELESQDVSDLTTVERED 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CV. RECORD: TISSUE-Stolon tip;
MEDLINE-93081725; PubMed-1450379;
Taylor M.A., Mad Arif S.A., Kumar A., Davies H.V., Scobie L.A.,
Pearce S.R., Flavell A.J.;
"Expression and sequence analysis of cDNAs induced during the early stages of tuberisation in different organs of the potato plant (Solanum tuberosum L.).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLY STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NON-SWELLING STOLON TIPS FROM STAGE B, AND LEVEL REMAINED HIGH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 20:641-651(1992).
 DOMAIN: TBP AND TAFII18 BIND TO DISTINCT DOMAINS OF TAFII28.
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING
                                                                                                                                                                                                                                                                                                                                           Score 70; DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                             59; Indels
                                                                                                                                                                                                                                                                    InterPro; IPR000166; Histone_core.
Transcription regulation; Nuclear protein.
SEQUENCE 211 AA; 23307 MW; 77C7BDC667D19A8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 SSLINPAAKKLKIDTKEKKEKKOKVDEDEIQKMQILVSSFSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 SDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                   SIMILARITY: BELONGS TO THE TAF2I FAMILY.
                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Induced stolen tip protein TUB8 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequ
01-FEB-1994 (Rel. 28, Last anno
                                                                                                                                                                                                                   EMBL; AL033520; CAB96725.1; -. TRANSFAC; T02114;
                                                                                                                                                                                    EMBL; X83928; CAA58780.1; -. EMBL; D63705; BAA23620.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 211679; CAA77741.1; -.
                                                                                                                                                                                                                                                                                                                                               9.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUBER INCREASED IN SIZE.
                                                                                                                                                                                                                                                                                                                                                             21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 21.69
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND ROOTS
                                                                                                                                                                                                                                                          600772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                        45 IEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEE 104
                                                                                                                                                                                                Levengood S.K., Webster R.E.; "Nucleotide sequences of the tolA and tolB genes and localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=97426617: Pubbed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their products, components of a multistep translocation system in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yano M., Horiuchi T.; **A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                            122 EPAAAEEPVAAAPVEEAAAPKAEPEEAPVSEPEAEKAEEASPVSEEPEKVEE 173
                                                                                              9.0%; Score 70; DB 1; Length 211; 23.2%; Pred. No. 1.4;
                                                                                                                                                                                                                                                      105 AEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                  67; Indels
                                                          AFF293F819951C4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
8 (APPROXIMATE)
9 (APPROXIMATE)
POLY-TYR.
                                                                                                                                                                                                                                                                                                                                                                                            421 AA
                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tola protein.
TOLA OR CIM OR EXCC OR LKY OR B0739.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-JM105;
MEDLINE-90078104; PubMed-2687247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 171:6600-6609(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
                                                          22638 MW;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Tue Oct 15 08:27:45 2002

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PRT;
                   STANDARD;
                 HTR2_HALVA
P42258;
         HTR2_HALVA
RESULT 28
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 DALQSEEAEVVQSDNAASD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                   Haloarcula vallismortis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFM_CHICK
P16053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 EERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEA 92
                                                                                                                                                                                                                                                                                                                                               "Filamentous phage infection: crystal structure of g3p in complex with its ocreeptor; the C-terminal domain of TolA.";
Structure 7:711-722(1999).
Structure 7:711-722(1999).
SCOLICINS (COLICINS A. El. E2. E3. AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFFER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OF BACTERIOPHAGE DNA.

SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                      inTeraction with Porins.
MEDLINE-97133271; PubMed-8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                           Levengood S.K., Beyer W.F. Jr., Webster R.E.; "TolA: a membrane protein involved in colicin uptake contains an extended helical region."; Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN II (ALPHA-HELICÁL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                               Lloubes R.; "TolA central domain interacts with Escherichia coll porins."; EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%; Score 70; DB 1; Length 421; 24.8%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 LADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8B2F52B4B97C655E CRC64;
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                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
MEDLINE-99332679; PubMed-10404600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 AA
                                                        MEDLINE-91296736; Pubmed-2068069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M28232; AAA24683.1; -.
EMBL, ABC00017; AAC73833.1; -.
EMBL, D90713; BAA35405.1; -.
PIR, JV0057; JV0057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Conservative
DNA Res. 3:137-155(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1TOL; 20-MAY-99
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TRANSMEM
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Matches

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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
56-BSOSSORY rhodopsin I transducer (HTR-II) (Methyl-accepting phototaxis protein II) (MPP-II) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.
NCBI_TaxID=28442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chórdata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 DELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2010 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 29715;
MEDLINE-95224074; PubMed-7708770;
Seidel R., Scharf B., Gautel M., Kleine K., Oesterhelt D.,
Engelhard M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 70; DB 1; Length 433; 21.5%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00304; HAMP; 1.
SMART; SM00283; Ma; 1.
Transducer; Photoreceptor; Transmembrane; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 1 1 1
SEQUENCE 433 AA; 45935 MW; 90507B8897D943C0 CRC64;
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InterPro; IPR004089; Chemotaxis_transducer.
InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Neurofilament medium polypeptide) (NF-M).
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MEDLINE=90174973; Pubmed=2106668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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MST2_DROHY
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                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                -i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND WHICH ARE INVOLVED IN THE MAINTERANCE OF WENDRONAL CALLBER.
-!- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.
                                                                                                                                                                                                                                      PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 LRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDA 89
                                                           SEQUENCE OF 259-857 FROM N.A.
MEDLINE-88112814; PubMed-3123320;
Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.;
Zidentification of gene products expressed in the developing chick visual system: characterization of a middle-molecular-weight neurofilament cDNA.";
Genes Dev. 1:699-708(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
"Isolation of the chicken middle-molecular weight neurofilament (NF-M) gene and characterization of its promoter.";
Nucleic Acids Res. 18:521-529(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL 2A.
LINKER 2.
COLL 2B.
C-LINKED (GLCNAC) (BY SIMILARITY).
O-LINKED (GLCNAC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intermediate filament, Coiled coil; Neurone; Phosphorylation; Glycoprotein.

INIT_MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> R (IN REF. 2).
4E2E0FC6AC64778B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 LEALADQTDALQSEEAEVVQSDNAASDAWEKAAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| : | | | : : | | | | : : | EKAAEQAAEEGEEKEEEEAEEEEEARKSDAAEEGGS 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; D
Pred. No. 5.
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LINKER 1.
COIL 1B.
LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A27040, A27040.
PIR; S08061, S08061.
PIR: S15762, S15762.
Interpro: Interpro: Interpro: Interpro: PR001664; IF.
PFam; PF00038; filament; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X17102; CAA34958.1; -. EMBL; X05558; CAA29073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
285
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857 AA;
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 GNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVK 81
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-95045538; PubMed-7957199;
Neesen J., Padmanabhan S., Buenemann H.;
Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axoneme-associated protein family Dhmst101 form extended
alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila hydei.";

Eur. J. Biochem. 225:1089-1095(1994).

- I FUNCTION: POSSIBLE STATE ROLE IN THE SPERM TAIL.

-! FUNCELLULAR LOCATION: Cytoplasmic.

-! SUBCELLULAR LOCATION: Cytoplasmic.

-! TISSUE SPECIFICITY: TESTIS, PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                     MSTI01(2).
Drosophila hydei (Fruit fly).
Fukarvota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.0%; Score 70; DB 1; Length 1391; 8.2%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%; Pred. No. 9.7;
tive 13; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olivariant STANDARD; PRT: 198 AA. 01142, 085733; 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Heparin-binding hemagolutinin (Adhesin). Mycobacterium tuberculosis, and
                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2)
1391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01032; 1C5A.
FlyBase; FBgn0020733; Dhyd\mst101(2).
                                                  (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X73481; CAA51876.1; -.
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Best Local Similarity 28.29
Matches 20; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S34154; S34154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPERMATIDS
                                                  01-FEB-1995
01-FEB-1995
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SCHPO
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
GAR2_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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MISCELLANEOUS: SERUM PROM PATIENTS DIAGNOSED WITH ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Neison W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                      <u>`</u>
                                                                                                                                                                                                                                                                                 s:
       Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID-1773, 1765;
                                                                                                                                                                                                   SPECIES-M.tuberculosis; STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris: Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulzen J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishal W .. "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                               Menozzi F.D., Bischoff R., Fort E., Brennan M.J., Locht C.; "Molecular characterization of the mycobacterial heparin-binding hemagglutinin, a mycobacterial adhesin."; Proc. Natl. Acad. Sci. U.S.A. 95:12625-12630(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pethe K., Alonso S., Biet F., Delogu G., Brennan M.J., Locht C.,
Menozzi F.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Menozzi F.D., Rouse J.H., Alavi M., Laude-Sharp M., Muller J., Bischoff R., Brennan M.J., Locht C.; Identification of a heparin-binding hemagglutinin present in
                                                      SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION SPECIES—W. tuberculosis, and M.bovis; STRAIN-H37Ra, and BCG / Paris 1173 P2; MEDLINE-98445421; Pubmed-9770536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-M.tuberculosis; STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-16, AND CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-M.tuberculosis, and M.bovis;
STRAIN-H37Ra, and BCG / Paris 1173 P2;
MEDLINE-97188915; PubMed-9064359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.tuberculosis, and M.bovis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-103, and BCG;
MEDLINE-21342355; PubMed-11449276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exp. Med. 184:993-1001(1996).
                                                                                                                                                                                                                                                                                                                                                                                  Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "gar2 is a nucleolar protein from Schizosaccharomyces pombe required for 18S rRNA and 40S ribosomal subunit accumulation."; Nucleic Acids Res. 23:1912-1918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 RIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQ 69
TUBERCULOSIS THAT HAD NOT BEEN VACCINATED CONTAINS ANTIBODIES TO RECOGNIZE HBHA, WHEREAS SERUM FROM HEALTHY INDIVIDUALS DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gulli M.-P., Girard J.-P., Zabetakis D., Lapeyre B., Melese T., Calzergues-Ferrer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=972;
Brown D., Churcher C.M., Barrell B.G., Rajandream M.A., Wood
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: HILPS THE ASSEMBLY OF PRE-RIBOSOWAL PARTICLES
CONTAINING 18S RRNA.
                                                                                                                                                                                                                                                                                                                                                                       TIGR; MT0493; -.
TubercuList; Rv0475; -.
Cell adhesion; Heparin-binding; Hemagglutinin; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%; Score 69; DB 1; Length 198;
25.3%; Pred. No. 1.7;
tive 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-1- SIMILARITY: BELONGS TO THE GAR FAMILY.
-1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> P (IN REF. 1).
513760F6F1EB6042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 LRSQOSFEEVSARAEGYVDQAVELTQEALGTVASQTRAV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P41891; 013707;
01-NOV-1995 (Rel. 32, Created)
01-NAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALA/LYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
                                                                      SIMILARITY: STRONG, TO M. LEPRAE HBHA.
                                                                                                                                                                                                                                                                                                                             EMBL; 277162; CAB00936.1; -.
EMBL; AE006951; AAK44716.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                       EMBL; AF074390; AAC26052.1; -.
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GAR2 OR SPAC140.02.
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Search completed: October 13, 2002, 04:38:41 Job time : 564.612 secs

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Sequence 1340, Application US/09619049

Sequence 1340, Application US/09619049

Sequence 1340, Application US/09619049

Sequence 1340, Application

TITLE OF INVENTION:

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TOWNER OF INVENTION:

TITLE OF INVENTION:

TOWNER OF INVENTION:

TOWNER OF ILLING DATE:

1000-07-18

PRIOR FILING DATE:

1099-12-23

PRIOR PELICATION NUMBER:

60/175,685

PRIOR FILING DATE:

2000-01-12

PRIOR PELICATION NUMBER:

60/175,685

PRIOR PELICATION NUMBER:

60/175,685

PRIOR PELICATION NUMBER:

60/175,685

PRIOR FILING DATE:

2000-03-03

PRIOR FILING DATE:

2000-03-03

PRIOR FILING DATE:

2000-03-03

NUMBER OF SEQ ID NOS:

1533

SOFTWARE:

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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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Matches:
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47.83%
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52.00
65.22%
47.83%
40.31%
                 ; TYPE: DNA
; ORGANISM: DROSOPHILA
US-09-614-150-35057
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                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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LENGTH: 16135
LENGTH: 16135
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GENERAL INFORMATION:
APPLICANT: APELICANTON VICKOLAI
APPLICANT: ALEXANDROY, NICKOLAI
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: THEREBY
TITLE REFERENCE: 2750-09659
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
LENGTH: 1244
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLO00728

CURRENT APPLICATION NUMBER: US/09/614,150

CURRENT APPLICATION NUMBER: 00/157,832

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-05

PRIOR PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-22

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2000-01-12-28

PRIOR PRIOR OFFICE SOURCES (60/173,383)

PRIOR FILING DATE: 2000-01-12-28

PRIOR PLICATION NUMBER: 60/173,383

PRIOR PLICATION NUMBER: 60/173,383

PRIOR PLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 2000-01-12-28

PRIOR FILING DATE: 2000-01-12-28

PRIOR FILING DATE: 2000-01-12-28

PRIOR FILING DATE: 2000-01-12-28
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
| LOCATION: (1)...(1244)
| OTHER INFORMATION: any n = a, g, c, t, unknown, or other
| NAME/KEY: misc_feature
| LOCATION: (1)...(1244)
| OTHER INFORMATION: (1)...(1244)
| STAG CONSENSUS (Clone Number:5tag_consensus)
| US-09-565-309A-52656
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
US-09-565-309A-52656/c
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Sequence 545, Application US/09595329A

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: VYACHESLAV, Brover
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
FILE REFERENCE: 2750-0948P

CURRENT APPLICATION NUMBER: US/09/595,329A

CURRENT FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3309

SOFTWARE: Patentin version 3.0
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.; OTHER INFORMATION: 40182 : FINISHED (Clone Number : FINISHED)
US-09-565-3098-62025
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Conservative:
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; OTHER INFORMATION: n is a, c, t, g, unknown, or
US-09-595-329A-545
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OTHER INFORMATION: Ceres Seq. ID no. 1013068
NAME/KEY: misc_feature
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ORGANISM: Arabidopsis thaliana
                                        NAME/KEY: misc_feature
LOCATION: (1)...(1230)
OTHER INFORMATION: any n = a,
NAME/KEY: misc_feature
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40.31%
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Best Local Similarity:
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APPLICANT: BROVER, Vyachesiav
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-0853P
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
SEQ ID NO 67147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62025, Application US/09565309A
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, NACAOLA1
APPLICANT: BROWER, VYGOHESIAV
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: UNMERR: US/09/565,309A
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
SEQ ID NO 62025
LENGTH: 1230
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OTHER INFORMATION: any n = a, g, c, t, unknown, or o

NAME/KEY: misc_feature

LOCATION: (1)..(999)

OTHER INFORMATION: 40182 : CDS (Clone Number : CDS)

US-09-565-309A-67147
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Conservative:
Mismatches:
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                 Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                           Sequence 67147, Application US/09565309A GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickola1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana
72.73%
50.00%
40.31%
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52.00
72.73%
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Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-565-309A-67147/C
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                                            Sequence 67148, Application US/09565309A

Sequence 67148, Application US/09565309A

GENERAL INFORMATION:
APPLICANT: ALEXAMINON, NICKOLAI
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-0833P
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
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Sequence 29368, Application US/09708427
Sequence 29368, Application US/09708427
GENERAL INFORMATION:
TATLE OF INVENTION: SEQUENCE-BETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION
CURRENT PELLING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 83364
SEQ ID NOS: 83364
SEQ ID NOS: 93368
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US-09-708-427-29368
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LOCATION: 1..984
OTHER INFORMATION: any
                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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Best Local Similarity:
Query Match:
 401 GCGGAT 396
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Pred' No.:
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RESULT 32
US-09-565-309A-32824/C
US-09-565-309A-32824/C
Sequence 32824, Application US/09565309A
; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 275-0-0853P
CURRENT APPLICATION NUMBER: US/09/565,309A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 68449
; SEQ ID NO 32824
; LENGTH: 641
                                                   TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(594)
CHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc_feature
LOCATION: (1)..(594)
COCATION: (1)..(594)
COTHER INFORMATION: 40182:107311 (Clone Number:Unique Sequence Identifier)
US-09-565-309A-32821
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| LOCATION: (1).(641)
| LOCATION: any n = a, g, c, t, unknown, or other
| NAME/KEY: misc_feature
| LOCATION: (1).(641)
| LOCATION: (1).(641)
| LOCATION: (1).(641)
| COTHEN INFORMATION: 40182:957281 (Clone Number:Unique Sequence Identifier)
| US-09-565-309A-32824
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Matches:
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Matches:
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 NUMBER OF SEQ ID NOS: 68449
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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458 GCGGAT 453
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US-09-565-309A-32821/C
; Sequence 32821/C
; Sequence 32821/C
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: THEREBY
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-0853P
; CURRENT APPLICATION NUMBER: US/09/565, 309A
; CURRENT FILING DATE: 2000-05-05
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TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
TITLE OF INVENTION: Sequences and Uses Thereof
FILE REPERENCE: CL000284
CURRENT APPLICATION NUMBER: US/09/528,237A
CURRENT APPLICATION NUMBER: US/09/528,237A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                          5 GlualaLeualaaspGlnThrAspAlaLeuGlnSerGluGlualaalaValValLysAla 24
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
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Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 1811, Application US/09528237A
; GENERAL INFORMATION:
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                                                 TYPE: DNA
ORGANISM: Drosophila
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                 SEQ ID NO 17589
LENGTH: 7206
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; SEO ID NO 13896
; LENGTH: 6398
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-681-13896
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND FILE REFERENCE: alono330
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 17580, Application US/60191637

Sequence 17580, Application US/60191637

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION UNMBER: US/60/191,637

CURRENT FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 42660

SOFTWARE: PASLEEQ for Windows Version 4.0

SEQ ID NO 17580
                                                                                                                                                                                                                                                                                             2298 GAGGAGGAGGAGGAGGAGGAGGAGGCCCCCAGGCAGAGGATGCCGCAGGGCTGCCGCC 2239
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Best Local Similarity:
Query Match:
DB:
                  TYPE: DNA
ORGANISM: DROSOPHILA
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Best Local Similarity:
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US-60-191-681-13896/c
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                                                    US-09-614-150-17530
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ORGANISM:
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SQUENCE 14400, Application US/60173464

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES;
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: PASSES for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: LJ, Perter W. D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOUIS2
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
                                                                                                                                                                                                                                                  2298 GAGGAGGAAGCTGACGAGGAGGACGCCCGAGGCAGGCAGCCGCAGCGCTGCCGCC 2239
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                   Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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Matches:
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CORGANISM: Drosophila
US-60-173-464-14400
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Best Local Similarity:
Query Match:
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Query Match:
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US-60-173-464-14400
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US-60-167-217-17589
                                                                Percent Similarity:
Alignment Scores:
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NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17530
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Best Local Similarity:
Query Match:
                          25 AspAsnAlaAla
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US-60-191-681-13897/c
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LENGTH: 3349
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APPLICANT: Venter.

APPLICANT: Venter.

TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING

TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL000392

CURRENT APPLICATION NUMBER: US/60/191,637

CURRENT APPLICATION NUMBER: US/60/191,637

NUMBER OF SEQ ID NOS: 42660

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17581

LENGTH: 3349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GlualaLeualaaspGlnThraspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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Mismatches:
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Mismatches:
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Matches:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,932
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PILING DATE: 1990-11-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-024
PRIOR FILING DATE: 2000-024
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
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; Sequence 17581, Application US/60191637
; GENERAL INFORMATION:
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41.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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LENGTH: 3349
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APPLICANT: L1, Peter, W.D.

TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
FILE REFERENCE: cl000390
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT APPLICATION NUMBER: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLO00728

CURRENT APPLICATION NUMBER: US/09/614,150

CURRENT FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PLING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR PLING DATE: 1999-12-28

PRIOR PLING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24
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Mismatches:
Indels:
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Sequence 17530, Application US/09614150
GBNRRAL INFORMATION:
APPLICANT: Venter, J. Craig
PAPLICANT: et al.
Sequence 13897, Application US/60191681 GENERAL INFORMATION:
APPLICANT: Li, Peter, W.D.
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957 GATGCTGCGGCG 946
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; LENGTH: 3046
; TYPE: DNA
; ORGANISM: Drosophila
US-60-173-464-14401
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; ORGANISM: Drosophila
US-60-167-217-17590
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-60-167-217-17590/c
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GENERAL INFORMATION:
APPLICANT: BOAZZI, VIVIEN:
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE
FILE REPREBUCE: CLO00058
CURRENT APPLICATION NUMBER: US/60/145,134
CURRENT FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 342
SEQ ID NO 143
LENGTH: 1785
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US-60-173-464-14401/c
US-60-173-464-14401/c
Sequence 14401, Application US/60173464
Sequence 114401, Peter W.D.
TITLE OF INVENTION: SOCIATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00173
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT PILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOCIWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                     5 GlualaLeualaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
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                                                                                             1783
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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; ORGANISM: Drosophila
US-60-145-134-143
                                : Drosophila
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
                                               US-60-142-845-289
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LENGTH: 1783
              TYPE: DNA ORGANISM: 1
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GENERAL INFORMATION:
Sequence 17580, Application US/60167217
GENERAL INFORMATION:
APPLICANT: LI, PETER W. D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLEUCIES ENCODING DROSOPHILA PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLO00152
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 3049
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US-09-614-150-17531/c
Sequence 17531, Application US/09614150
Sequence 17531, Application US/09614150
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: BETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL00078
CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
                                                                                                                                                                           5 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
                                                                                                                                         US-09-847-539A-6_COPY_59_86 (1-28) x US-60-173-464-14401 (1-3046)
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Mismatches:
Indels:
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Mismatches:
  Length:
Matches:
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US-08-621-425-49
                                                                                COUNTRY:
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GENERAL INFORMATION:
APPLICANT:
DOUGLAS Smith
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 495
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
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Matches:
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SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,002A
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
NAME: Mandragouras, Any E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
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STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                              ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity:
Query Match:
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US-08-621-425-49
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US-60-142-845-289
Sequence 289, Application US/60142845
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/142,845
CURRENT APPLICATION NUMBER: US/60/142,845
NUMBER OF SEQ ID NOS: 704
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 289
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
SOFTWARE: tar
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,425
FILING DATE: 25-MACH-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/561,469
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,032
FILING DATE: 07-JUNE-1995
ATTORNEY-YAGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 37-001CP2
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Helicobacter pylori
FEATURE:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 8mm cartridge
COMPUTER: SPARC station LX
OPERATING SYSTEM: sunOS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.9
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Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                02109-1875
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Best Local Similarity:
Query Match:
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145 ATACAAGCCTACAGGAGCAAATTGACGTTTAGATTCTCAAGAAAAGTCGTTAGCAAA 204
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Mismatches:
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Matches:
                                                                                                                                                 PFILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,405
FILING DATE: 01-APRIL-1996
FILING DATE: 01-APRIL-1996
PRIOR APPLICATION DATA: US 08/660,742
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA: US 08/736,791
FILING DATE: 05-SOCT-1996
PRIOR APPLICATION DATA: US 08/736,791
FILING DATE: 25-OCT-1996
PRIOR APPLICATION DATA: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/739,150
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELEFAX: (617)227-5941
INPORMATION FOR SED 1D NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 1239 base pairs
TYPE: NUCLEL CACLE
TYPE: NUCLEL CACLE
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                                                                    SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,739
FILING DATE:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
MEDIUM TYPE: CD/ROM ISO9660
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57.00
69.578
52.178
44.198
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                                              OPERATING SYSTEM:
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205 TGGGATAAC 213
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Query Match:
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GENERAL INFORMATION:
APPLICAT: DOUGLAS SMITH ET AL
APPLICAT: DOUGLAS SMITH ET AL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI VACCINE COMPOSITIONS THERE
NUMBER OF SEQUENCES: 608
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LeuGlualaLeualaaspGlnThraspalaLeuGlnSerGluGlualaalaValValLys 23
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mandragouras, Amy E.
RECISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19575
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/739,150
FILING DATE: 28-OCT-1996
PRIOR APPLICATION NUMBER: US 08/759,739
FILING DATE: 06-DEC-1996
PRIOR APPLICATION NUMBER: US 08/759,739
FILING DATE: 14-JULY-1997
ATTORNEY APPLICATION NUMBER: US 08/891,928
FILING DATE: 14-JULY-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature;
COCATION: 1...1239
PCT-US97-19575-51
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STATE: Massachusetts
COUNTR: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
                                         OPERATING SYSTEM:
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Best Local Similarity:
Query Match:
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ORIGINAL SOURCE
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                                                                    SOFTWARE
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Massachusetts

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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
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GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6_COPY_59_86 (1-28) x US-08-759-739-92 (1-666)
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Mismatches:
Indels:
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Matches:
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 37.001CP8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 Dase pairs
LENGTH: 666 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                       PRIOR AFPLICATION DATE:

PRIOR AFPLICATION NUMBER: US 08/487,032
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/60,742
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/60,742
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/736,791
FILING DATE: 25-OCT-1996
PRIOR APPLICATION NUMBER: US 08/736,791
FILING DATE: 28-OCT-1996
PRIOR APPLICATION NUMBER: US 08/736,791
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: US 08/739,150
FILING DATE: 28-OCT-1996
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US/08/759,739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.59
57.00
69.57%
52.17%
44.19%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AlaAspAsn 26
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US-08-993-002A-4234
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-759-739-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
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229 ATACAAGCCCTACAGGAGCAAATTGACGCTTTAGATCTCAAGAAAAAGTCGTAGCAAA 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-847-539A-6_COPY_59_86 (1-28) x US-08-993-002A-4234 (1-666)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELLCOBACTER PYLORI AND VACCINE COMPOSITIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                            APPLICATION ...
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: MANdragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)722-7400
TELEPHONE: (517)742-4214
INFORMATION FOR SED ID NO: 4234:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
TYPE: OLIVERISS: OLIVER
                                                                                                SUFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
FILLIG DATE:
              ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pCT-US97-19575-51
; Sequence 51, Application PC/TUS9719575
GENERAL INFORMATION:
; APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COC
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1...666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.59
57.00
69.57%
52.17%
44.19%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NC TITLE OF INVENTION: RE TITLE OF INVENTION: VP NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 TGGGATAAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 AlaAspAsn 26
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STATE: Massa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-993-002A-4234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
COUNTRY:
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COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-847-539A-6_COPY_59_86 (1-28) x US-08-759-739-43 (1-576)
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CP8
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617)227-7400
IELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/561,469
FILING DATE: 17-NOV-1995
FILING DATE: 01-APRIL-1996
FRIOR APPLICATION NUMBER: US 08/630,405
FILING DATE: 01-APRIL-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,742
FILING DATE: 06-JUN-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/736,791
FILING DATE: 25-CCT-1996
PRIOR APPLICATION APPRIL
APPLICATION NUMBER: US 08/736,791
FILING DATE: 28-OCT-1996
FILING DATE: 28-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
1...576
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-993-002A-4232
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US-08-759-739-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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Sequence 92. Application US/08759739
Sequence 92. Application US/08759739
GENERAL INFORMATION: WOLLET AL
TITLE OF INVENTION: WOLLETC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: WOLLETC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI VACCINE COMPOSITIONS THERE NUMBER OF SEQUENCES: 608
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE STREET: 60 State Street, Suite 510
STREET: Massachusetts
COUNTRY: USA
COUNTRY: USA
ZIP: 03109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
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Matches:
Conservative:
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Indels:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOCHWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                  NAME: MANDEAGOURAS, AND ERECTSTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 576 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Helicobacter pylori
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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57.00
69.57%
52.17%
44.19%
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 TGGGATAAC 213
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Query Match:
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Sequence 282, Application US/08561469A

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF SEQUENCES: 994
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-847-539A-6_COPY_59_86 (1-28) x US-08-487-032A-282 (1-576)
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEGITICS NUMBER OF SEQUENCES: 880 CORRESPONDENCE ADDRESS:
                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,032A

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-001

TELEPHONE: (617)227-7400

TELEPHONE: (617)227-7401

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 282:

SEQUENCE CHARACTERISTICS:

LENGTH: 576 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                               STATE: MAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STATE: Massachusetts COUTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.41
57.00
69.57%
52.17%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109-1875
COMPUTER READABLE FORM:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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Sequence 43, Application US/08759739
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH ET AL
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI VACCINE COMPOSITIONS THERE
NUMBER OF SEQUENCES: 608
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6_COPY_59_86 (1-28) x US-08-561-469A-282 (1-576)
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,469A
FILING DATE: 17 *NOV-1995
PRIOR APPLICATION NUMBER: US 08/487,032
PRIOR APPLICATION NUMBER: US 08/487,032
FILING DATE: 07-*JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGOLICAS, AMY E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: GTN-001CP
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
CUNTRY: USA
21P: 02109-1875
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APPLICATION NUMBER: US 08/487,032
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APPLICATION NUMBER: US/08/759,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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US-08-561-469A-282
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09847539A
GENERAL INFORMATION:
APPLICANT: BJOTCK, LARS H
APPLICANT: RASABNUSSEN, MAGNUS
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084.415US / N.75312B
CURRENT APPLICATION UNMBER: US/09/847,539A
CURRENT FILING DATE: 2001.05-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 13
LENGTH: 777
APPLICANT: Rassmussen, magnus
TITLE OF INVENTION: STREPTOCCCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100.084.4150.12
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 764
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US-09-847-539A-15
Sequence 15, Application US/09847539A
GENERAL INFORMATION:
APPLICANT: Bjorck, Lars H
APPLICANT: Rassmussen, Magnus
                                                                                                                                                                                                                                                                                                                                                                        379 GTTGTTAAAGCGGATAACGCTGCT 402
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                                                                                                                                        ; ORGANISM: Streptococcus pyogenes US-09-847-539A-27
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Query Match:
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Best Local Similarity:
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US-09-847-539A-13
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US-09-489-039A-318
US-09-489-039A-318
Sequence 318, Application US/09489039A
GENERAL INFORMATION:
TOTAL TRED OF INVENTION:
TITLE OF INVENTION: NUGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUGLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 928
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US-08-487-032A-282
; Sequence 282, Application US/08487032A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6_COPY_59_86 (1-28) x US-09-489-039A-318 (1-828)
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TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN FILE REFERENCE: 100084.415US / N.75312B CURRENT APPLICATION NUMBER: US/09/847,539A CURRENT FILING DATE: 2001-05-01 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO.15 LENGTH: 853
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Matches:
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                                                                                                                                          TYPE: DNA ORGANISM: Streptococcus pyogenes
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Pred. No.:
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APPLICANT: Bjorck, Lars H
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50148, A
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35057, A
1340, Ap
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GENERAL INFORMATION:
APPLICANT: Blorck, Lars H
APPLICANT: Blorck, Lars H
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084.415US / N.75312B
CURRENT APPLICATION NUMBER: US/09/847,539A
UNUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 469
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US-60-191-681-13897
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US-60-173-464-14400
US-60-173-464-14400
US-60-173-464-14400
US-69-55-3094-32821
US-09-565-3094-32824
US-09-565-3094-67148
US-09-565-3094-67147
US-09-565-3094-67147
US-09-565-3094-67147
US-09-565-3094-67147
US-09-565-3094-67147
US-09-565-3094-5255
US-09-614-150-35657
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Conservative:
Mismatches:
Indels:
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US-60-171-627-1945
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US-09-614-150-17531
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ORGANISM: Streptococcus pyogenes
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US-09-847-539A-14
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Query Match:
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Sequence 12. Application US/09847539A
GENERAL INFORMATION:
APPLICANT: Bjorck, Lars H
APPLICANT: Rassmussen, Magnus
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084 4150S / N.75312B
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ 1D NOS: 30
SOFFWARE: Patentin Ver. 2.1
APPLICANT: RASSENCESEN, MAGINES
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084 41512 S/
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEO ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
LENGTH: 504
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; ORGANISM: Streptococcus pyogenes
US-09-847-539A-12
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Best Local Similarity:
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LENGTH: 654
                                                                                                                                                                 TYPE: DNA
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-WODEL-frame+_pin.model -DEV-x1h
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-Q-COGO12_1/USPFO_SPOOL/USOB47539_Frunat_10102002_092549_3486/app_query.fasta_1.526
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -FRANS-human40.cd1
-LIST-45 -DOCALIGN-200 -THR-SCORE=-pct -THR_MAX-100 -THR_MIN-0 -ALIGNA40
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-YGAPOP-60 -YGAPEXT-60 -DELEXT-7
                                                                                                              Search time 553.112 Seconds
(without alignments)
1095.215 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                          - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                   21979536 seqs, 10817449327 residues
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                            129
1 SDALEALADOTDALOSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          US-09-847-539A-6_COPY_59_86
                                                                                                              October 13, 2002, 02:20:12
                                                                                                                                                                                                                                                                                       Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                      Scoring table:
                                                                          OM protein
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                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| SUMMARIES | Description                      | Sequence 14, Appl | Sequence 16, Appl | Sequence 12, Appl | Sequence 27, Appl | 13,               | 15,               | Sequence 318, App  | Sequence 282, App  | Sequence 282, App  | Sequence 43, Appl | Sequence 4232, Ap   | Sequence 92, Appl | Sequence 4234, Ap   | Sequence 51, Appl | Sequence 250, App | Sequence 4235. Ap   |
|-----------|----------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|---------------------|-------------------|---------------------|-------------------|-------------------|---------------------|
|           | Ω                                | US-09-847-539A-14 | US-09-847-539A-16 | US-09-847-539A-12 | US-09-847-539A-27 | US-09-847-539A-13 | US-09-847-539A-15 | US-09-489-039A-318 | US-08-487-032A-282 | US-08-561-469A-282 | US-08-759-739-43  | US-08-993-002A-4232 | US-08-759-739-92  | US-08-993-002A-4234 | PCT-US97-19575-51 | US-08-759-739-250 | US-08-993-002A-4235 |
|           | DB                               | 32                | 32                | 32                | 32                | 32                | 32                | 18                 | ထ                  | σ                  | 11                | 13                  | 11                | 13                  | -                 | 11                | 13                  |
|           | %<br>Query<br>Match Length DB ID | 469               | 504               | 654               | 764               | 777               | 853               | 828                | 576                | . 576              | 576               | 576                 | 999               | 999                 | 1239              | 1239              | 1239                |
|           | %<br>Query<br>Match              | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 45.0               | 44.2               | 44.2               | 44.2              | 44.2                | 44.2              | 44.2                | 44.2              | 44.2              | 44.2                |
|           | Score                            | 129               | 129               | 129               | 129               | 129               | 129               | 58                 | 57                 | 57                 | 57                | 57                  | 57                | 57                  | 57                | 57                | 57                  |
|           | Result<br>No.                    | 1                 | 7                 | ٣                 | 4                 | ស                 | 9                 | 7                  | 8                  | σ                  | 10                | 11                  | 12                | 13                  | 14                | 15                | 16                  |

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```
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr]
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharcomyces bayanus var. uvarum, Saccharcomyces ervazzii, Zygosaccharomyces rouxii, Saccharcomyces servazzii, Zygosaccharomyces rouxii, Saccharcomyces kluyverimyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <577. .>846
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/note="similar to Saccharomyces cerevisiae ORF YOL109w [
2E01 ; zeocin resistance ]"
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a 205 c 189 g 240 t 3 others
2 (bases 1 to 848)
Souclet,J.L., Algle,M., Artiguenave,F., Blandin,G.,
Souclet,J.L., Algle,M., Artiguenave,F., Casaregola,S.,
Belotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
Malpertuy,J., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
yeast species for molecular evolution studies(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to Saccharomyces cerevisiae ORF YOL110w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 LysAlaAspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 AAAGCTGAAACTGCCGCTGAAGACGTCCAACAAAAGCTGGATGAAACCAAGGAGTCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Saccharomyces bayanus"/strain="CLIB 533"
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHR5; RAS suppressor]
1 putative frameshift(s)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="end : T7"
                                                                                                                                                                                                                                                                            3 (bases 1 to 848)
Genoscope.
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58.82%
41.18%
11.33%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
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       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                       PUBMED
REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                               JOURNAL
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Search completed: October 13, 2002, 03:00:40 Job time : 1854.74 secs

gene

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gene

CDS

gene

gene

CDS

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DEARSLGLNYTRLRYFULYCATLITASTVATAGITGWYGLVVPHIARLLTGHNHQOLL
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                                                                                                                    /note="probable ABC transporter protein (permease),similar to ABC transporter permeases e.g. [Haemophilus influenzae] gi|2501391|sp|Q57130|YE71_HAEIN percent identity 40 in 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSO618W 848 bp DNA linear STS 10-JAN-2001 T7 end of clone ASOAA018G01 of library ASOAA from strain CLIB 533 of Saccharomyces bayanus, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 111928 GCTGACATTCAGCAGGGATGCATCGAGTCAGCCGGCAGGCGGCAGAAAGTGCAGCC 111987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 112048 AGTGAGTCATTACAAAGTGCAACAGATGCTGAGTTGTCAAAAAAGACGGCAGAAAGTGCA 112107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 848)
Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P., Aigle,M. and Durrens,P.
Genomic Exploration of the Hemiascomycetous Yeasts: 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ECs1699"
/note="probable ABC transporter, weakly similar to iron
(iii) ABC transporter, ATP-binding protein [Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 111988 GCTGCAAAGCAGTCAGAGGCGTCCTCGGCCTCTGCGGCCCGCTCAAAAGCC
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27
7
34
0
TQGLPTEQLTTNKLAALYRVSADQIHHHLSAISH"
Complement(4854. .5834)
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Mismatches:
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Matches:
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FEBS Lett. 487 (1), 37-41 (2000)
11152880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5834, ,6856)
/gene="ECs1699"
complement(5834, ,6856)
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                                                /gene="ECs1698"
complement(4854. .5834)
/gene="ECs1698"
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::: ||||||||||
Db 112108 GCCGGTAATGCAGCCAGGGATGCA 112131
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AL399990.1 GI:12155259
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Saccharomyces bayanus
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Best Local Similarity:
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<u>N</u>O.
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KEYWORDS
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Shiga toxin 1 genes of the prophage VTI-Sakai carrying the Ol57:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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/product="putative TonB dependent outer membrane receptor"
/protein_id="baB35116.1"
/db_xref="G1:13361158"
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YDGNIDILARILITNNLGAVEVSKGYSSLLQGPNQMGGAINITTQKPTKPLEASLGYRQG
WSRSQDNAYDMHASFAASSELGYLOVSGSQLKODFLGLPHGVNNDIAGKHGKMINSSA
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QGTTQLNDRFTLKSRLYRDTFENTLMMYNSLADLKNKKGSYSHYSDYSDGAGLQLAAD
VRENDLLTFAVNWKDDVHREKGAPHAAYDRYEDRTWSLASEYOWAAADNVDVVAGISY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="probable TonB dependent outer membrane receptor, similar to TonB dependent outer membrane receptor PrrA [Escherichia coli CFT073] gi|3661477|gb|AAC61709.1| percent identity 97 in 656 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MRLKKHYLCTALSLAFTQQAVAAQESDSLTVWSSPVSSTTTTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:kenegen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to YMCE_ECOLI g1|1787445 percent identity 97 in 84 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                           Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                4 (sites)
Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Ida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
Syst. Appl. Microbiol. 23 (3), 315-324 (2000) 20557356
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/organism="Escherichia coli 0157:H7"
/strain="0157:H7"
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/product-"inyothetical protein"
/protein_id="BAB35115.1"
/db_xref="G1:13361157"
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/gene="ECs1693"
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/gene="ECs1693"
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126. .380
/gene="ECs1692"
126. .380
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/transl_table=11
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/gene="ECs1692"
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                                                                       Yokoyama, K.,
Yutsudo, C.H.
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                                                                                                                                                                                                                                                                                                                                                                      of LMFLCHR34 from base 1600001 (AL499623 Leishmania major chromo
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Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S.,
Makino, K., Ishli, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T.,
Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaqa, T., Honda, T.,
Sasakawa, C. and Shinagawa, H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
derived from the Sakai outbreak
Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP002556 291136 bp DNA linear BCT 07-MAR-2001
Escherichia coli 0157:H7 DNA, complete genome, section 7/20.
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli O157:H7 (strain:O157:H7, sub_strain:RIMD 0509952)
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 AsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 AlalleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGlu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp 83
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Mismatches:
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AP002556.1 GI:13361156
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Best Local Similarity:
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LMFLCHR34_11
LMFLCHR34_11
LMFLCHR34_13
LMFLCHR34_14
LMFLCHR34_15
LMFLCHR34_16
                          LMFLCHR34_03
LMFLCHR34_04
LMFLCHR34_05
LMFLCHR34_06
LMFLCHR34_07
LMFLCHR34_08
LMFLCHR34_09
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NLNSMWAVKLQQMQDGRLYIAGIGAGIENTPAGMQSQVLLAADRIAMINPANGNTKPM
FYQQGDQIFMUEVFLKYLTRATITSGGNPAFSIFPDGRLTARNADISGNVANSGTL
NNVTINENCRVLGKLSANQIEGDLVKYVGKAFPRDSRAPERWPSGTITVRVYDDQPFD
RQIVIPANAFSGARHEKEHTDIYSSCRLIVRKNGAEIYNRTALDNTLIYSGVIDMPAG
HGHMTLEFSVSAWLVNNWYPTASISDLLVVVWKKATAGITIS"
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//functe="Residues Related)"
//note="Residues 1 to 451 of 451 are 96.93 pct identical to residues 1 to 391 of 391 from Genpept121:
db)|Rab19563.11 (AP000400) host specificity protein J (Escherichia coli 0157:H7]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Phage or Prophage Related)" of 224 of 224 are 92.37 pct identical to residues 14 to 246 of 247 from Genpept121: dbj|BAB19565.11 (AP000400) tail assembly protein K [Escherichla coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AaKi6946.1"
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//db_xref="GI:13259575"
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SVRNGKWRLIYSGEGGGGGGGGGGRAHPPREARDNLKGTOMMSVIDAIGEGPIEGPVKGL
GSILVNKTPLTDTDGNPVIHGVTAVWRAGEQEGTPPEGFESSGAETGLGVEVTRAKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRTITSANIDRLRVTFGVQSLLETTSKGDRNHSSVRLLIQLQRNGNWVTEKDVTINGK
TTSQFLASVTLDNLPERPENIRWVEETADSTSDQLQNKTLWSSYTEIIDVKQCYPNTA
TYGQPDAGOGGGGGGWTVNTHRGRILQVPSNYDPEKRTYSGINDGSLKPAYSNNPAW
CLWDMLTHPRYGWGKTGAADVRANLYALAQYCDGTVPGGFGGFERPRATFRYLLSGO
RKAWDVLSDFCSAMRCMPVWNGQTLTFVQDRPSDVVWPTPAVMWWMITAWGFATASA
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SLOVPGFREGONBGWYQIRALMGSLASPAVARLHEGLGGGTYVHIVPRLAGAGKGGL
SLULGAAAIVGSFFTAGASBALMGSALAAGGFSATTMLFSLGASMILGGVAOMLAPKA
KTPDYRATDNGROUTYFSSLDNMIAQGNPMVPYGEMLYGSRRISODISTRDBGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="z6032"
/function="putative factor; DNA packaging, phage assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function "putative factor; DNA packaging, phage assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"putative tail component of cryptic prophage CP-933p"
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/transl_table=11
product="putative tail assembly protein of cryptic
prophage CP-933P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAK16947.1"
/db_xref="G1:13259576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="z6031"
complement(7105. 7785)
/gene="z6031"
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complement(7683. .8357)
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                                                                                                                                            complement(5588, .6943)
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                                                                                                                                                                                                                                        /gene="26030"
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0157:H7]"
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Alignment Scores: 0.496 Length: 9331
Score: 89.00 Matches: 27
Score: 50.00$ Conservative: 7
Best Local Similarity: 39.71$ Mismatches: 34
Query Match: 11.45$ Indels: 0
DB:
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50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69

US-09-847-539A-6 (1-159) x AE006458 (1-9331)

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18) of LMFLCHR34 from base 1700001 (AL499623 Leishmania major chr
                                                    1971 GCTGCAAAGCACTCAGAGGCGTCCTCGTCCTCGCGCCCCTCAAAAAGCC 1912
                                                                                                            111 | 11|::: | 11|11| | 11| | 11| | 11| | 2031 GCTGACAGACAGAGAGAGGCGGCAGAAAGTGCAGCC 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 AsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGlu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 GCCGAGCATGCCCGCGTGGTTGCTGCGCTGAGGCGAAGGCGTGTGCTGCCGAGCGTGAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AlaileGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGlu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GluAlaGluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence split into 18 fragments LOCUS LMFLCHR34 Accession AL499623 Fragment Name Begin End LMFLCHR34_00 110000 LMFLCHR34_01 100001 210000
                                                                                                                                                                                                                                         LOCUS LMFLCHR34 Accession AL499623
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36
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Mismatches:
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Matches:
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210000
310000
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510000
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                  Fragment Name
LMFLCHR34_00
LMFLCHR34_01
LMFLCHR34_02
LMFLCHR34_03
LMFLCHR34_04
LMFLCHR34_05
LMFLCHR34_06
LMFLCHR34_06
LMFLCHR34_06
LMFLCHR34_06
LMFLCHR34_06
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LMFLCHR34_13
LMFLCHR34_14
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LMFLCHR34_10
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Continuation (18
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EAGRYSMDVEGGYSTILLVEGFPPHAGTTTVYEDSOPGTLANFLGAMSEDDVRPEA
LRRFELMVEEAARHAEEAKRAGFAETSARAAGISASOAEERNANADTSAGDASESAR
QAAESAAAAROSEEASSASAAQARASESLOSATDAELSKKTAESAAGNARDATTA
AEKARESAESAGSAGAARAKASESLOSATDAELSKKTAESAAGNAARDATTA
AEKARESAESAGSAGAARANIPTVVGPPGFKGEPCPAGPOGPKGDKGERGD
TGPAGATGERGPAGDAGPKGDRGERGETGLTGNAGPOGPKGDTGAGP
TFLARKDTTRYQGFFKGDFKGDFGFYOIRFRLGPASIIETNNGWFPGTDGALITGL
CFLARKDTTRYQGFFQLLQVRRGDGFWQDVKGLDEVGSDTGRTGE"
complement(2624..3223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prophage Related)...
/note="Residues 1 to 199 of 199 are 96.48 pct identical to residues 1 to 199 of 199 from GenPept121: dbj|BAB19561.1|
(APD000400) outer membrane protein Lom precursor [Escherichia coli 0157:H7]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MVVDDNGVGFRYSFSALKDRHTAVEVNYTDPQNGWQTSTELVED
PEAILRYGRILKMDAFGCTSRGQABRAGIAVIKTGLLETQTVDFTLGSGGIRHTPGD
ITAICDNYAGTWTGGRVLSTDAASRTJTLDFEVTPETGAATVNLINGSGRVVSVDI
TAHPAPDRIQVSTLEDGOVETYGVWGLSLPSICRRLFRCVSYRENTDGTFATRAVOHVP
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IIPEQDRVITQVVILDADKKQIQCVVRPLQILRADGFWENIGGMK"
complement(1159. .2472)
/gene="z6027"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLRLTSGKGTDARLVTTAITADTEHRFSGLPLGEYTLTVRAINSYGQGEPATTTFRI
AAPAARSKIELTPGYFQITAPPLLAYYDPTVQFERWSEKRIKIDIRQYGTAARYLGSA
LVWIAGSIN IKPGHPYYFYTRYPWYGKSAPVBAVGRASDDAEGYLDFFKGEIGKTHL
AQELWTQIDNGQLAPDLAEIRTSITNVSNEITQTVNKKLENQSAAIQQIQKVQVDTNN
                                                                                                                                                                                                                                                         or Prophage Related)"

Ante-"Residues 1 to 437 of 437 are 94.96 pct identical to residues 1 to 437 of 437 from GenPept121: dbjlBAB19560.11 (AP0000400) tail fiber protein [Escherichia coli 0157:H7]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mrkicavilsavvwqvaaatpasaaehgstlsagylhastnvpg
spobdkgivktrktrekmaletlstrstranaebgvtrytsdyrrenebsyrnkwag
psyravnewtsayamagvaysrytbygdylstrytdynkgkthdyltgsddgrhsytslaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="putative structure; Structural component (Phage
                                                                                                                                                                                                                             /function="putative structure; Structural component (Phage
                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="putative tail fiber protein of cryptic prophage
CP-933p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative membrane; Other or unknown (Phage or
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/product=Poutative Lom-like outer membrane protein of cryptic prophage CP-933P*
/protein_id="AAM16944.1"
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/transl_table=11
/product="putative tail component of cryptic prophage
CP-933p"
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/gene="lomp"
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                                                                                                                                                                        complement(1159. .2472)
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/note="Residues 1 to
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                                                                                                                   gene
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ELEFIZGFWNROFEALRORMLSMLSDSGEAQSOBSIQOKISQCKFPVSSGNFQCPPESI
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KCVYDPIKGNFIIKOF
                                                                                                                                                                                                    AE006458 9331 bp DNA linear BCT 21-MAR-2001
Escherichia coli 0157:H7 EDL933 genome, contig 2 of 3, section 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Residues 53 to 176 of 176 are 37.50 pct identical to residues 13 to 140 of 140 from GenPept121: db]|BAA36750.1| (AB016764) ORF4 [Escherichia coli]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 9331)
Plunkett,G. III.
Direct Submission
Submitted (12-FEB-2001) Laboratory of Genetics, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706-1577, USA
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 9331)
Perna, NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Maybew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grobbeck, E.J., Davis, N.W., Lim, A., Dimalanta, R., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A.
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/product="unknown protein encoded by cryptic prophage
CP-933P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
21074935
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/product="unknown protein encoded by cryptic prophage
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complement(201. 731)
/gene="26025"
complement(201. 731)
/gene="26025"
/function="orf; Other or unknown (Phage or Prophage
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    9331 / Organism="Escherichia coli 0157:H7 EDL933"

                                                        108 ValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
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/serotype="0157:H7"
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AE006458.1 GI:13259569
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KKOVRSAQKGNLTNTINSKSYSDAVREVVAIREVENEKMLAOQEADKAALES
KOJENONAINTVAANTKOJE BINKAALATORAQLEAAQLELSAQLTTYONEKASLIQAK
AQAECAARKAARARAAEAKAQAEAKAQAESVAKAQAAAVESATAPTETVOTOPRTE
SYDSSYTTYPMOSCTTAATATATREPKYTOPSVYTYRAVEAPKAVVSSTPRAVSKPVR
SYDSSYTTYPMOSCTAGARAARAANGRYWGNANGNGASARAACYSVOTTPRVOAVAVWP
YDGGGYGHVAVVTSVANNSSIOWMESNYAGNNSIGNYRGSFNPSASGSVYIIYPN"
Identification and molecular analysis of PosB, a protein required for cell wall separation of group B streptococcus J. Bacteriol. 183 (4), 1175-1183 (2001)
                                                                   2 (bases 1 to 2437)
Reinscheid, D.J.
Burect Submission
Submitted (06-APR-2000) Reinscheid D.J., Microbiology and
Blotechnology, University of Ulm, Albert-Einstein-Allee 11, Ulm,
D-89081, GERMANY
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1029 GTTGCTATTCGTGAGGTTGTTTCAGCTAATGAAAAGATGTTAGCACAAAAGAGGCTGAC 1088
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/strain="6313"
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Conservative:
Mismatches:
Indels:
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/protein_id-"CAC28144.1"
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1979. .2002
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.47. .2002
/gene="pr
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607. .613
/gene="pscB"
627. .2002
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/gene="pcsB"
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TITLE
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Streptococcus agalactiae
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Reinscheid, D.J., Gottschalk, B., Schubert, A., Eikmanns, B.J. and
Chhatwal, G.S.
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-441L2"
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160980:
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Mus musculus clone RP23-441L2, WORKING DRAFT SEQUENCE, 56 unordered
pieces.
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DOE Joint Genome Institute.
Direct Submission
Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 15, 2000 this sequence version replaced gi:6980210.
                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 269726)
DOE Joint Genome Institute.
                  Summary Statistics
Consensus quality: 205453 bases at least Q40
Consensus quality: 22960 bases at least Q30
Consensus quality: 229624 bases at least Q30
Consensus quality: 229624 bases at least Q30
Consensus quality: 229624 bases at least Q30
Estimated insert size: 240000; pulse field gel estimation
Estimated insert size: 240205; sum-of-contigs estimation
Quality coverage: 8.31 in Q20 bases; pulse field gel estimation
Quality coverage: 8.11 in Q20 bases; sum-of-contigs estimation
• NOTE: This is a "working draft' sequence. It currently
• consists of 56 contigs. The true order of the pieces
• is not known and their order in this sequence record is
GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125
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Web site: http://www.jgi.doe.gov
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Center: Joint Genome Institute
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="FLYBASE: FBan0004067"
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/evidence=not_experimental
join(46218. .46232,46434. .
48515. .51130)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "gene-"pug"
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Best Local Similarity:
Query Match:
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Pred. No.:
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HPAFNAITFSNRVREICWQLNYNKPAVCQSMYIYKNPGVGGEVTPHQDSWFLHTDPNS
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FTPMQVSKGTCILIHGNVVHKSEPNRSQKSRHAYTFHVIETENNVKYSEDNWLQAPKD
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                                                                                                                                                                  TEDFRALNVGFAMDEGLASPDEOLPLFYAERAVWRVYFNISGTAGHGSLLLPNTAGEK
LNYTVGKMBERRSQVQRLAVDNNELLYGGOVTTINTEKGGGGVGNVVPPEDLMVCPDCR
LALDVDFEBFEANHKWGADVGGGTEITYEOGKQPKVPPTAIDGSNPFWLAFKRATDEM
HISIKPQIFTGGTDSRYIRAVGIPALGFSPMNNTPVLLHDHDEFIQADIYLRGVOIFO
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RRYRNKDVTLSLPEGKTLRDIKWFSVWCDEFAVNFGDVSIPPNLDFPRPQKISALRGV
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RYERKTIVLTLPEDLTIFDIGHFGVWCEAFTVDFGHVRLPEGLNVPFSLKMLGISPQV
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/db_xref="FLYBASE:FBgn0037821"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CG14688"
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Arthropoda; Tracheata; Hexapoda; Insecta;
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MEDLINE
REFERENCE
AUTHORS
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JOURNAL
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AE003688 AE002708
HTG.
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4AWLDLRFLFWLAPIVFSLILSPFVSVISSRATVGLRTKRWKLFLIPEEYSPPQVLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D 185857 GCCACGACGCATCCACGAAGGCGACAGGGAGCTGGTAGTGCGACGCAGCAGCAGCTCAG 185916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 185737 AGCGCAGAATCCTCAAAAACGCTGCCGCATCGTCAGCCAGTTCGCGGGGTCATCGGCA 185796
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to MSYB_ECOLI 91|1787289 percent identity 99 in 125 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 185797 TCATCTGCGTCTGCTTCAAAAGATGAGGGGGACCAGACAAGGGGTCAGCAGCGAAGAGGG 185856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 SerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspVal 129
                                                                                                                                                   note="identical to YCEK_ECOLI gill787288 (Conserved C.coli K-12)"
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Mismatches:
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                                                                                                               7832. .8059
/qene="ECs1428"
                                                                                             /gene="ECs1428"
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Drosophila melanogaster
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AE003688/c
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EUKARYOGEA MEGEZORA ATLINOGORA; TERGRAGAEA; HERADOGEA; INSECTA;

RUSCOMORPHA: EPHOYGICIGA: DIOSOPHILIGAE: DESOPHILA.

EL (DASSES I TO 224759).

RADAMALIGAE, C. SCHEEF, S. E., LI, P. W., HOSKINS, R.A., GAILE, R.F., GAOGOGER, R.A., LEWISS, E.P., LI, P. W., HOSKINS, R.A., GAILE, R.F., GAOGOGER, R.A., LEWISS, E.P., RICHARGE, S.C., CABMDE, M., PREDIGER, B.D., BRANCHIGAE, G., BAYCHER, E.G., Hell, G., Nalburner, M., PREDIGER, B.D., MAIN, C., ROGPER, Y. H., BLAZE, R.G., CHAMDE, M., PREDIGER, B.D., MAIN, CANDON, R.C., ROGPER, Y. H., BAYCHARL, D., BAILA, M., BASU, A.,

HAINOS, C.L., ADVILL, J.F., AGDASHON, M., BASU, A.,

BAXORGHE, J., BAYCHARCH, D., BAILAW, R., BESON, K.Y.,

BANCHAL, M., BERMAN, B.C., BAYCHARL, D., BOLSHAKOY, S., BOLKOYA, D.,

BOCK, D., BOUCK, J., BOCKSELIP, P., BOCHIGLE, P., BURLIS, K.C.,

BUSCA, M., CAWIER, J., CANGREIL, D., BOLSHAKOY, S., BOLKOYA, D.,

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ROLLAGA, J., PULLI, V., PEASED, D., MELSON, K., NELSON, K., NELSON, K., MUSSKEN, M., WAGASATHAN, M., SALDAR, M., WOLLAGA, M., WELSON, K., MUSSKEN, M., WELSON, K., SHIP, M., SALDAR, M., WOLLAGA, M., SALDAR, M., WOLLAGA, M., WELSON, K., MUSSKEN, M., WELSON, K., SHIP
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Adams, M.D., Cellhker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="CT20161"
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us-09-847-539a-6.rge

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                                                                                                                                                                                                                                                                                                            Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin I genes of the enterchemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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NSLRLVAANSYTSVAFPAISTGVYGYPRAAAABIAVKTVSEFITRHALPEQVYFVCXD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6679-2047)
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"similar to B1045_ECOLI g1|1787283 percent identity 100 in 177 aa (Conserved in E.coli K-12)"
                                                                                                                                                                             3 (sites)
Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishil,K., Hattori,M., Abe,H., Iida,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (bases 1 to 222605)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ECs1424"
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                                Comparative analysis of the whole set of rRNA operons between an enterchemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yokoyama, K., Han, C.-G., Ohtsubo, E., Nakayama, K., Murata, T., Tanaka, M., Tobe, T., Iida, T., Takami, H., Honda, T., Sasakawa, C., Ogasawara, N., Yasunaga, T., Kuhara, S., Shiba, T., Hattori, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .222605
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                                                                                                            Syst. Appl. Microbiol. 23 (3), 315-324 (2000) 20557356
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MEDLINE
REFERENCE
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JOURNAL
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MEDLINE
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AUTHORS
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                                                   TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGQVYGLSARGLAIDTALPSGEEFPRFKEFWIERPKPTDKRLTIYALLDSPRATGAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGSILSHDFVEAALMRRAGWGVWIAYDLPGSYEELPPNILDEIKRDRRWCHGNIMNF
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gill787287 percent identity 100 in 847 as but differs at
N-ter (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                       complement(2038. .3195)
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Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishli, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T., Sanamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and Shinagawa, H. Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7 Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AP002555 222605 bp DNA linear BCT 07-MAR-2001
Escherichia coli 0157:H7 DNA, complete genome, section 6/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 151518 GAGGAGGCAGCCGCCAAAAAGGCCGCCGAGGAAGCTGCCCAAAAAGGCTGCCGAAGAAGGC 151459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 151698 GAAGAGGCTCTCCTGGCTGAAGCTGCCGCAAAAAGCAGCCGAAGAAGCTAAAGCCCTA 151639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 151578 GCCGCCCAAAAGGTCGCCGAAGAAGCTGCCCAAAAAGCTGCTGAGGAAGCTCGCCTAGCA 151519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                    /map- cc. cc. bacRE29B06 (D712)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6)"
a 38195 c 37760 g 51671 t
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
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                                                                                      melanogaster"
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                                                                                                     /strain="y; on bw sp"
/db_xref="taxon:7227"
/chromosome="3R"
/map="86C-86C"
                                                                                   /organism-"Drosophila
                             Location/Qualifiers
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AP002555.1 GI:13360886
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E (Dases 1 to 179669)

S Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.M., Evans, C.A., Goczyne, J.D., Amanatidea; P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D. Banzon, J., Beson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., McIntosh, T.C., Moyim, Murphy, B., Nelson, C., Melson, K.A., Nunco, J., Paragas, V., Park, S., Patel, S., Patel, S., Pteiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 3R, region 86C-86C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO08089 179669 bp DNA linear INV 24-FEB-2001
Drosophila melanogaster, chromosome 3R, region 86C-86C, BAC clone
BACR29806, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                            24842 AAAGCCGCTGAAGATGCTGCCCAGAAAGCTGCCGAAGAAGCGCGTCTAGCGGAGGAGGCCT 24783
                                                                                                                                                                                                                            86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
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                                                                                                                                                                                                                                                                         GCCGCCCAAAAGGTCGCCGAGGAAGCTGCCCAAAAAGCTGCTGAGAAGGTCGCCTAGCA
                                                        24902 GAAGAGGCTCTCCTGGCTGAAGCTGCCGCCCAAAAAGCAGCCGAAGAAGCTAAAGCCCTA
GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu
                                                                                                              66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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AC008089 AC007806
AC008089.3 GI:13027515
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fruit fly.
Drosophila melanogaster
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AC008140
HTG.
                                  AC017732 54784 bp DNA Linear HTG 10-DEC-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA dentified as CDM:10211903 by the submitter. For more information on this record e-mail to fly@celera.com.
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                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 54784)
Adams,M. and Venter,J.C.
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                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
15347 a 11327 c 11357 g 16753 t
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fruit fly.
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/transl_table=11
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/gene="Z1920"
7240. .7821
/gene="Z1920"
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NUSWAAYKUKQMOGCRLYIAGIGAGIENTPAGAGGSQVLLAADRIAAURANBAGNTKPH
FUGGGOOIFWNEVELKYLTAPTITSGGNPPAFSLFPDGRLTAANADISGNVANNSGTL
NNVTINENCRYLGKASNOIEGDLVKTVGKAPPRDSRAPERWPSGTTTVRVVDDQPFP
RGIVIPAVAFSGAKHEKEHFDIYSSCRLIYNKNGAEIYNRTALDNTLIYSGVIDMPAG
HGHMTLEFSVSAWLVNNWYPTASISDLLVVVMKKATAGITIS*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AaG56006.1"
/db_xref="G1:12514846"
/translation="mrklchvillsavvwQvaaatpasaaehOsTlsagyLhastnvPG
SDDLNGINVKYRYEFWDALGLITSFSYANAEDEQKTRYSDTRWHEDSVRNRWFSVWAG
PSVRVREWFSAXYAMQVAYSRVSTFSGOYLRYTDVKCKTHDVLTGSDDGRHSNTSLAW
GAGVQFNPXESVVAIDIAXEGSGSGDWRTDGFIVGVGYKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Residues 1 to 498 of 973 are 95.78 pct identical to residues 1 to 498 of 1122 from GenPept 118 : gridles 1 to 498 of 1122 from GenPept 118 : gridle 11787636|gb|AAC74454.1| (AE000234) putative membrane protein [Feberichia coli] /codoi_start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                            /note="Residues 1 to 199 of 199 are 75.87 pct identical to residues 1 to 199 of 199 from GenPept 118 : 91|7532789|gb|AAF63231.1|AF151091_2 (AF151091) Lom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEGLTDGTVYSLYTPSEQFYPPGAPIPWPSDTVPSGÄALMQGQTFDKSAYPKLAAAYP
SGVIPDMRGWTIKGKPASGRAVLSQEQDGIKSHTHSASASSTDLGTKTTSSFDYGTKS
TNNTGAHTHSVSGTAASAGNHTHSVTGASAVSQWSQNGSVHKVVSAASVNTSAAGAHT
                         AAPAAPSRIELTPGYFQITATPHLAVYDPTVQFEFWFSEKRIADIRQVETAARYLGSA
LYWIAASINIKPGHDYYFYIRSVNTVGKSAFVEAVGRASDDAEGYLDFFKGEIGKTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MNMAVKISGVLKDGTGRPVENCTIQLKARRNSATVVVNTVASEN
PDEAGRYSMDVEYGQYSVILLVVEGFPPSHAGTITVYEDSQPGTLNDFLGAMTEDDVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSVSGTAASAGAHAHTVGIGAHTHSVAIGSHGHTITVNAAGNAENTVKNIAFNYIVRL
  SLRLTSGKGTDARLVTTAITADTEHRFSGLPLGEYTLTVRAINSYGQQGEPATTTFRI
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                                                                                                                                                                                                                                                                                                                 or unknown (Phage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative membrane protein of prophage CP-933X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="putative membrane; Not classified (Phage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
/product="putative outer membrane protein of prophage
CP-933X"
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                                                                                                                                                                                                                                                                                                               /function-"putative membrane; Other
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/db_xref="GI:12514847"
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/gene="21919"
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                                                                                                                                                                                                                                                                 3661. .4260
/gene="21917"
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/note-"Residues 1 to 289 of 296 are 84.42 pct identical to residues 1 to 289 of 292 from GenPept 118 : [34] profile [Salmonella typhimurium] (1918) putative catalase [codon_start=1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-*MARRMSEOPRTIKIYNLLTGTNEFIGEGDAYIPPHTGLPANSTY
IAPPDIPAGFVAVFNSDESSWHLVEDHRGKTVYDVASGDALFISELGSLPENTWLSP
EGEFOKWNGTAWVKDAEARELRRIREAEETKNSLMQVASEHIAPLQDAVDLEIATEEE
ASLLEAWKKYRVLLNRVDYSTAPDIEWPVIPEV"
complement(7941. .8831)
/product-"unknown protein encoded by prophage CP-933X"

/brotein_id="AAG56008 1"

/db_xref-"GI:12514848"

/translation-"MDAVVALLEAADACLVASSFEADADDADDAAELADDAAAVFEDS

ALVSDAFARYSDVFAARAELSAALACSVASPAFVVAVEADDAALSADFPAAVALAEAC

PALVDAALADNAAAVFEDAAABALCSSAAVSEDLAFVSDVLAAFAELPAAVAEAAAL

LEAALVSDDFASFEDASLAEBAASDAFVVAVDAEVAADGCDFAAFVSDVFAAPALV

AAALFEDSAAAALFDASVAFVDAVPALEDAD"
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/protein_id="AAG56009.1"
/db_xref="GI:12514849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Residues 1 to 191 of 193 are 94.76 pct identical residues 1 to 191 of 191 from GanPept 118 : gil2367120|gb|AAC74619.1| (AE000252) orf, hypothetical protein [Escherichia coli]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5614
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/protein_id="AAG56010.1"
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111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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/gene="21921"
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/transl_table=11
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23

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ETAKLEEEDKINRALEKKKALEGORDLYOELKRAVSALEKRALEGORGKINROTERALLAS
ETAKLEEEDKINRALEKKKALEGORDLYOELKRAVSALEKRYETLEGOLTERALLAS
BOLDVKGGDVKALADLKOKVEGELEDLRRQVEELKKAVSALEKTRETLEAGLNDANNA
LAESNARATLOGUKALEDINALKAREEDLALANGKLAEEGRAKAKLLETELAAGUNDANNA
LAESNARATLOGUNLKATEELDLALANGKLAEEGRAKAKLLETELAAGONVEGLIDE
KKGRDIVDRRSDLESELANLENDFYSELSORTKOGLEKAKKLLETELAAGORGKOGLDE
KKGRDIVDRRSDLESELANLENDFRSORTSORYTENDLODVOEKLDEEGRAR
AROKAGOWI LIELQNADSGOSLODAEAARKI ERORRTLENDLODVOEKLDEEGRAR
VRFOKOLAKTDEELROAKLKIDDLTNATSORYTAGENSORNOHRELEALDEKTAG
WNRLRKQAEVOLEDLKAGLERAISAKLVEKOKROHERER FYPTVSSKSDEPKKYLTEELA
VLKTELDGEKAMRCHAEFARKRELLAKPRKOKROHERER FYPTVSSKSDEPKKYLTEELA
VLKTELDGEKAMRCHAEREALAKPROKOKROLENTER FYPTVSSKSDEPKKYTTEELA
VLKTELDGEKAMRCHAEREALAKPROKGRGATER FYPTVSSKSDEPKKYTTEELA
VLKTELDGEKAMRCHAEREALAKPROKGRAGTER FYPTVSSKSDEPKRYTTELA
DEESSATKTOSENLAGKLEETAK KLEGEAELTLKMDELRKOFERDTRYV
DEESSATKTOSENLAGKLEETAK KLEDENDLINIKLDAETKRYTERTER
DEESSATKTOSENLAGKLEETAK KLEDENDRYKOKALI ERTRKLEVECEERARKYNIRES
EARGRANAAKLRROAENELEDLRSGVUDAFDEFTGODLLSDKTTOMES
EARGRANAAKLRROAENELEDLRSGVUDAFDEFTGODLLSDKTTOMES
EDLENKYNEEVTORTELSKLKNOLDSDLRSTTSQLESEIERRGILEGLOKKLEAALAS
                                                                                                                                                                                                                                                                                                                                                                                                 RAKLEREVKAAAAGTKLLQTAKADADKLKARVQALEKMEADYKKLQARCTEEEDARRA
                                                                                                                                                                                                                                                                                                                                                                                                                    AENEKKKATADLNEARADVLFYQQQAEKIRTDVEKEKKSNEDLQANLASLLGLTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 21-MAR-2001
3, section 2 of
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Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4904 GCCGAGTTGCTCGCGAAGCCCAGAGGAAAGGAAGGCGCGCACCGAAATCAAGCCCCACAGTC 4963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 SerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAspVal 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIleGluAspLysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr
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genome, contig 2 of
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221
231
58
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
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Escherichia coli 0157:H7 EDL933
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90.00
44.76%
24.76%
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Best Local Similarity:
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9
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KEYWORDS
SOURCE
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/note="Residues 8 to 366 of 388 are 81.05 pct identical to residues 11 to 369 of 1132 from Genepat 118 : gil2151251gblAAA96553.1| (J02459) J (tail:host specificity.1132) [bacteriophage lambda]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANIDRIRVTFGVQSLLETTSRGDRHISSVRLLIQLQRGNWTERDVTINGKTTSOF
LASVILDNLEPRPRINTRAVBETADSTTDQLQNRTLMSSYTEIIDVRQCYPNTAIVGLO
VDAEOFGGGQWTVNYHIRRNENIQVPSTTDQLQNRTLMSSYTEIIDVRQCYPNTAIVGLU
LTHPRYGMGRRLGAADVDKNALTAIAQTCDQTVPDGFGGTEPRMTFAAYLSQDRRAWD
VLSDFCSAMRCMPVWNGQTLTFVQDRPSDVVWPTPAVMWWWIITAWGFATASAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAG56004.1"
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/db_xref="G1:12514844"
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NKTPLTDTDGNPVIHGVTAVWRAGEQEQTPPEGFESSGAETALGVEVTKAKPVTRTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="putative structure; Structural component (Phage or Prophage Related)"
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/translation="MYVDDNGYGFRYSFSALKDRHTAVEVNYTDPQNGWQTSTELVED
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TAHPAPDRIQVSTLPDGVETYGVWGLSLDSCRRLFRCVSVRBNTDGFFAITAVOHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="putative structure; Structural component (Phage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="VO-island #52; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                2 (bases 1 to 10432)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N. W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R. Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7 Nature 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"putative tail protein (partial) of prophage CP-933x"
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Submitted (22-OCT-2000) Laboratory of Genetics, University
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers

    10432
    organism="Escherichia coli 0157;H7 EDL933"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /serotype="0157:H7"
/db_xref="taxon:155864"
/note="enterohemorrhagic"
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/gene="21916"
1245. .3593
/gene="21916"
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/gene="Z1915"
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PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
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**EKEAIVDNGARFEPOSGSLNSVIPPAVQHLTVEVSAADGQYLAQAKWDTPRVVKGVRF** 

REFERENCE AUTHORS 1234 GAAGAGGCTCTCCTGGCTGAAGCTGCCGCCCAAAAAGCAGCCGAAGAAGCTAAAGCCCTA 1293

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Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
Direct Submission

AL Submitted (30-OCT-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley, CA 94720, USA
Sequence Submitted by:
Berkeley, CA 94720, USA
Sequence Submitted by:
Berkeley, CA 94720, USA
Sequence Submitted by:
Berkeley, CA 94720 as part of a high-throughput process to
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
This clone was sequenced as part of a high-throughput process to
This clone was sequenced as part of a high-throughput process to
This clone was sequenced or polyA tail and contiguity
This clone was sequenced of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAS, and
reverse transcription of unspliced precursor RNAS, and
reverse transcription and volut this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu, or send email to
cdna@fruitfly.berkeley.edu, or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVRVITSPYRSYPSYLKRLPPGYGARALITYINEPPTTFSEETRRINGASCLRICE
HTPVVRRARGCTPFPYTGYTYEPAGOLALDAYVARYTNPVRHIAKEVHNISHYPRPAV
KYDAELDANDRPSRKFSAPREDEDPLUDAKRKROKIRQGERLTYNEERALGEVHNISHYPRPAV
AQKADBEAKREERALEERDRIJABAEKQAAAKAKKAAEEBAKIAAEEALLEKKR
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EAARLEEGORVREQELERLEGSKYTPTGGASCABLAETARQESELAAQELQAIQKNE
NETSEBYVEEPYTBEYVEEDETIEKEGSKYTPTGGASYEEDLDAEEEEBEEEEF**
616 C 549 9 335 t
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SYSVPRRVYGATRVVTSPIRVVTSPARVVSRVIHSPSPVRVVRTTTRVISSPERTTYS
YTTPSTYYSPSYLPSTYTSTYIPTSYTTYTPSYAYSPTVTRVYAPRSSLSPLRITPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="alignment with genomic scaffold AE0036BB"
/db_xref="FLYBASE:FBgn0020439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAL28545.1"
/db_xref="GI:16768652"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="86C4-86C4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Longest ORF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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GluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeu

46

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EEEQEAIFRVIAGILHIGNVNFTQSYCDASVIODKTSLNYAPSLFNTASQLEKGLIE
PRIQTGKELVSTQLTPAKAKSGRDALTKAIYHRLFLMIVKK NLLVLSQQNRYSFIGV
DIAGFELFRYNSFEOLCINFYNBEKLQQFRNHHMFTLDGDETYKRRINOMFIDFGNDSQ
ATIBLIESKTPPGILALLDEQSYFPHTATDGTLITKLHTHFGGGGGAGGKAKKHRYYE
BERFANSPNFGIYHTAGTVSYDYTMALEKNROPLQPDLEATMRDSKOSFVRRLFTS
FEDLPTSLAEYQRKGTRGAAFVTVAAQYKSQLSNLMSTLQATHPHFFYRCILLPHQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="major plasmodial myosin heavy chain"
/protein_id="AaK17202.1"
/db_xref="GI:13272546"
/translation="MASERQHADYQRYLKFRKDDLFQVPSDKKFAWFNPDPKDRDTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAEVLKEGKDEWVVRTEEGGTLFVKMDFISPRNPAKFDGVEDMSELGYLNEAGYLHNL
RLRYNKDVIYTYSGLFLVAINPYKRFPIYSDTIIDIYKGRRRNEVAPHIFAIADVAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMLGDKLNQSILITGESGAGKTENTKKVIQYLTSVAGRVSNDPNQVSLEAQILQANPI
LESFGNAKTTRNNNSSRFGKFIEVQFNSAGYISGAKIQSYLLEKSRVVFQAERERTFH
IFYQLLAGATPEERKSMFLGPPDTYHYLNQSGCFDVPGINDANDFQDTKNACKIMNIT
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HFRQAREKSVSARIIODNIRAYLEFKNWAWWKLFAKARPLLVGRNMDKELKERDSQIK
DLSSQLAAEKAARAELERQLKEAEHKIAQLQDSLKAEKANVVNLQDANADLKOEIATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning of the major plasmodial myosin II of Physarum polycephalum
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JAN-2001) Biochemistry, Eotvos L. University, Puskin u.3., Budapest H-1088, Hungary Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physarum polycephalum major plasmodial myosin heavy chain (mynPl)
                                                                                                                              1294 AAAGCCGCTGAAGATGCTGCCCAGAAAGCTGCCGAAGAAGCGCGTCTAGCGGAGGAGGCT 1353
                                                                                                86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla 105
                                                                                                                                                                                           106 GluValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIle 125
85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 6484)
Nyitray.L., Farkas.L., Nagy.A., Kovacs.M., Nakamura,A. and
Kohama.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nyitray, L., Farkas, L., Nagy, A., Kovacs, M., Nakamura, A. and
Kohama, K.
  66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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8. .6454
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1 (bases 1 to 6484)
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AF335500
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/codon_start=1
/transl_table=11
/transl_table=11
/transl_table=11
/product="protein having the same IgG specificity as
protein G from group G streptococci strain G148"
/protein_id="caa01034.1"
/protein_id="caa01034.1"
/db_xref="G14"
/translation="EPNKYGVSDYKNLINNAKTVEGVKDLQAQVVESAKKARISEAT
DGLSDFLKSQTPAPDTVKSIELAEAVLANRELDKYGVSDYHKNLINNAKTVEGVKDL
QAQVVESAKKARISEATDGLSDFLKSGTPAEDATOKTKLKGETTEAVDAATAEKVF
KQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTATKVF
KQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTAGETT
EAVDAATAEKVFKOYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTEKUV
INGKTLKGETTTARDAETAEKAFKQYANDNGVDGWTYDDATKTFTVTEKPEVIDASELTPAVTEKUV
INGKTLKGETTTARDAETAEKAFKQYANDNGVDGWTYDDATKTFTVTEKPT
RQTABATAEKPEASIPLANDAETAEKAFKQYANDNGVDGWTYDDATKTFTVTEKPTTG
APTEBFFRAALAVWAGGALAVASKKKED"
EGSNPFFTAALAVWAGGALAVASKKKED"
15 a 280 c 297 9 347 t

    .1443
/note="Protein sequence is in conflict with the conceptual

                                       PAT 04-JAN-1994
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FUI_CDNA.

fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Nooptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 2022)

Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,

Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AspValLysLysThrLysAspThrLysProValValLysLysGluGluArgGlnAsnVal 147
                                                                                                                                                                                                                               METHOD AND MEANS FOR PRODUCING A PROTEIN HAVING THE SAME 19G SPECIFICITY AS PROTEIN G
Patent: WO 8705631-A 4 24-SEP-1987;
Location/Qualifiers
                                       A12446 . Ilnear 1.5 kb EcoRI/HindIII restriction fragment of pSPG1.A12446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY060997 2022 bp mRNA linear Drosophila melanogaster HL01392 full length cDNA.
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Mismatches:
                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnThrLeuProThrThrGlyGluGluSerAsnPro 159
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                                                                                                                                                                            artificial sequence.
1 (bases 1 to 1469)
                                                                                                                                                                                                                                                                                                                                                                                                              translation
                                                                                                                                      synthetic construct. synthetic construct
                                                                                                 A12446.1 GI:491352
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62.50%
56.25%
11.58%
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Best Local Similarity:
Query Match:
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TITLE
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                                                                                 SG148IGG 148 gene fragment for IgG-binding protein G. X04015
                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                     1 (bases 1 to 1469)
Guss, B., Eliason, M., Olsson, A., Uhlen, M., Frej, A.K., Jornvall, H., Flock, J.I. and Lindberg, M.
Elock, J.I. and Lindberg, M.
Extracture of the 19G-binding regions of streptococcal protein G
EMBO J. 5 (7), 1567-1575 (1986)
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Conservative:
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/organism="Streptococcus sp."
/strain="G 148"
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Quality coverage: 13.20x in Q20 bases; sum-of-contigs Quality coverage: 12.22x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAlaLeuGluAla
                                       * NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AlaileGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 LeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGlnSerAspAsn
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Matches:
Conservative:
Mismatches:
Indels:
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47567. .67691
67792. .91151
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fragment_chain:1"
193304. .220820
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fragment_chain:1"
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40568 c 40361 g 70932
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                                                                                              Location/Qualifiers
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92.00
49.12%
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11.84%
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Best Local Similarity:
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YTKVRBNAKTARDVKKXTFEESONEVTRTKTREKTKARAALELLEKKYGOBY
YIKLINNGKTABGVYALKDELLASKPAVIDAPELTATYKLVINGKTARGATLKKYGIGDY
YIKLINNGKTABGVATKDELLASKPAVIDAPELTATYKLVINGKTEKGETTTKA
VDAETARRAFKQYANDGVAYTODATKTFTVTEMTTEVDGDAPTEBKKFETA
                                BCT 16-AUG-1994
                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function-"binding of macroglobulin, albumin and IgG" /product-"unnamed" 242 c 305 g 426 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'function="binding of macroglobulin, albumin and IgG"
                                                                                                                                                   Streptococcus.

1 (bases 1 to 1555)
Jonsson, H., Frykberg, L., Rantamaeki, L. and Guss, B.
MAG, a novel plasma protein receptor from Streptococcus
Gene 143, 85-89 (1994)
                            Streptococcus dysgalactiae (mag) gene, complete cds. L27798
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1555
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/db_xref="taxon:1334"
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/gene="mag"
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288. .1529
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Best Local Similarity:
Query Match:
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RESULT 23
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EKLEHNPGQVIPASLREENHAQHVQLDLNRPLRDVMQDLARLPVGTRVSLSGPIVVAR
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QADIDAAKEVWSESKRMLADKRYDLVVLDELLYMLAYHYLDTEEVIASLQNRPAQQSV
IVTGRGCHSQILKMADTVSEIRPVKHAFDNGIQAQPGIDW"
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QAAGGSLVMLSKGNRSQQVTDACHKHGGFNLGSIGGAAALLAQEYVKSLRCLEYPELG
MEAVWMMEVENLPAFILVDDKGNNFFSQFEQQHRCASCPAGH"
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TIFLRLIKMIIAPLVVSTLVVGIAKMGDAKALGRIFSKTLFLFICASLLSIALGLITV
NFFMPGTGINFVAHGAETTGVVAAEPFTLKVFISHAFPTSIVDAMAHNEILQIVVFSI
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VSAGIRMGERFTMLLLWVLJGLAIVYVGPCIRKITRALSEPALLAFTSSSBAAFP
GTLEKLEOPGVSPKI ASFVLPIGYSFNLVGSMAYCSFATVFIAQACNIHLSIGEOITM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-*probable fumarate hydratase, similar to fumarate
hydratases e.g. fumarate hydratase class I, aerobic
(fumarase) - Escherichia coli
gi|120598|sp|P00923|FUMA_ECOLI percent identity 68 in 545
                                                                                                                                                                                                                                                                                                                            /note="probable cob(1)alamin adenosyltransferase, similar to cob(1)alamin adenosyltransferases (corrinoid adenosyltransferases) e.g. [Escherichia coli] gill15148[sp[Pl3040]BTUR_ECOLI percent identity 67 in 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate/aspartate transport proteins (proton glutamate symport proteins) e.g. [Bacillus stearothermophilus] g1[121467]sp[ps24943]gTT_BACST percent identity 38 in 416 aa,also similar to C4-dicarboxylate transpor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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/gene="ECs0758"
complement(6092. 7372)
/gene="Ecs0758"
/note="probable transport protein, similar to
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/transl_table=11
/evidence=not_experimental
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/db_xref="G1:13360216"
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complement(4332. .5984)
/gene="ECs0757"
                                                                                                                                                                                                                                /gene="ECs0756"
complement(3720, .4322)
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/db_xref-"GI:13360214"
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Mus musculus chromosome 11 clone RP23-239H6, *** SEQUENCING IN PROGRESS ***, in unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutolcostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84022 AGTGAGTCATTACAAAGTGCAACAGATGCCGAGTTGTCAAAAAAGACGGCAGAAAGTGCA 84081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AlaThrThrAlaileGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: De-terminator Big Dye; 100% of reads Consensus quality: 218850 bases at least 040 Consensus quality: 219288 bases at least 030 Consensus quality: 219708 bases at least 030 Insert size: 220120; sum-of-contigs Insert size: 237848; 1.5% error; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL663060.2 GI:18135362
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                /product="hypothetical protein"
/protein_id="BAB34182.1"
                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                             /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bM23946
                                                                                                                                                                                                                                                                                                                                                                  indels:
                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-539A-6 (1-159) x AP002553 (1-297816)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..... Summary Statistics
complement(7533, .7850)
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complement(7533, .7850)
/gene="ECS0759"
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                                                                                   /note="unknown"
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                                                                                                                                                                                                                                                                   2.6
96.00
51.47%
39.71%
12.36%
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Burton, J.
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/evidence-not_experimental
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GTTHHGLPYENTYREAVAATGATASVIYVPAPFCKDSILEAIDAGIKLITITEGIPT
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AVKQTTDYGFGGOTGOODIPGSNFIDILEMFEKDPQTEAIWHGEIGGSAEEBA
AAYIKTHVYKPVVGYIAGVTAPKGKRMGHAGAIIAGGKGTADEKFAALEAAGVKTVRS
                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:kendgen-info.osaka-u.ac.jp,
URL.http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
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/gene="ECS0754"
/note="similar to SUCD_ECOLI gil1786949 percent identity
100 in 289 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                5 (bases 1 to 297816)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to SUCC_ECOLI gi|1786948 percent identity 100 in 388 aa (Conserved in E.coli K-12)" /codon_start*1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="probable transcriptional regulator,similar to
transcriptional regulators e.g. glycine cleavage system
transcription activator (gcv operon activator) -
Escherichia coli gil417043|sp|P92064|GCVA_ECOLI percent
identity 31 in 300 aa"
Ogasawara, N., Yasunaga, T., Kuhara, S., Shiba, T., Hattori, M. and
                                                           Complete genome sequence of enterohemorrhagic Escherichia co. 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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/protein_id="BAB34178.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Escherichia coli 0157:H7"
/strain="0157:H7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref-"taxon:83334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/transl_table=11
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79. .1245
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/gene="ECs0754"
1245. .2114
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2781. .3686
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                                                                                                                                                                           21156231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                    JOURNAL
                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli O157:H7 DNA, complete genome, section 4/20.
AP002553 BA000007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterchemorrhagic Escherichia coli OI57:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli O157:H7 (strain:O157:H7, sub_strain:RIMD 0509952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (sites)
Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (sites)
Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishi,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1229 TCTGCAAAGAAGTCAGAGGGTCCTCGTCCTCAGCCTCTGAGGCCCCTCAAAAAGCC 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1169 GCTGATACTTCAGCAGGATGCATCGGAGTCAGCCCGGCAGGCGGCAGAAAGTGCAGCC 1228
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Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaGluValValGln 109
                                                                                                                                                                                                                                                                                                                                                                                                    AlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGlnThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 AspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAspAla 89
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S.,
                                                                                                     13501
                                                                                                                                 27
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33
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                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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complement(8203. .9492)
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96.00
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                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                                              Alignment Scores:
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9
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FTTSGSNBEVTSEVRCFNOYYGGSAEKIYGNNGDIIGIRMDKINGESLINISSLPAQ
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SRAESOKYSPLLLEEARTVGLGAFSEEVLSENKFHEEIGMPRRTSYPXDSALIHDDNT
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                                                                                                                                                                                                                                                                                                                                          /translation="MKIPSLQSNFNFSAPAGYSAPIAPNRAENAYADYVLDIGKRIPL
SAADLSNYESVIRAVHDSRSRLIDQHTVDMIGNTVLDALSRSQTFRDAVSYGIHNEK
VHIGCIKYRNEYELNEESSVKIDDIQSLTCNELYEYDVGQEPIFPICEAGENDNEEPY
                                                                                                                                                                                                                                                                                                                                                                                                                             VSFSVAPDTDSYEMPSWQEGLIHEIIHHVTGSSDPSGDSNIELGPTEILARRVAQELG
WSVPDFKGYAEPEREAHLRLRNLNALRQAAMRHEENERAFFERLGTISDRYEASPDFT
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YDGAAPPKGETHRYIFTVHALDVERIDVDEGASGAMVGFNVHFHSLASASITAMFS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYSAYSNIGYGFIQQHDFPGLAINDNLQDANQIQLYHGAPYIFTFGDVDKHNQQ"
5350. 6231
7gene="2.0989"
7gene="2.0989"
                                                                                                                                                                                                                                                             protein encoded by prophage CP-933K"
                                                                                                                       'function="orf; Other or unknown (Phage or Prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="orf; Other or unknown (Phage or Prophage
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/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAG55144.1"
/db_xref="G1:12513759"
                                                                                                                                                                              /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="No significant matches"
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                                                                                                                                                                                                                                                                                       /protein_id="AAG55i41.1"
/db_xref="G1:12513756"
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/gene="ybhB"
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/transl_table=11
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/gene="Z0986"
3530.
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/note="20993"
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/db_xref="G1:12513752"
/db_xref="G1:12513752"
/ranslelion="MRKVCAAILSAAICLAVSGVPAWASEHOSTLSAGYLHASTDAPG
SDDLNGINVKYRYEFTDTLGLITSFSYANAEDEQKTHYSDTRWHEDYVRNRWFSVWAG
PSYRVNEWPSAYAMAGVAYSRVSTFSGDYFRYTDNKRKTHDVLTGSDDARYSNTSLAW
GGGVQFNTPESVAVDVAYEXSGSGDNRTDGFIVGVGYKF"
                                                                                                                                                                                                                                                                                                                                                                                                                             /function="putative structure; Structural component (Phage or Prophage Related)"
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KLEROFENNAIIREDVDFSWYDRKLSDIYHDIICEORLRTEDKRDFYLLNLLEKELR
EISRAQDSLISMYAKKRNHAWFDFFRUALLKAGEIFRCTYWTKNHGISFGEGCIYLD
MDMILTGKLGTIYABOGISHHVDRRNDSWNIENSAIIVNRSWHPALLEGLSFWHSKVD
AHPYYDGLGKGVKKYPNFTPLHNYNHFCDFIEFNHPNIIMNTSQYTCSSW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Residues 1 to 102 of 102 are 98.03 pct identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MKWAVIQAELENDMNILRKLMQSLCGCGKHDDCENGRSLTAQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 are 68.79 pct 1dentical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Residues 164 to 440 of 440 are 68.79 pct 1dentical to residues 381 to 645 of 645 from GenPept 118 : gi|4585436|gb|AAD25464.1|AF125520_59 (AF125520) putative tail fiber protein [Bacterlophage 933W]"
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/protein_id="AAG55139.1"
/db_xref="GI:12513754"
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/protein_id="AAG55140.1"
/db_xref="G1:12513755"
                                                                                           membrane protein of prophage
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//codon_start=1
                                                                                              'product-"putative outer
              P-EibA]"
                                       /codon_start=1
/transl_table=11
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/gene="20985"
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719. .2041
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/gene="20985"
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Bayles, R.W., Schreier, P.H. and Buchel, D.E.
Determination of the endpoints of partial deletion mutants of the
attachment site of bacteriophage lambda by DNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                        bacteriophage
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Schwarz,E., Scherer,G., Hobom,G. and Kossel,H.
Nucleotide sequence of cro, cII and part of the O gene in phage
               20 (bases 39062 to 39170)
Denniston-Thompson,K., Moore,D.D., Kruger,K.E., Furth,M.E. and
                                                              Physical structure of the replication origin of bacteriophage
lambda
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                                                                                                                                                                                   Structure and function of two regions of DNA controlling the synthesis of prokaryotic RNAs Thesis (1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    operators of bacteriophage lambda
ss : MGG. 166 (1), 61-73 (1978)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence of the bacteriophage gama cI gene
Nature, 276 (5685), 301-302 (1978)
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Nichols, B.P. and Donelson, J.E.
178-Nucleotide sequence surrounding the
                                                                                                    Science. 198 (4321), 1051-1056 (1977)
78054731
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Molecular & general genetics
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Scherer, G.
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                                                       Blattner, F.R.
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Mismatches:
Indels:

0.152 99.00 53.16% 32.91% 12.74%

Percent Similarity: Best Local Similarity: Query Match: DB:

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/nofe="Residues" 1 to 199 of 199 are 72.86 pct identical to residues 1 to 199 of 199 from GenPept 118 : gil7532789|gb|AAF63231.1|AF151091_2 (AF151091) Lom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear BCT 21-MAR-2001
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Direct Submission
Submitted (12-Corr-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grobeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
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1 (Dases 44588 to 44780)

Lebowitz,P., Weissman,S.M. and Radding,C.M.

Nucleotide sequence of a ribonucleic acid transcribed in vitro from lambda phage deoxyribonucleic acid

The Journal of biological chemistry. 246 (16), 5120-5139 (1971)
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In vitro transcription products of lambda DNA: Nucleotide sequences and regulatory sites
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virus RESEARCH. PROCEEDINGS OF 1973 ICN-UCLA SYMPOSIUM: 533-544;
Academic Press, New York (1973)
6 (bases 37945 to 38027)
Maniatis, T., Ptashne, M., Backman, K., Kield, D., Flashman, S., Jeffrey, A. and Maurer, R.
Recognition sequences of repressor and polymerase in the operators
                                                                                                                                                                               circular PHG 31-OCT-2000
                                                                                                                                                                                                                                                                                                  bacteriophage lambda
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
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Weigel,P.H., Englund,P.T., Murray.K. and Old,R.W.
Weigel,P.H., Englund,P.T., Murray.K. and Old,R.W.
The 3'-terminal nucleotide sequences of bacteriophage lambda DNA
Proceedings of the National Academy of Sciences of the United
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                             39535 CATGCAGACTCCGCGAAGAGTGAAGAGAAAAGGCGAAGAAATTGCCGATCTGTTAGAT 39476
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Kleid, D.G., Agarwal, K.L. and Khorana, H.G.
The nucleotide sequence in the promoter region of the gene N in
bacteriophage lambda
The Journal of biological chemistry. 250 (14), 5574-5582 (1975)
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Dahlberg,J.E. and Blattner,F.R.
Sequence of the promoter-operator proximal region of the major leftward RNA of bacteriophage lambda
Nucleic acids research. 2 (9), 1441-1458 (1975)
109 GlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProIleAlaLeuAsp 128
                                                                                                                                                                                          Bacterlophage lambda, complete genome.
J02459 M17233 M24325 V00636 X00906
J02459.1 G1:215104
DNA-binding protein; circular; coat protein; complete genome;
origin of replication; repressor; unidentified reading frame,
bacterlophage lambda.
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Mu.R. and Taylor,E.
Nucleotide sequence analysis of DNA. II. Complete nucleotide sequence of the cohesive ends of bacteriophage lambda DNA Journal of molecular biology. 57 (3), 491-511 (1971)
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Nature New Biol. 233, 230-231 (1971)
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Cell. 5 (2), 109-113 (1975)
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Humayun, Z., Jeffrey, A. and Ptashne, M. Completed DNA sequences and organization of repressor-binding sites in the operators of phage lambda number of molecular biology. 112 (2), 265-277 (1977)
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Ptashne,M., Backman,K., Humayun,M.Z., Jeffrey,A., Maurer,R.,
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Autoregulation and function of a repressor in bacteriophage lambda Science, 194 (4261), 156-161 (1976)
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Lambda repressor regulates the switch between PR and Prm promoters
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Maniatis,T., Jeffrey,A. and Kleid,D.G.
Nucleotide sequence of the rightward operator of phage lambda
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Sklar,J., Yot,P. and Weissman,S.M.
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Smith,G.R., Elsen,H., Reichardt,L. and Hedgepeth,J.
Deletions of lambda phage locating a prm mutation within the
rightward operator
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Seperer.G., Hobom.G. and Kossel,H.
DNA base sequence of the po promoter region of phage lamdba
Nature. 265 (5590), 117-121 (1977)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 (bases 38041 to 38241)
Roberts,T.M., Shinmatake,H., Brady,C. and Rosenberg,M. Sequence of Cro gene of bacteriophage lambda
Nature: 270 (5634), 274-275 (1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oţ
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Davies, R.W., Schreier, P.H. and Buchel, D.E.
Nuclectide sequence of the attachment site
Nature. 270 (5639), 757-760 (1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 (bases 37206 to 37263; 37914 to 37970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 (bases 37905 to 37989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 (bases 27617 to 27934)
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78071724
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MEDLINE
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gene

CDS

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Complement(1647 . 2489)

Complement(1647 . 2489)

Gene="HCM2.0006c, possible lipoprotein, len: 280 aa;

//doce="HCM2.0006c, possible lipoprotein, len: 280 aa;

//doce="HCM2.0006c, possible lipoprotein, len: 280 aa;

shows weak similarity to TR:AAF10061 (EMBL:AE001907),

DR0482, Deinococcus radiodurans B-cell receptor associated protein-related protein (328 aa), fasts scores; E(): 4.9e-07, 23.4% identity in 265 aa overlap. Highly similar to TR:CAB55231 (EMBL:AL117211), YPMT1.49C, Yersinia pestis CO-92 putative lipoprotein from plasmid pwr1 (276 aa), fasta scores; E(): 0, 97.5% identity in 280 aa overlap and TR:C68763 (EMBL:AF074611), Y1114, Yersinia pestis KIM5 hypothetical protein from plasmid pwr1 (276 aa), fasta scores; E(): 0, 97.5% identity in 280 aa overlap. Contains a possible N-terminal signal sequence and an appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           highly similar to TR:CAB62372 (EMBL:AL117211), YPWT1.49AC, Yersthia pestis CO-92 hypothetical protein from plasmid pWT1 (66 aa), fasta scores; E(): 3.5e-25, 97.0% identity in 66 aa overlap. Contains hyrophobic, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2493. 2693)
/gene="HCM2.0007c"
/note="HCM2.0007c, possible membrane protein, len: 66 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39715 GAGGCGTTAAACTCTAAACAAGCAGCTGCGGGCAGCGAAGCTAATGCTAAGGCAAGTGAA 39656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39655 AACGCTGCAGCTGCCTCTCAGCAGCAGCGGCTACCAGTGAAAGTAACGCCCGGGCAAGC 39596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2427. .2459)
/gene="HCM2.0006c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GluAlaThrThrAlaIleGluAlaAlaSerSerAspAlaLeuGluAlaLeuAlaAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 ThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAlaAlaSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106516
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Conservative:
                                                                                                                                                                                                                                                                                                         repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-847-539A-6 (1-159) x STYPPHCM2 (1-106516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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complement//
                                                                                                                                                                                                                                                                                                                                         complement(1647, .2489)
/gene="HCM2.0006c"
complement(1647, .2489)
                                             complement(1137. .1141)
/gene="HCM2.0005c"
                                                                                                                  /note="possible RBS"
complement(1492, 1497)
/note="possible RBS"
                                                                                                                                                                                                                                                           1565. .1621
/note="repeat 1; 57 bp
    PFRAAMTVFLLMOEKKHEETV'
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/trans1_table=11
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Best Local Similarity:
Query Match:
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complement(1113. .1484)

/gane="HCM2.0005c",

complement(1113. .1484)

/gane="HCM2.0005c",

foote="HCM2.0005c",

foote="HCM2.005c",

foote="HCM2.0005c",

                                                                                                                                                                                                                                                                                                                                    224. .6722

// note="96.5% identical to Yersinia pestis CO-92 plasmid pMT1 (EMBL:ALI17211) bases 48733. .55208"

complement(375. .650)
/gene="HCM2.0003c"
complement(375. .650)
/gene="HCM2.0003c, hypothetical protein, len: 91 aa;
/note="HCM2.0003c, hypothetical protein len: 91 aa;
/sinia pestis CO-92 hypothetical protein from plasmid pMT1 (91 aa), fasta scores; E(): 0, 94.5% identity in 91 aa overlap and TR:QSZGX9 (EMBL:AF074611), Y1117, Yersinia pestis KIM5 hypothetical protein from plasmid pMT1 (91 aa), fasta scores; E(): 0, 94.5% identity in 91 aa), fasta scores; E(): 0, 94.5% identity in 91 aa overlap"
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/gene="HCM2.0004c"

/gene="HCM2.0004c"

/gene="HCM2.0004c"

/force="HCM2.0004c"

/force="HCM
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/protein_id="CAD09870.1"
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MDADSYYDDDGVCWRINGSCMYVDDTWTVSDEDAAHLERILGISTFE"
complement(658..663)
/note="possible R85".
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IGPNGAGTFDWCNDPEDAWDIIYRHRIGVIPARQPGEWRAAHRKVDSSTPQHLIQNPN
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FYVVRDDRVLSSPYLTKRNGKLSGVGEDKFVYNKSGDVYGVHAKNASYLFDDCKEVG"
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                                                                                                                                                                                                                                                                                                    'note-"possible RBS"
                                                                                                                                                                                                                      complement(36, .43)
/gene="HCM2,0002c"
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/transl_table=11
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/transl_table=11
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CDS

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/codon_start=1
/transl_table=11
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 AL513384.1 GI:16505981
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                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 106516)
Parkhill, J.
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                KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                               TITLE
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 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /procein_id="AAA66376.1"
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1 857 c 1035 g 603 t
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FSVAXGFPVPPSLRNIYAELHRSLPEFSPPDHGCLDAWASQGVLLLNTIIITVQKGKPG
                                                                                                                                                                                                                                                                                                                                                                                                     SHADIGWAWFTDHIIALLSERLKACVPMLWGAKAGDKASLINSKKHLVLTSQHPSPLA
QNSTRKSAQQKFVGNNHFVLANNFLREKGLGEIDWRL"
3019. .>3222
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AL513384
                                                                                                                                                     /Lranslation-*MHAAIRVFVSLSLVALFVLPTWGNWAYPCCHVTQLSQQHHLALE
NISDIYLVSNKTCDGFSLASLNSPKNGSNQLVISRCANGLNVASYFIAVLRRSRSALT
                                                1843. 2259
/note="potential 15kDa protein; similar to BKRF2 of EBV,
Swiss-Prot Accession Number P03212"
                                                                                                                                                                                       SQLLELLNTLESLYASFSVEDLFGANLNRYAWHHAG"
2241. .3008
/note="slmilar to BKRF3 of EBV encoded by GenBank
Accession Number V01555; similar to to EBV uracil DNA
glycosylase, Swiss-Prot Accession Number P12888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 AspAsnAlaAlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSer 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 GluGluAlaGluValValValGlnSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAla 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 ThrProIleAlaLeuAspValLysLysThrLysAspThrLysProValValLysLysGlu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to BKRF4 of EBV, Swiss-Prot Accession Number P30117"
/citation=[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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.622
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1843.
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56.47%
28.24%
13.38%
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Best Local Similarity:
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1...25.7% identical to Yersinia pestis CO-92 plasmid pWT1 (EMBL:AL117211) bases 48304. .48535" complement(29. .334) complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement(29. .334) /gene="HCM2.0002c" complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement complement comp
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1 (bases I to 106516)
Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
Sebalhia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N.,
Farrar, J., Peltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S.,
Jagels, K., Krogh, A., Larsan, T.S., Leather, S., Moule, S., O'Gaora, P.,
Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J.,
Stevens, K., Whitehad, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HCM2.0001c"
/note="HCM2.0001c"
/note="HCM2.0001c, hypothetical protein, len: 68 aa;
highly similar to TR: CAB5527 (EMB1:AL117211), YPMT1.45c,
Yersinia pestis CO-92 hypothetical protein from plasmid
pMT1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity
in 60 aa overlap and TR: 668760 (EMB1.AF074611), Y1119,
Yersinia pestis KIM5 hypothetical protein from plasmid
pMT1 (71 aa), fasta scores; E(): 5.9e-25, 93.3% identity
in 60 aa overlap. Spans the end of the sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Notes:
Details of S. typhi sequencing at the Sanger Centre are available
on the World Wide Web.
Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

    .1065i6
/organism="Salmonella enterica subsp. enterica serovar

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Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (URL, http://www.sanger.ac.uk/Projects/S_typhi/).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413 (6858), 848-852 (2001)
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complement(1. .29)
/gene="HCM2.0001c"
complement(1. .29)
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160 TCAGAGACAACACTGGCTTTGCGTAATGAAGAGAGTGCT 198
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                                             DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA66372.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral episome"
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                                                                                                    U23857.1 GI:775213
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                                            LOCUS
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AUTHORS
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                     RESULT 17
HPU23857
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                                                                                                                           SOURCE
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Fahnestock,S.R.
CLONED PROTEIN G VARIANT GENES AND THE PROTEIN G VARIANTS EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 02-DEC-1994
                                                                                                                                                                                                                                          106 GluValValGinSerAspAsnAlaAlaSerAspAlaTrpGluLysAlaAlaThrProile 125
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                                                                                                                                                                                                                               85
                                                                                                                                     GluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeuLysLysGlnAlaIle 45
                                                                                                                                                                                                                             66 AlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsnAla
                                                                                                                                                                                                                                                                          86 AlaSerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAla
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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Gaps:
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Location/Qualifiers
1. .798
                                                                                                                                                                                                                                                                                                                                                                                                                                   798 bp
Sequence 4 from Patent WO 8810306.
109107
109107.1 GI:588179
                                                                                                              US-09-847-539A-6 (1-159) x AC020602 (1-167227)
                                                                                          Gaps:
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161 c 177 g
17009. .17747
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105.00
72.73%
69.70%
                           0.00915
113.00
50.00%
26.67%
14.54%
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Best Local Similarity:
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                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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 repeat_region
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                     Alignment Scores:
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
109107
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FEATURES
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GDWPYANWYGGRNSCYNLRRCLGCCVPWCRLTPLSRLPYGHSWGTGPBFTPLMESCV
SYELVFLPTGGSAECVRDAUVI STRPQPTSSVKVTFCTFDPPVMLPIFYPPBEAPT
GSGAEGGEGARGDDGGBEGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="GDLEDPVSEARASTPLPPGDEGIEEFEAWLESQNPSLEDVQQEF
AGMRVTGEEAEDNSDDGEFSDWDASDSDHEGDEDGGTSGGGRSLHSLYSLSAV"
VRL 30-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <1. 294
/note="similar to BRRF2 of Epstein-Barr virus, Swiss-Prot
Accession Number P03210"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to EBNAl of Epstein-Barr virus, Swiss-Prot
Accession Number P03211"
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yates, J.L.

Pirect Submission
Submitted (31-MAR-1995) John L. Yates, Department of Human
Genetics, Roswell Park Cancer Institute, Elm and Carlton Streets,
Buffalo, NY 14263, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /citation=[1]
/function="encodes heptamer repeat of Gly, Ser and Ala"
/rpt_family="analogous to IR3 of EBV"
/rpt_type=tandem
             Herpesvirus papio BRRF2 homolog gene, partial cds, EBNAl, BKRF2 homolog gene, partial cds, and BKRF4 homolog gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           612. .770
/note="The 21-bp repeat unit encodes the heptapeptide Gly-Gly-Ser-Gly-Ala-Gly-Ala; approximately seven and one-half copies of this repeat in strain 594-S encode amino acid repetitive domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="binds to oriP to permit replication of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EcoRI HVP DNA insert)"
                                                                                                                                                                                                                                                                                       1 (sites)
Yates,J.L., Camiolo,S.M., Ali,S. and Ying,A.
Comparison of the EBNA1 proteins of Epstein-Barr virus and
Nirology 222 (1), 1-13 (1996)
                                                                                                                                                                                                          Herbesvirus papio
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
  linear
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'rpt\_family="GA-rich"

repeat\_region

7

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Center project name: H_NHO461M18
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NOTICE: This sequence may not represent the entire insert of this folor. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/jsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genemics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com) or Pieter de Jong (http://www.resgen.com) or Pieter de Jong (http://www.resgen.com). The clone sequenced to the left is RPI1-341H1, 2000 bp overlap; the clone sequenced to the right is RPI1-289K3. Actual start of this clone is at base position 162181 of RPI1-341H1; actual end is at base position 167227 of RPI1-461H8. NEIGHBORING SEQUENCE INFORMATION: pBACe3.6

ţ Data from AC016725 and AC017031 was used to finish this clone, AC020602. There is a tandem repeat from base position 33099 t

Location/Qualifiers
1. 167227
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2361. .2391
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/rpt\_family-"L1"

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12983. 13285
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13257. 13292
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1202, .11400
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9210. .9343
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11531. 11600
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8486. .8631
/rpt_family="L1"
8668. .8693
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14335. 14439
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16313. .16664
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SVKEKIKASYDRDETTELSAQADQIVSAQADNEAITKAEEDSSKAWEBAADQANTAKA
SVKEKIKASYDRDETTELSAQADQIVSAQAALKEEDSSKAWEBAAADQANTAKA
BADELAKAEKESSDAWEKAAALDQAKQAALKEEPRYGYSOSYYKNLINKAKTVBGIMEL
QAQVVESAKKARISBATDGLSPELKSOTSABDTLKSIKLSEAKEMAIRELDAQGVSDF
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/product="albumin-binding protein"
/protein_id="AAA26847.1"
/db_xref="G1:153555"
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Sjobring, U.
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Maligorski, J., Cotton, M. and Doebber, A.
The sequence of Homo sapiens BAC clone RP11-461M18
Unpublished (2002)
3 (bases 1 to 167227)
Materston, R. H.
Materston, R. H.
Direct Submission
Submitted (05-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, M. 63108, USA
4 (bases 1 to 167227)
Materston, R. H.
Materston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO20602 167227 bp DNA linear PRI 10-JAN-2002
Homo sapiens BAC clone RP11-461M18 from 2, complete sequence.
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( pases 1 to 167227)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (07-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MM 051108, USA
6 (bases 1 to 167227)
Waterston, R.H.
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
7 (bases 1 to 167227)
Waterston, R.
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Submitted (10-JAM-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Dec 6, 2001 this sequence version replaced 91:14029092.
LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValLys
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Center code: WuGSC
Center code: NtGSC
Contact: sapiens@watson.wustl.edu/gsc
                                                                                                                                                                                                             102 SerGluGluAlaGluValValGInSerAspAsnAlaAlaSerAspAlaTrpGluLysAla
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Fahnestock, S.R.
CLONED STREPPOCOCCAL GENES ENCODING PROTEIN G AND THEIR USE TO CONSTRUCT RECOMBINANT MICROORGANISMS TO PRODUCE PROTEIN G Patent: WO 8705025-A 2 27-AUG-1987;
Location/Qualifiers
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/note="cell-wall spanning region"
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//note="inverted repeat A" 2172. 2180
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Sequence 2 from Patent WO 8705025.
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RNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAABNAGQOLGKORQQQM
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Goward, C.R., Murphy, J.P., Atkinson, T. and Barstow, D.A.
Expression and purification of a truncated recombinant
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// Acrain="Streptococcus sp. 'group G'"
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/gene="Protein G'gene"
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Fahnestock.S.R.
CLONED STREPFOCCCAL GENES ENCODING PROTEIN G AND THEIR USE TO CONSTRUCT RECOMBINANT MICROORGANISMS TO PRODUCE PROTEIN G Patent: WO 8705025-A 4 27-ANG-1987;
Location/Qualifiers
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LINNAKTVEGVKALIDEILAALPKTDTYKLILNGKTIKGETTTEAVDAATARKVFKOY

ANDNGYOGEWTYDDATKTETVTEKPEVIDASELTTEAVDAATAKKLINGKTIKGETTEAV

BAATAEKVYKOYANDNGVDGEWTYDDATKFETVTEKPEVIDASELTEAV

KTIKGETTTRAVDAATAETAKTUNGVOGWTYDDATKFETVTEWYTEVVING

KTIKGETTRAVDATPTATPIAKDDATKFETVTERVIDNGVOGWTYDDATKFETVTEWYTEVPGGDAPT
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Streptococcus G148 gene for protein G.

X06173.1 G1:47084

G protein; IgG receptor.

Streptococcus Sp. G148.

Gardenia; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
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                                                                                                         21 LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
676 GTTGACTCCACCAATCGAAGATACCCCAATTATTCGTAATGGTGGAATTAACTAATCTT
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Olsson,A., Eliasson,M., Guss,B., Nilsson,B.,
Lindberg,M. and Uhlen,M.
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Product-"mature G protein (AA 1

694. .765

/note-"repetitious region 1"
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335. . 340 |
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/note="repetitious region 2"
1144. .1215
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/note="repetitious region
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/note="repetitious region
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ACAGCAGCAGCGGTAGCCGATACTGTGGCCAGCAGCGGCAGCTGAAAATGCTGGGGCAGCA 856
                                                                                                  LysLysGlnAlaileGluAspLysGluAlaThrThrAlaileGluAlaAlaSerSerAsp 60
    LeuGlyAsnAlaProGluLysLeuAlaLeuArgAsnGluGluArgAlaIleAspGluLeu
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AUTHORS
TITLE
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                    / LEALOID - WREEKKYKYFLEKSAFGLASVSAAFLVGSTVFAVDSPIEDTPII
RNGGELTNLLGNSETTLALRNEESATALTAAAVADTVAAAAAENAGAAAWEAAAAD
RAGARAABALKEENKYGVSDYYKNLINNAKTVEGIKDLOAQVVESAKKARISEATDGL
SDFLKSOTPAEDTVKSIELAAKVLINNELDKYGVSDYKKNLINNAKTVEGYKELIDE
ILAALFKTDYTKLILGKTLKGETTTEAVDAATAEKVFKOYANDNGVDGEWTYDDATK
TPTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKOYANDNG
VGVWTYDDATKTFTVTEWYTEVPGDAFTEPERFEASIPLVPLTARVDBAKKD
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VGCWTYDDATKTFTVTEWTEVPGBSNPFTAAALAVMAGAGALAVASKRKED"
677. . 1921
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                                                                                                                                                 /product="1gG binding protein mature peptide" 706 a 323 c 398 g 523 t 1 bp upstream of HindilI site.
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/db_xref-"SWISS-PROT: P19909"
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SDFLKSQTPAABDTVKSIELABARVLANRELDKYGVSDYHKNLINNAKTVEGVKDLQAO
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LINNAKTVEGVKALIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVFKOY
ANDNGVDGEWTYDDATKTFTVTEKPINDASELTPAYTTYKLY INGKTLKGETTTEAV
BATAEKVFKOYANDNGVDEMTYDDATKTFTVTKP PEVIDASELTPAVTTYKLY ING
KTATAEKVFKOYANDNGVDEMTYDDATKTFTVTKP PEVIDASELTPAVTTYKLY ING
KTATAEKTTKANDATAEKATKOYANDNGVOGVWTYDDATKTFTVTEWTTEWTTEVFGOAPT
EPEKPEASIPLVPLTPATPIAKDDARKDDTKKEDAKKPEAKKEETLPTTGGGS
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Submitted (12-0CT-1987) Fahnestock S.R., Genex Corp., 16020
Industrial Dr., Gaithersburg, MD 20877, USA
2 (bases 1 to 2384)
Filpula,D., Alexander,P. and Fahnestock,S.R.
Nuclectide sequence of the protein G gene from Streptococcus GX7805, and comparison to previously reported sequences
Nucleic Acids Res. 15 (17), 7210 (1987)
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                                                                                                                                                                   Streptococcus sp. spg gene for protein G. Y00428
                                                                                                                                                                                                                                                                          G protein; IgG binding protein; spg gene. Streptococcus sp. GX7805. Streptococcus sp. GX7805
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986. 1435
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577. .2358
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Fahnestock, S.R.
                                577. .2358
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AAVKKADNAASDTLEALADOTDALGSEEAEVVGSDNAASDAMGKAATPIALDVKKTKD
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Rasmussen, M., Muller H.P. and Bjorck, L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the bacterial surface by binding alpha2-macroglobulin
J. Biol. Chem. 274 (22), 15336-15344 (1999)
                                                                                                                                                                                                                                                                                                            BCT 14-AUG-2000
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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pyogenes strain KTL9 GRAB precursor, gene, partial
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/note="Region: alpha2-macroglobulin-binding A domain"
/note="grab"
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                                                                                                  61 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaYalVal
                                    LysLysGlnAlaIleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp
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/note-"Region: cell-wall attachment"
/140 c 163 g 157 t
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/organism="Streptococcus pyogenes"
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constant region; immunoglobulin binding protein.
Streptococcus sp. (Lancefield group G; strain GX7809) DNA, clone
mGX4547.
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Fahnestock, S.R., Alexander, P., Nagle, J. and Filpula, D. Gene for an immunoglobulin-binding protein from a group streptococcus
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578. .676
/note="IgG binding protein signal peptide"
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IEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQS
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2 (bases 1 to 469)
2 (bases 1 to 469)
2 Insulation Muller, H.P. and Bjorck, L.
Direct Submission 1999 (Cell and Molecular Biology, Molecular Submitted (28-JAN-1999) (Cell and Molecular Biology, Molecular Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden Location/Qualifiers
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Rasmussen,M., Muller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates p
bacterial surface by binding alpha2-macroglobulin
J. Biol. Chem. 274 (22), 15336-15344 (1999)
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Rasmussen, M., Muller, H.P. and Bjorck, L.
Protein GRAB of streptococcus pyogenes regulates proteolysis at the Jacterial surface by binding alpha2-macroglobulin 574 (22), 15336-15344 (1999)
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EEAAVVOSDNAAGDALAADQTDALQSEERAVVKADNAASDALEALADQTDALQSEE
ASVVKADNAASDALEALADQTDALQSEERAVVKADNAASDALEALADQTDALQSEE
ASVVKADNAASDALEALADQTDALQSEERAAVKADNAASDALEALADQTDALQSEERA
AF124403 804 bp DNA linear BCT 14-AUG-2000
Streptococcus pyogenes strain AP49 GRAB precursor, gene, partial
                                                                                                                           Streptococcus pyogenes.
Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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<1. .>804
/note="grab"
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Direct Submission
Submitted (28-JAN-1999) Ceil and Molecular Biology, Molecular Pathogenesis, Seelbegatan 39, Lund 221 00, Sweden
Location/Qualifiers
1. 804
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/strain="App9"
/db_xref="taxon:1314"
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Indels:
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/product="GRAB precursor"
/protein_id="AAD26342.1"
/db_xref="GI:4589087"
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/note="Region: c
a 161 c 185
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                                                            AF124403
AF124403.1 GI:4589086
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536.00
94.26%
92.62%
68.98%
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BCT 14-AUG-2000
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Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                               /translation="VOSPIEOPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQA
IEDKEATTALEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQS
EEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQNVNTLPTTGEE"
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Streptococcus pyogenes strain AP1 GRAB precursor, gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                       /note="Region: alpha2-macroglobulin-binding A domain"
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/note="Region: repeat motif"
343. .468
/note="Region: cell-wall attachment"
91 c 100 g 99 t
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Matches:
Conservative:
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Indels:
                     /note="grab"
/codon_start=1
/transl_table=11
/product="GRAB precursor"
/protein_id="AAD26340.1"
/db_xref="GI:4589083"
                                                                                                                                                                                                                                                                                                                                (1-468)
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AF124400.1 GI:4589080
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                                                                                                                                         misc_feature
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Rasmussen, M., Muller, H.P. and Bjorck, L.
Direct Submission
Submitted (28-JAW-1999) Cell and Molecular Biology, Molecular
Pathogenesis, Soelvegatan 39, Lund 221 00, Sweden
Location/Qualifiers
                                                                                                                                                                                                                LysLysGlnAlalleGluAspLysGluAlaThrThrAlaIleGluAlaAlaSerSerAsp 60
                                                                                                                                                                                                                                                                  AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 80
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Protein GRAB of streptococcus pyogenes regulates p
bacterial surface by binding alpha2-macroglobulin
J. Bioll Chem. 274 (22), 15336-15344 (1999)
10029
159
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    .468
    /organism="Streptococcus pyogenes"
/strain="KTL3"

                          Conservative:
Mismatches:
Indels:
 Length:
Matches:
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11. >468
/product="GRAB"
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Streptococcus pyogenes
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AF124401.1 GI:4589082
2.15e-89
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TITLE
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MEDLINE
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MYTHYDTFTVATMINIALSNIRITYDLKTVEQYMIPITDYGYLCEDSSVEEPWTLIKK
TROVREPVLDYKRKVIGVSHRDVYDOLPTTKLTKVYSKNITTARPNTSLANISOKMI
FEDLAMLPYTDEENNLLGAMFRQAMENLPNHOPNNPYTYSEQILSNLEETVDYYOVV
VEPTWALDSAGNMSWYYELHAIQIEDELKI
YPKIITENRRSSTIDIEIFVDDQVIAKAITTKIN*
(gene="SPY1356" - 5690)

Complement(5148 . 5690)
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FPEQKTKAASDYLLVHSFIKFPLGOWAIEDKATHQVIGSIRIEHYDAKTRCADIGYFL
NYAFWGQGIMTEVVIKLYYLSFHEFGLKTLRIITHLENKASQKVAKKAGFQLKTCFKG
                                                                                                                                                                                                                                                                        /translation="makhodildylerlaigkwyrksishhikwsdgtavralkere
//translation="makkowildklaigk"
//translatiwggilhigherijollalehinailwyggipyskyuemandrid
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/product="protein GRAB (protein G-related alpha 2M-binding
protein)"
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PNGGTLTILLGNAPEKLAIREERALDELKKOAIEDKERATA TEAASSDALEALADOT
DALGSEEAAVVKADRASDALEALADOTDALGSEEAAVVGSDARSDAWEKAATPIAL
DVKKTKDTKPVVKKEERQNVNTLPTTGEESNPFFTAAALAIMYSTGVLVVSSKCKEN.
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UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE 2
UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE 2
(ENOYLPPRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE
ENOLPPRUVAT TRANSFERASE) (EPT) >9412127263|pir|(B32354
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) murz - Bacillus subtilis
yqi|(B53767|emb|CAA89875.1| (Z49782)
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bacillus subtilis] >941|2636235|emb|CAB15727.1| (Z9912)
      (AF008220) YtoI [Bacillus subtilis]
>91|2635392|emb|CAB14887.1| (Z99118) ytoI [Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Best Blastp hit = emb[CAA03913.11 (AJ0000084) putative acetyl transferase [Proteus mirabilis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Best Blastp hit - gb|AAD26340.1|AF124401_1
(AF124401) GRAB precursor [Streptococcus pyogenes]"
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1-carboxyvinyltransferase"
/protein_id="AAK34186.1"
                                                                                                                                                                              hypothetical protein"
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/product="putative acetyl transferase"
/protein.id="AAK184184.1"
/db_xref="G1:13622465"
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/protein_id-"AAK34183.1"
/db_xref-"GI:13622464"
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/db_xref="GI:13622466"
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/note="SPy1358"
complement(6939. .8198)
/gene="murz"
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/note="SPy1357"
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                                                                                       /note="Best Blastp hit = spiP43905|AROA_LACLA
3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE
(5-ENOLPYRUYYLGHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP
8-SYNTHASE) (EPSPS) >q1|1075724|pir|1552580
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
- Lactococcus lactis >q1|683583|emb|CAA55180.11 (X784.3)
5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cranslation="MAEKWPENKVLSKWOYEPIQVFWRHLQSAEMDLSAIAVAYYLIL
THPPLIVIPENFSKPSGSVLGVA
TLTGLWTWSRSLTSLOKAINKAYGACQHRDFFIGHLYGLLTSLIILFLLAFALIFES
SKAAIQVLDKHYHLSDNITTIFLLIQPITVLIIFVGLMLLYFFLLDNYKIKK RYILE
GTLFTSEPWPFLSNLYGNYVYNVERWYDIKNEGSYMIFIIMWFIFLARILILGAIF
COMPIEMSLGKLEGSGDMIAILKKTLGNDSDLSPSQSIEDSHTD"
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RRRCKEDNYLJLGGGVDGHMADYPYATCCGLNDEVAHAFPHYILKEGDLLKVDMVLS
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ITYTLPISSAQVKSAILLAALQAKGTTOVVEKEITRNHTEEMIQOFGGRLIVDGKRIT
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DAQELRVKETDRIQVVTDIINSMGANIKATADGMIIKGPTVLYGANTSTYGDHRIGMM
TAIAALLVKQGQVHLDKEEAIMTSYPTFFKDLERLCHD"
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/note="SPy1355"
/note="Best Blastp hit = pir||A69998 hypothetical protein
yto! - Bacillus subtilis >gi|2293258||gb|AAC00336.1|
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ANINOPEPTIDASE (MAP) (PEPTIDASE M)

941111264635|plr||144405 methionyl aminopeptidase (EC 3.4.11.8) map (imported) - Bacillus halodurans

9414512426|db||BAA75293.11 (AB017508) map homologue (identity of 818 to 8. subtilis ) [Bacillus halodurans]

94110172768|db||BAB03875.11 (AP001507) methionine aminopeptidase [Bacillus halodurans]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Best Blastp hit - dbj|BAB07074.1| (AP001518)
unknown conserved protein [Bacillus halodurans]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-carboxyvinyltransferase"
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complement(2013. .2978)
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                                                           /EC_number="2.5.1.19"
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/product="GRAB"
100. .273
/note="Region: alpha2-macroglobulin-binding A domain"
274. .441
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Sweden
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                                                                           Streptococcus.

1 (bases 1 to 832)
Rasmussen,M. wuller,H.P. and Bjorck,L.
Protein GRAB of streptococcus pyogenes regulates p
bacterial surface by binding alpha2-macroglobulin
9269061_chem_274 (22)7-15336-15344 (1999)
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Direct Submission
Submitted (28-JAN-1999) Cell and Molecular Biolognesis, Soelvegatan 39, Lund 221,00, Swellon/Qualifiers

Companism="Streptococous pyogenes" (45-Jan - Arcc: 700394")

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QHGEIAFRTIESQVLKDLLFANDNSIIVTGGGVVVLQENRQLLRKNHQHNILLVASFF
TLYQRLKHDKKSQRPLFLKYSKEAFYEFYQQRMVFYEGLSDLVIRVDHRTPEEVANII
                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
of 167 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 10029)
Perretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E. Complete genome sequence of an M1 strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Therefti, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Vuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.
Direct Submission
Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 SL Young Blvd, Oklahoma City, OK 73104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Best Blastp hit = pir||D82693 shikimate kinase
Kr1335 [imported] - xylella fastidiosa (strain 9a5c)
>gi|9106332|gb|AAR84144.1|AE003966_5 (AE003966) shikimate
kinase [Xylella fastidiosa]"
460 GCAGCAACTCCCAATCGCTTTAGATGTTAAGAAAACTAAAAGATACAAAACCTGTAGTTAAA 519
                                                                                                                                                 121 AlaAlaThrProileAlaLeuAspValLySLySThrLySASpThrLySProValValLyS 140
                                                                                                                                                                                                                                  AE006573 10029 bp DNA linear BCT Streptococcus pyogenes MI GAS strain SF370, section 102
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/protein_id-"AAK34179.1"
/db_xref-"G1:13622460"
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complement(135. .626)
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/note="SPy1352"
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AE006573 AE004092
AE006573.1 GI:13622459
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em_htg_hum:*
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-UNITG-b1ts -START=1 -END-1 -MATRIX-b100sum62 -TRANS-human40.cdi -LIST=45
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-WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                   October 13, 2002, 02:12:06 ; Search time 1551.74 Seconds (without alignments) 2144.253 Million cell updates/sec
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1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159
                           GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                     OM protein - nucleic search, using frame_plus_p2n model
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SUMMARIES

| Res  | Result               |          | %<br>Query                  |                       |                |                      |                       |
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| ;    | ₽                    | Score    | Match                       | Length                | DB             | aı                   | Description           |
|      | 1                    | 777      | 0.00                        | 832                   |                | AF124399             | F124399 Strep         |
| Ö    | 7                    | 777      | 0                           | 10029                 | Н              | AE006573             | AE006573 Streptoco    |
|      | ო .                  | 760      | œ (                         | 468                   | <del>, ,</del> | AF124401             | AF124401 Streptoco    |
|      | <b>→</b> u           | 754      | 0 0                         | 469                   | Н-             | AF124400             | AF124400 Streptoco    |
|      | n ve                 | 534      | ٠.                          | 717                   |                | AF124403<br>AF124402 | AF124403 Streptoco    |
|      | ۰,                   | 155      | 6                           | 1950                  | ٠.             | STRSPGIGP            | M13825 Streptococc    |
|      | 80                   | 155      | o.                          | 1950                  | 9              |                      | 109115 Sequence 23    |
|      | ο (                  | 155      | o, c                        | 2384                  |                | SGSPG                | Y00428 Streptococc    |
|      | 3:                   | 155      | אַ ס                        | 2384                  | - م            | 108537<br>SGPROTG    | 108537 Sequence 4     |
|      | 17                   | 153      | , ~                         | 1950                  | 9              | 108536               | 108536 Sequence 2     |
|      | 13                   | 142      | m                           | 1576                  | -              | SG148PG              | X53324 Streptococc    |
|      | 14                   | 126      | N                           | 696                   | Н              | STRABP               | M95520 Streptococc    |
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| t    | 1 8 1                | 107      | • <                         | 3222                  | 1              | HFU2363/<br>STVDDGGW | 02383/ Herpesvirus    |
| ,    | 16                   | 50       | • -                         | 48502                 | , ,            | LAMCG                | TO2459 Bacteriopha    |
|      | 20                   | 96       | 4                           | 13501                 |                | AE005258             | AE005258 Escherich    |
|      | 21                   | 96       | 4.                          | 297816                | -              | AP002553             | AP002553 Escherich    |
|      | 22                   | 92       | œ ۱                         | 220820                | ~              | AL663060             | AL663060 Mus muscu    |
|      | 5 7                  | 2 6      | ٠. ر                        | 1555                  | ٦,             | STRMAG               | L27798 Streptococc    |
|      | 2 C                  | )<br>n d | ی بو                        | 1409                  | - v            | 36148166<br>A13446   | AU4U15 Streptococc    |
|      | 26                   | 0 0      | ب و                         | 2022                  | m              | AY060997             | AY060997 Drosophil    |
|      | 27                   | 06       | φ                           | 6484                  | m              | AF335500             | AF335500 Physarum     |
|      | 28                   | 06       | 9.                          | 10432                 | -              | AE005333             | AE005333 Escherich    |
| ပ    | 53                   | 06       | ا ب                         | 54784                 | 7              | AC017732             | AC017732 Drosophil    |
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| y.   | 33                   | 200      | ی ہ                         | 222605                | n -            | ACUUBUB9<br>AD003555 | ACOUBORY DIOSOPHIL    |
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|      | 35                   | 68       | 'n                          | 2437                  | -              | SAG277292            | AJ277292 Streptoco    |
| ပ    | 36                   | 68       | 'n                          | 9331                  | Н              |                      | AE006458 Escherich    |
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| o c  | 42                   | 80       |                             | 43658                 | 17             | HSV3PRGEN            | 17 7890               |
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| AF1  | AF124399             |          |                             |                       |                |                      |                       |
| TOCU | US                   | :        | AF124399                    |                       |                | 832 bp DNA           | _                     |
| DEF  | DEFINITIO            | z        | streptococcus complete cds. | ccus pyogenes<br>cds. | gene           | strain ATCC/00294    | GRAB precursor, gene, |
| ACC  | ACCESSION<br>VERSION |          | AF124399<br>AF124399 1      | Ţ                     | .458907        | ď                    |                       |
| KEY  | KEYWORDS             |          |                             | ;                     |                | )                    |                       |
| son  | RCE                  | Stre     | aptococ                     | treptococcus pyogenes | gene           | . 25                 |                       |
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<sup>;</sup> 0 0; Gaps Query Match
Best Local Similarity 54.8%; Pred. No. 0.043;
Matches 17; Conservative 2; Mismatches 12; Indels

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Search completed: October 13, 2002, 02:08:14 Job time: 66.6203 secs

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                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                            Synthetic; protein G; IgG; Fc receptors; heavy chain; leukaemia; lymphoma; cancer; autoimmune disease.
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| 990x - 0132480.<br>990x - 0132480.<br>990x - 0132488.<br>990x - 0132488.<br>990x - 0132488.<br>990x - 0132488.<br>990x - 0132488.<br>990x - 0132421.<br>990x - 0134219.<br>990x - 0134219.<br>990x - 0134219.<br>990x - 0134219.<br>990x - 0134219.<br>990x - 0134219.<br>990x - 0139445.<br>990x - 0140695.<br>990x - 0140695.<br>990x - 0140695.<br>990x - 0142390.<br>990x - 0142390.<br>990x - 0142390.<br>990x - 0142390.<br>990x - 0142390.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 9US-014<br>9US-014<br>9US-014<br>9US-014<br>9US-014<br>9US-014                                           |
| 30-APR-1999;<br>04-MAY-1999;<br>05-MAY-1999;<br>06-MAY-1999;<br>07-MAY-1999;<br>07-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11-MAY-1999;<br>11                                                                                                                                                                                                                                                                                                                                                                                                      | - JUL-19<br>- JUL-19<br>- JUL-19<br>- JUL-19<br>- JUL-19<br>- JUL-19<br>- JUL-19                         |
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                       The sequence is that of 'SG-3 (synthetic protein G). SG-3 is capable of specifically binding the constant region of the heavy chain of 1gG in the same way as neutral Fc receptors. It can be used to analyse the structure and function of Fc receptors, as well as in antibody production, cell culture, diagnosis and therapy. They can be used to treat disorders such as leukaemia and lymphoma, cancer and immune
                                                                                                                                                     New peptide(s) which bind the Fc region of an immunoglobulin comprising a nontotal portion of the amino acid sequence of Protein A and/or Protein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 83; DB 16; Lengtu ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 22243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 DVKKTKDTKPVVKKEERQNVNTLPTTGEESN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG20163 standard; Protein; 168 AA.
                                                                                                                                                                                                                            Disclosure; Fig 2C; 61pp; English.
                                    (IMMU-) APPLIED IMMUNE SCI INC.
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99US-0131449.
99US-0132048.
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99US-0126264.
93US-0110653.
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99US-0123548.
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                                                                    Talib
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       termination sequence
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                                                                                                   WPI; 1995-106854/14.
N-PSDB; AAQ84884.
                                                                                                                                                                                                                                                                                                                                                                                    See also AAR71123-8.
                                                                    Okarma TB,
                                                                                                                                                                                                                                                                                                                                                                                                                      46 AA;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
 23-AUG-1993;
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09-MAR-1999
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30-APR-1999;
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                                                                  Lee YM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| | : :::: | | || : || : : | | || 327 APETEAAAKTTESSNDVVEVATEGKETVLEVPAAEPKEAESTVESAEELLETSTVVVTEP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 APEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKAD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic; protein G; IgG; Fc receptors; heavy chain; leukaemia; lymphoma; cancer; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 2757; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 NAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKK 131
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                                                                                                                   23-MAR-2001; 2001WO-US09231
                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                  Drosophila melanogaster,
                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072).
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N-PSDB; ABL02758.
                                                                                                                                                                                                          (PEKE ) PE CORP NY
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                                                  WO200171042-A2.
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                                                                                    27-SEP-2001
                                                                                                                                                                                                                                          Venter JC,
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SG-3.

RESULT 37 AAR7112

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MUELLER H.
RANTAMAKI L K.
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N-PSDB; AAQ89196.
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nes 18; Conserv
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LINDBERG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to obtain prods. for binding inhibition
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                                                                                                                                                                                                                                                                                                                                                                         (MUEL/)
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                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating of sources involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Asgounces of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 EDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 86; DB 22; Length 1107; 26.8%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIG; fast alpha-2-macroglobulin binding protein; FAM; plasma proteinase-inhibitor binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 EVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKE 142
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/label- Sig_peptide
209..278
/label- 1gGl
/note- "igG binding domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                         Claim 20; SEQ ID No 48606; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus dysgalactiae strain SC1
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                                     Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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 dysgalactiae MIG.

                                    Drmanac RT, Liu C,
                                                           WPI; 2001-639362/73
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           (HYSE-) HYSEQ INC.
                                                                        N-PSDB; AAS82434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding fast alpha 2-macro:globulin-binding proteins - use to obtain prods. for sepn., detection or quantification or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rantamaki LK;
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                                                                                                                                                                                                                                                                                 630..635
//note= "putative wall anchoring motif"
639..664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 2757.
                                                                                                                                                                                                                                                                      /note= "cell wall spanning region"
                                                                                                                                                                                                                                                                                                                                                           /note- "membrane spanning domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
279..348
/label= 1gG2
/note= "IgG binding domain 2"
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                                                                                                                                                                                                            /label= 19G5
/note= "1gG binding domain
                                                                                                          domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 DVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 85; 56.2%; Pred. No.
                                                                                  /label= IgG3
/note= "IgG binding
                                                                                                                                               /label= IgG4
/note= "IgG binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 31; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB58655 standard; Protein; 489 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lindberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93SE-0002855.
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                                                              ..418
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                                                                                                                           .488
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a GRAB peptide EKL 18 useful in vaccine composition. It was used to produce immunoglobulin G (1gG) antibodies specific for native GRAB protein in sheep. The peptide has a cysteine insert at the C-terminal for attachment to a hetero-bifunctional linker.
                                                                                                                                                                                                                                                                                   New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                         alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; peptide EKL 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 21; Length 15,
Pred. No. 0.0011;
           GRAB; protein G related alpha2M binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #18238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG18247 standard; Protein; 1107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Sc..
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                              Example 9; Page 31; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                  99WO-GB03631,
                                                                                                                                                                          98GB-0023975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.1
Best Local Similarity 100.
Matches 18; Conservative
                                                                 Streptococcus pyogenes
                                                                                                                                                                                                     (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                          WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AA;
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                                                                                           WO200026240-A2
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                                                                                                                                                 02-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG18247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity as protein G from Streptococcus G148 (AAN70757) is claimed. See, for example, AAN70754, AAN70755 and AAN70756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                  Gaps
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                                                                 ö
                                      DB 16; Length 413;
                                                                                                                                                                                                                                                                       Sequence of polypeptide possessing 1gG-binding activity of protein G from Streptococcus G148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA molecules - for producing proteins IgG-binding specificity of protein G or proteins A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
8
                                    Score 91; DB 16.
Pred. No. 0.011;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uhlen CEM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes GRAB peptide EKL 18.
                                                                                                                                                                                                                                                                                                                Antibody-binding; IgG; IgA; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 DVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 DTKKEDAKKPEAKKEDAKKAETLPTTGEGSNP 455
                                                                                           128 DVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                          AAP70468 standard; Protein; 480 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Fig 2; 39pp; English.
                                    11.7%;
59.4%;
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                                                                                                                                                                                                                                            21-MAY-1991 (first entry)
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Matches 18; Conservative
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guss BM, Lindberg KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA AB. (GUSS/) GUSS B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1987-277686/39.
                                                                                                                                                                                                                                                                                                                                           Streptococcus G148.
                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 AA;
           413 AA;
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                                                                 19;
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            Sequence
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                                    Query Match
                                                      Local
                                                                Matches
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A phage lambda EMBL3 library of S. dysgalactiae 8215 DNA was analyzed for alpha-2-macroglobulin. BSA- and IGG-binding activity. Clone lambda-SD1, which expressed all 3 activities, was analyzed to obtain DNA encoding the SA-binding protein, MAG. The mag gene (given in 086080) encoded a 44 kba MAG protein (R71670). Recombinant, immobilized MAG was used for serum albumin affinity purification, detection and assay.
                                                                                                                                                                                                                                                                                                                            Mag gene; serum albumin binding protein; protein stabilization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a serum albumin binding protein - used to obtain prods. for sepns., detection, quantification, protein stabilisation or vaccine development
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- A2-M
/note- "alpha-2-macroglobulin binding domain"
                      11.7%; Score 91; DB 16; Length 413; llarity 59.4%; Pred. No. 0.011; Conservative 1; Mismatches 12: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cell wall binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "membrane-spanning region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Alb
/note- "albumin binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243..312
/label= IgG
/note= "IgG binding domain"
313..387
                                                                                         128 DVKKTKDTKPVVKKEERQNVNTLPTTGEESNP 159
                                                                                                             Streptococcus dysgalactiae strain 8215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 29-30; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      1..34
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                       Locatión/Qualifiers
                                                                                                                                                                                                   AAR71670 standard; Protein; 413 AA.
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                                                                                                                                                                                                                                                                                             S. dysgalactiae MAG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93SE-0002856.
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                                                                                                                                                                                                                                                               (first entry)
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388..413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GUSS/) GUSS B.
(JONS/) JONSSON H.
(LIND/) LINDBERG M.
                                           Local Similarity
les 19; Conserv
413 AA;
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Sequence
                                                                                                                                                                                                                                AAR71670;
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                Best Loc
Matches
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S
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                                                                                                                                                                                                                   50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
                                A phage lambda EMBL library of S. dysgalactiae 8215 DNA was analyzed for fast-acting alpha-2-macroglobulin (FAM)-, BSA- and IgG-binding activity. Clone lambda-SDL, which expressed all 3 activities, was analyzed to obtain DNA encoding the FAM-binding protein, MAG. The mag gene (given in Q89197) encodes a 44 kDa protein (R71929).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding fast alpha 2-macro:globulin-binding proteins - used to obtain prods. for sepn., detection or quantification or for binding inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "alpha-2-macroglobulin binding domain"
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                                                                                                                                                                                                                                                                                                          MAG; fast alpha-2-macroglobulin binding protein; FAM;
plasma proteinase-inhibitor binding protein.
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388..413
/label= membrane-spanning region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "albumin binding domain"
243..312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label = IgG /note = "IgG binding domain"
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/label- Sig_peptide
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                                                                                                                                                                                  AAR71928 standard; Protein; 413 AA.
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    dysgalactiae MAG protein.

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                                                                                                                                                                                                                                               (first entry)
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LINDBERG M.
MUELLER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-123382/16.
N-PSDB; AAQ89197.
                                                                        110 SDNAASDA 117
                                                                                                     447 ETNASSSA 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JONS/)
(LIND/)
(MUEL/)
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Domain

AAR71928 RESULT

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Conditional partner of the invention of mutations and acid sequences of the invention.

Conditional partner of the invention of mutations of the invention but was obtained in electronic format directly from MIPO are the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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0.0063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 46397; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93;
Pred. No. (
                                                                                                                                                                                                                                   Novel human diagnostic protein #16029.
                                                                                                                        ABG16038 standard; Protein; 422 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 35.39
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS80225
                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                           ABG16038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                          ABG16038
                                                                                        RESULT
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in chagnostics, forensics, gene mapping, identification of mutations constitutions in the polypeptide and disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.0%; Score 93; DB 22; 35.3%; Pred. No. 0.0069; tive 13; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 50668; 103pp; English.
                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #20300.
                                                                                                                                                                                          ABG20309 standard; Protein; 459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                      110 SDNAASDA 117
                                                                                           410 ETNASSSA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS84496
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity
                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-0CT-2001.
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Gaps

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24; Conservative

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Gaps

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.31; Indels

13; Mismatches

50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109

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us-09-847-539a-6.rag

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Gaps

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Indels

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Length 20;

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from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a GRAB peptide KKT 19 useful in vaccine composition. It was used to produce immunoglobulin G (IgG) antibodies specific for native GRAB protein in sheep. The peptide has a cysteine insert at the C-terminal for attachment to a hetero-bifunctional linker.
                                                                                                                                                                                                                                                                                                                                                                                  GRAB; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; peptide DSP 18.
                                                                                                                                           97; DB 21;
No. 5e-05;
                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes GRAB peptide DSP 18.
                                                                                                                                                                 Mismatches
                                                                                                                                           Score 97;
                                                                                                                                                        Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 31; 67pp; English
                                                                                                                                         12.5%; Sco
100.0%; Pri
tive 0;
                                                                                                                                                                                                                                                                                   AAY71047 standard; peptide; 19
                                                                                                                                                                                           130 KKTKDTKPVVKKEERQNVN 148
                                                                                                                                                                                                        1 KKTKDTKPVVKKEERQNVN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-0023975.
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACTI-) ACTINOVA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365572/31.
                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                  20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200026240-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                    29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bjorck LH,
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                           AAY71047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                          RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                  Protein G isolated from Streptococcus has IgG-binding activity which has been localised to the B repeating structure (see AAR53290). The sequence AAR53294 represents a claimed Streptococcal Protein G variant comprising the B domain active site and retaining
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
immune response; Streptococcus pyogenes infection; peptide KKT 19.
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                     New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy
                                                                                                                                                                                                                                                                                                                        Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein G related alpha2M binding protein; vaccine;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                       Score 105; DB 15;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes GRAB peptide KKT 19.
                                                                                                                                                                                                                                                                                                                                                                                   PIEOPRIIPNGGTLTNLLGNAPEKLALRNEERA 36
                                                                (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB.
                                                                                                                                                                                         Claim 3; Column 46; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                     13.5%;
             88US-0209236.
90US-0540169.
 87us-0063959
                                      92US-0871539
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71051 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0023975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-GB03631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 31; 67pp;
                                                                                                                                                                                                                                                                                                                                              23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ACTI-) ACTINOVA LTD.
                                                                                                                WPI; 1994-159179/19.
                                                                                                                                                                                                                                                                     IgG-binding activity
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                             265 AA;
                                                                                                                            N-PSDB; AAQ64648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200026240-A2
                                                                                         Fahnestock SR;
 19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-1999;
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                                      21-APR-1992;
              20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000
                          .9-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9;
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                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71051;
                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRAB;
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
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                                                                                                                                                                                                                      related alphazM binding procedul) from Streptococcus progenes which have the ability to bind alpha2-macroglobulin (alphaZM) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus progenes infections. The protein is also useful for purifying alphaZM from a sample. The present sequence is a GRAB peptide DSP 18 useful in vaccine composition. It was used to produce immunoglobulin G (IgG) antibodies specific for native GRAB protein in sheep. The peptide has a cysteine insert at the C-terminal for attachment to a hetero-bifunctional linker.
New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                              The patent discloses a new family of proteins termed GRAB (protein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Lv
. 6.3e-05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 96; DB 100.0%; Pred. No. 6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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RESULT 23 AAR07004

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Protein G variant product carries active regions B1 and B2, it may be imobilised and exhibits different binding profiles. The bound protein is useful in purification and detection of Igs and framents.
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/label- secretion_sequence
31..262
/label- Protein_G_variant
/note- "claimed without the secretion sequence"
                                                                                                                                                                                                                                                                                                                      Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.5%; Score 105; DB 12; Best Local Similarity 69.7%; Pred. No. 0.00012; Matches 23; Conservative 1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus Protein G variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PIEQPRIIPNGGTLTNLLGNAPEKLALRNEERA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 11; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR53294 standard; Protein; 265 AA.
                                                                                                                                                                                                                                                      Wroble MH;
                                                                                                                        89US-0354264.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86US-0829354
86US-0854887
                                                                                                 89US-0354264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                 Streptococcus sp GX7809
                                                                                                                                                                                                                                                     Lee T,
                                                                                                                                                                                                                                                                               WPI; 1991-006758/01.
                                                                                                                                                                                                                           (GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus sp.
                                                                                                                                                                                                                                                                                              Q-PSDB; Q10007
                                                                                                                                                                                                                                                     Fahnestoc SR,
                                                                                                 19-MAY-1989;
                                                                                                                                                       23-APR-1986;
17-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1986;
23-APR-1986;
                                                                                                                                                                                               20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IgG-binding
                                           US4977247-A.
                                                                                                                                           14-FEB-1986;
                                                                       11-DEC-1990
                                                                                                                            19-MAY-1989
                                                                                                                                                                                    19-JUN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR53294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR53294
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  ö
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence may be incorporated into a non-pathogenic host eg. E.coll, where they may be expressed at high levels. The proteins have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifyling, detecting and isolating antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 69.7%; Pred. No. 0.0001;
Matches 23; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
 9; Indels
                                                                                                                                                                                                                                                               Streptococcus sp. Lancefield Group G strain.
 1; Mismatches
                          4 PIEQPRIIPNGGTLTNLLGNAPEKLALRNEERA 36
                                          4 PIEDTPIIRNGGELTNLEGNSETTLALRNEESA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PIEQPRIIPNGGTLTNLLGNAPEKLALRNEERA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PIEDTPIIRNGGELTNLLGNSETTLALRNEESA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 9-16; 48pp; English.
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                                                                                                                        AAR07004 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                         88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                                                                                                                                                                                                                                 88US-0209236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1991 (first entry)
                                                                                                                                                                               17-JAN-1991 (first entry)
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-297491/39.
N-PSDB; AAQ06009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulins; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AA;
                                                                                                                                                                                                           Protein G variant.
                                                                                                                                                                                                                                       Immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                 20-JUN-1988;
                                                                                                                                                                                                                                                                                           US4956296-A
                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1986;
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AAR1001

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Gaps

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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective from it are used in vaccine compositions for generating a protective are useful for treating Streptococcus, pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a GRAB peptide EKL 24 useful in vaccine composition. It was used to produce immunoglobulin G (IGG) antibodies specific for native GRAB protein in sheep. The peptide has a cysteine insert at the C-terminal for attachment to a hetero-bifunctional linker.
New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene for protein G variant of non-pathogenic streptococcus sp. allowing isolation of the protein and variants, useful as bacterial Fc receptors eg in purification and detection of Abs., screening of hybridoma clones and treatment of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressing proteins having immunoglobulin-binding properties of protein G and derived from Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 10; Length 235;
Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 115; DB 21; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 110; 2011
100.0%; Pred. No. 4e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein G; immunoglobulin; Fc receptor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP94785 standard; protein; 235 AA.
                                                           Page 31; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 88; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 EKLALRNEERAIDELKKQAIEDKE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EKLALRNEERAIDELKKQAIEDKE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloned protein G variant genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88WO-US02084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUL-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AA;
                                                                                                                                                                                                                                                                                                                                                             25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN91099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                           Example 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP94785;
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus, natibodies against GRAB are useful for treating Streptococcus, pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a fragment of GRAB protein from S, pyogenes strain SF370 corresponding to residues 34-56. This fragment is capable of binding alpha2M and useful in vaccine composition.
                                                                                                                                                                                                                                                                                               New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRAB; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; peptide EKL 24.
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Pred. No. 8.7e-08;
Mismatches 0;
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100.0%; Pred. No. c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71048 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 55; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDSPIEQPRIIPNGGTLTNLLGN 23
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                                                                                                99WO-GB03631
                                                                                                                                     98GB-0023975
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Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3jorck LH, Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes
                                                                                                                                                                                                                     Rasmussen
                                                                                                                                                                            (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                        WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                             New alpha2M binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPI; 2000-365572/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                  WO200026240-A2.
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                                                                                              32-NOV-1999;
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                                                                                                                                     32-NOV-1998;
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                                                       11-MAY-2000
                                                                                                                                                                                                                   Bjorck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Gaps

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Streptococcus pyogenes strain SF370 GRAB protein fragment #3.

(first entry)

29-AUG-2000

AAY71038;

A.

AAY71038 standard; peptide; 28

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RESULT 19
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Also described are: (1) a liposomal delivery vehicle comprising: (a) a liposome are: (1) a liposomal delivery vehicle comprising: (a) a liposome; and (b) a connecting moiety connected to the liposome, which specifically binds the Fc region of an antibody, for connecting the attibody to the liposome; and (2) forming a liposomal carrier comprising: (a) providing liposomal components having binding moieties, for forming a liposome; (b) providing a construct comprising a linking moiety and a connecting the liposomal accomponents and the construct and sonicating the liposomal components and the construct and sonicating the liposomal components and the construct and sonicating the liposome, for binding to the linking moiety, and to facilitate the binding between them. The binding moiety, and to facilitate the binding between them. The construct can be used for the delivery of diagnostic or therapeutic agent, e.g. antiblotics, antidepressants, cor therapeutic agent, e.g. antiblotics, antidepressants, courtenessing agents, councilly moiety provides a liposomal delivery of cytotoxic agents to maily an used particularly for the delivery of cytotoxic agents to mailgnant cells. The protein G' connecting moiety provides a liposomal delivery complex having improved the connecting moiety provides a liposomal delivery complex having improved the connecting moiety provides a liposomal delivery complex protein g' connecting moiety provides a liposomal delivery complex may be connected to the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the liposom of the li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New liposome constructs comprising a liposome connected to an antibody, used, e.g. for delivery of cytotoxic agents to malignant cells \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a construct for connecting an antibody
                                                                                                                                                                                                                                                                                                                                                           Streptococcus strain G 148; protein G'; protein G primer; liposome; liposomal delivery complex; connecting moiety; antibody; Fc region; diagnosis; therapeutic agent; antibotic; antidepressant; antiviral; antitumourigenic; cytokine; hormone; imaging agent; neurotransmitter; stimulant; cytotoxic agent; malignant cell.
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Pred. No. 1e-09;
                                                                                                                                                                                                                                                                Streptococcus strain G 148 protein.
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57.9%;
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                                                                                                                                                    10-MAR-2000 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus sp.
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                                       AAY57611;
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence S. pyogenes strain SF370 corresponding to residues 92-119. This fragment is useful in vaccine composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                          GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.6%; Score 129; DB 21; 100.0%; Pred. No. 8.6e-09;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SDALEALADQTDALQSEEAAVVKADNAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 SDALEALADQTDALQSEEAAVVKADNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 56; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71036 standard; peptide; 23
                                                                                                                                                                                                                                                                      99WO-GB03631.
                                                                                                                                                                                                                                                                                                     98GB-0023975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Bjorck LH, Rasmussen M;
                                                                                                                                                                          Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                     (ACTI-) ACTINOVA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 AA;
                                                                                                                                                                                                       WO200026240-A2.
                                                                                                                                                                                                                                                                      02-NOV-1999;
                                                                                                                                                                                                                                                                                                    02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2000
                                                                                                                                                                                                                                      11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY71036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
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ID AAY7
XX AC AAY7
XX XX
DDT 29-A
XX XX
KW GRAB
KW alph
KW immu
XX Immu
XX SETE
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Gaps

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21; Indels

3; Mismatches

33; Conservative

Matches

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A 2.4kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7805 using the 1.9kb Protein G coding sequence from Streptococcus GX7809. The Protein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 155; DB 15; Length 5:
Pred. No. 2.2e-10;
4; Mismatches 25; Indels
"involved in IgG binding activity"
                                      373 ..427
/label- B3
/note= "involved in 1gG binding activity"
                                                                                                                                               note= "involved in 1gG binding activity"
                                                                                                                                                                                                                                                                                                 /note= "corresponds to GAA codon"
                                                                                 'note= "corresponds to CCT codon"
                                                                                                                                                                   'note- "corresponds to ACT codon
                                                                                          428..442
/label = b
/note = "linking region"
443..497 |
/label = B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB.
                              'note- "linking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Fig 9; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   860S-0829354.
860S-0854887.
870S-0063959.
88US-0209236.
90US-0540169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 19.9%;
Local Similarity 56.1%;
Nes 37; Conservative
                                                                                                                                                                            531..535
/label- c1
                                                                                                                                                                                                 536..540
/label= C2
                                                                                                                                                                                                                       541..545
/label= C3
                                                                                                                                                                                                                                                                                                                                                                86US-0829354
                                                                                                                                                                                                                                           546..550
/label- C4
                                                                                                                                                                                                                                                                  551..555
/label- C5
                     /label- b
/note= "1
358..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-159179/19.
N-PSDB; AAQ75036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593 AA;
                                                                        Misc-difference
                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                               14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1986,
19-JUN-1987,
20-JUN-1988,
19-JUN-1990,
                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-1992;
                                          Active-site
                                                                                                                           Active-site
                                                                                                                                                                                                                                                                                                                      US5312901-A
                                                                                                                                                                                                                                                                                                                                           17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                             Region
                                                                                                                                                                                                                        Region
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein G gene product may be modified allowing the variant to be imobilised and exhibit different binding profiles. The bound protein is useful in purification and detection of Igs and fragments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VDSPIEQPRIIPNGGTLTTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 VDSPIEDTPIIRNGGELTNLLGNSETTLALRNESSATADLTAAAVADTVAAAAAENAGAA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immobilised protein G variants - used for detection, isolation and purificn. Immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
19.9%; Score 155; DB 12;
Best Local Similarity 56.1%; Pred. No. 2.2e-10;
Matches 37; Conservative 4; Mismatches 25;
                                                                                                                                                      304..358
/label= Active Site B1
374..428
/label= Active Site B3
444..498
/label= Active Site B2
                                                                                                                                             Location/Qualifiers
           AAR10005 standard; protein; 594 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY57611 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       Wroble MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9; 52pp; English.
                                                                           ö
                                                                          Streptococcus GX7805 protein
                                                                                                                                                                                                                                                                                                     89US-0354264.
86US-0829354.
86US-0854887.
                                                                                                                                                                                                                                                                                                                                     87WO-US00329.
87US-0063959.
88US-0209236.
                                                                                                                                                                                                                                                                                89US-0354264
                                                     (first entry)
                                                                                                                       Streptococcus sp GX7805
                                                                                                                                                                                                                                                                                                                                                                                                        Lee T,
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-006758/01.
Q-PSDB; Q10002.
                                                                                                   fmmunoqlobulins; Iq.
                                                                                                                                                                                                                                                                                                                                                                                   GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 AWEAAA 99
                                                                                                                                                                                                                                                                                                                                                                                                        Fahnestoc SR,
                                                                                                                                                                                                                                                                                                               14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
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                                                     13-MAR-1991
                                                                                                                                                                             Active-site
                                                                                                                                                                                                    Active-site
                                AAR10005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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ID AAYS
AAR10005
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Gaps

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1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60 

61 ALEALA 66

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1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed at high levels.

The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                           19.9%; Score 155; DB 11; Length 593; llarity 56.1%; Pred. No. 2.2e-10; Conservative 4; Mismatches 25; Indels (
                                                                                                                                                                                        Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus Protein G derived from strain GX7805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "corresponds to GGA codon" 303..357
/label= B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106..140
/label- Al
141..178
/label- al
/note- "linking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216..253
/label= a2
/note= "linking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR62944 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                  Disclosure; Fig 9; 48pp; English.
88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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/label- A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label- A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus sp. GX7805.
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                                                                                                                                              WPI; 1990-297491/39.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 37; Conserve
                                                                                       (GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                593 AA;
                                                                                                                                                             N-PSDB; AAQ06019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 AWEAAA 99
                                                                                                                  Fahnestock SR;
                            23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR62944;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                A 1.9kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7809. The Protein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
0
                                                                                                                                                                                                                                                                           New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 155, DB 15;
Pred, No. 1.5e-10;
4; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus sp. Lancefield Group G strain.
                                                                                                                                                                                                                                                                                                                    Example 2; Fig 3 and Fig 8; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein G variant with three active sites
                                                                                                                                                                         (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR07014 standard; protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.9%;
56.1%;
                                                                                     86US-0854887,
87US-0063959,
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                                           86US-0829354
                                                                        86US-0829354
                                                                                                               88US-0209236
90US-0540169
                                                                                                                                             92US-0871539
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/label=B3
443..497
/label=B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303..372
/label-Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.1
                                                                                                                                                                                                                                WPI; 1994-159179/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                       448 AA;
                                                                                                                                                                                                                                                N-PSDB; AAQ64644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 AWEAAA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin
                                                                                                                                                                                                      Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-1988;
                                           14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                         are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US4956296-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1990,
                                                                                                                20-JUN-1988;
                                                                                    23-APR-1986
                                                                                                                                             21-APR-1992
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Active-site
               17-MAY-1994
                                                                        14-FEB-1986
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Protein G gene product may be modified allowing the variant to be imobilised and exhibit different binding profiles. The bound protein is useful in purification and detection of 1gs and fragments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
19.9%; Score 155; DB 12; Length 448;
Best Local Similarity 56.1%; Pred. No. 1.5e-10;
Matches 37; Conservative 4; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus Protein G derived from strain GX7809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283.297
/label b
/note="linking region"
298.352
/label B2
  B1
/label= Active site
298..352
/label= Active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
228..282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR53290 standard; Protein; 448 AA.
                                                                                                                                                                                                                                                       Wroble MH;
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 52pp; English.
                                                                                                                                89US-0354264.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                          89US-0354264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus sp. GX7809.
                                                                                                                                                                                                                                                       Lee T,
                                                                                                                                                                                                                                                                                 WPI; 1991-006758/01
Q-PSDB; Q10001.
                                                                                                                                                                                                                              (GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ALEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 AWEAAA 99
                                                                                                                                                                                                                                                       Fahnestoc SR,
                                                                                                                                              14-FEB-1986;
23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
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                                                    US4977247-A
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                                                                                11-DEC-1990
                                                                                                                                   19-MAY-1989
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Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5312901-A
               Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 19.9%; Score 155; DB 11; Length 448; Local Similarity 56.1%; Pred. No. 1.5e-10; es 37; Conservative 4; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                           Streptococcus sp. Lancefield Group G strain.
                                                   Location/Qualifiers
228..282
/label=B1
298..352
/label=B2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 8a-c; 48pp; English.
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228..282
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                                                                                                                                                                                                           88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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N-PSDB; AAQ06018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 AA;
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Immunoglobulin
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                                                                                                                                                                                    20-JUN-1988;
                                                                                                                                                                                                            20-JUN-1988;
14-FEB-1986;
23-APR-1986;
17-FEB-1987;
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Active-site
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Best Loca Matches

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RESULT 13 **AAR10004** 

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1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
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                                                                                                                                                                                                                                                                                                                         Streptococcus sp
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AWEAAA 99
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                                                            61 ALEALA 66
                                                                                       94 AWEAAA 99
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                                                                                                                                                                                                                                                               Protein G.
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is a fragment of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-91. This fragment is capable of binding alpha2M and useful in vaccine composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein G expressed by inserting the gene into an expression vector. A second vector may also be used as a cryptic helper plasmid to stably maintain the first plasmid in the host cell. Bacterial Fc receptors such as Protein G can be used to detect and purify antibodies, and in the treatment of disease. Fc receptors are useful to purify antibodies to be used in the purifice. of protein drugs and as therapeutics. High levels of Protein G can be obtd. in conditions favourable for isolation, using a non-pathogenic host. Suitable cloning vectors are lambda gtll, MI3mp9 and pGX1066.
                                                                                                                          Gaps
                                                                                                                                                                      1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAAS 58
                                                                                                                                                     1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloned Protein G gene - used for producing Protein G for detection and purificn. of antibodies and treatment of diseases
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Pred. No. 1.5e-10;
4; Mismatches 25; Indels
                                                                                          Length 58
                                                                                        36.7%; Score 285; DB 21;
100.0%; Pred. No. 1.2e-27;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus Lancefield Group G strain.
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228..297
/label=active site B1
298..352
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                                                                                                                                                                                                                                                                                                                                                                                  Protein G; antibody; Fc receptor;
                                                                                                                                                                                                                                                            AAP70493 standard; protein; 448
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56.1%;
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86US-0829354
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                                                                                                       Best Local Similarity 100.
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Matches 37; Conservative
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(FAHN/) FAHNESTOCK S R.
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N-PSDB; AAN70811.
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                                                            58 AA;
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14-FEB-1986;
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                                                                                                                                                                                                                                                                                                                                                      Protein G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 VDSPIEDTPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAA 93
1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloned protein G variant genes - expressing proteins having immunoglobulin-binding properties protein G and derived from Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.9%; Score 155; DB 10; 56.1%; Pred. No. 1.5e-10; iive 4; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein G; immunoglobulin; Fc receptor; ds.
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                                                                                                                                                                                                                                                   AAP95030 standard; protein; 448 AA.
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                                                                     The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective manner response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus, pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence the protein has alpha2M binding region and is useful in vaccine
New alpha2M binding protein for generating a protective immune response to group. A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                       61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                               4 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 63
                                                                                                                                                                                                                                                                                                                                               1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
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                                                                                                                                                                                                                                                                                      Length 271;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes strain KTL9 partial GRAB protein.
                                                                                                                                                                                                                                                                     Score 536; DB 21; L
Pred. No. 9.4e-58;
                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 59-60; 67pp; English
                                                                                                                                                                                                                                                                                     69.0%;
92.6%;
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                                            67pp;
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                                            5; Page 61-62;
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                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                         271 AA;
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The patent discloses a new family of proteins termed GRAB (protein G

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related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is a lso useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. pyogenes strain KTL9. The protein composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective are useful for treating Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                    61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                     81 ALEALADQADALQSEEAAVVQSDNAASDALEALADQTDALQSEEAAVVKADNAASDTLEA 140
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAB protein; protein G related alpha2M binding protein; waccalpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                          Length 259;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                        Score 534; DB 21;
Pred. No. 1.6e-57;
4; Mismatches 6;
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                                                                                                                                                                                                                                                          68.7%;
91.8%;
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Matches 112; Conservative
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus, pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a frament of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-174. This fragment is devoid of the trans-membrane and cell wall anchor regions. It is useful in vaccine composition.
                                                                                                                    New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.4e-76;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%; Score 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71045 standard; Protein; 271 AA.
                                                                                                                                                                                  Claim 5; Page 57; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AATPIALDVKKTKDTKPVVKK 141
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Matches 141; Conservative
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                                          Bjorck LH, Rasmussen
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  (ACTI-) ACTINOVA LTD.
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                                                                              WPI; 2000-365572/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AA;
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The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                            New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 750; DB 21; Length 155;
Pred. No. 2e-84;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                         Claim 5; Page 60-61; 67pp; English.
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99.4%;
                                        99WO-GB03631
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Matches 154; Conservative
                                                                                                                                                            Rasmussen M;
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                                                                                                                      (ACTI-) ACTINOVA LTD.
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                                        02-NOV-1999;
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11-MAY-2000
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99WO-GB03631
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Best Local Similarity
Matches 156; Conserv
                                                                                                                                                                                                                                                                                                                   Sequence 167 AA;
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                                                                                                                 N-PSDB; AAD00564
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                     02-NOV-1999;
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 11-MAY-2000
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                                                                                  Bjorck LH,
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                                                                                                                                                                                                                    New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 217;
         /note= "consensus sequence for gram-positive surface cell wall anchored proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 777; DB 21; 100.0%; Pred. No. 1.4e-87;
                                        label- Membrane_spanning_region
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                                                                                                     99WO-GB03631,
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Matches 159; Conservative
183..188
                                                                                                                                                                  Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
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                                                                                                                                                                                                                                                                                                                                                                              217 AA;
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Region
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2 macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a partial GRAB protein from S. Pyogenes strain KTL3.

The protein has alpha2M binding region and is useful in vaccine
New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \cdot
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Pred. No. 1.3e-85;
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                                                                                                           Claim 5; Page 62-63; 67pp; English.
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        The patent discloses a new family of proteins termed GRAB (protein Grelated alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a fragment of GRAB protein from S. pyogenes strain SF370 corresponding to residues 34-192 and devoid of the membrane spanning region. This
                                                                                                                                                                                                                                                                    61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                                                                                          61 ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
                                                                                                                                                                                                                       1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                   1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
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0
                                                                                                                                                                           Length 159;
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/note= "consensus sequence for gram-positive
surface cell wall anchored proteins"
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/label- alpha2-macroglobulin_binding_site
                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response; Streptococcus pyogenes infection.
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/label* Cell_wall_spanning_region
                                                                                                                                                                        100.0%; Score 777; DB 21;
100.0%; Pred. No. 9.9e-88;
11ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                               AAY71039 standard; Protein; 184
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                                                                                                                                                                                    Best_Local Similarity 100.
Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
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Binding-site
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                                                                                                                                                    Sequence
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                                                                                                    New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEK 120
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/label= Cell_wall_spanning_region
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100.0%; Pred. No. 1.2e-87;
ive 0; Mismatches 0;
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/label= Signal_sequence
34..217
/label= Mature_GRAB_protein
34..91
/label= alpha2M_binding_site
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/label- Repeat_region_2
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                                                                                                                                                                                      Claim 5; Page 56; 67pp; English.
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/note=
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                                                  WPI; 2000-365572/31.
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Bjorck LH,
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77
1 VDSPIEQPRIIPNGGTLTNL.....KKEERQNVNTLPTTGEESNP 159
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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21. (SIDSI)gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:\*
22. (SIDSI)gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\* A\_Geneseq\_032802:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|     | . Description            | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Streptococcus pyod | Protein G. Strept | Protein G. Strept |
|-----|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|
|     | ID                       | AAY71041           | AAY71039           | AAY71042           | AAY71046           | AAY71044           | AAY71040           | AAY71045           | AAY71043           | AAY71037           | AAP70493          | AAP95030          |
|     | 08                       | 21                 | 21                 | 21                 | 77                 | 21                 | 21                 | 71                 | 21                 | 21                 | æ                 | 10                |
|     | Ouery<br>Match Length DB | 159                | 184                | 217                | 167                | 155                | 141                | 271                | 259                | 28                 | 448               | 448               |
| op. | Query                    | 100.0              | 100.0              | 100.0              | 97.8               | 96.5               | 87.8               | 0.69               | 68.7               | 36.7               | 19.9              | 19.9              |
|     | Score                    | 777                | 777                | 777                | 160                | 750                | 682                | 536                | 534                | 285                | 155               | 155               |
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| 4448<br>4448<br>5993<br>5993<br>6593<br>665<br>665<br>665<br>665<br>665<br>665<br>665<br>665<br>665<br>66                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | peptil t entr enes s ein G in; gr trepto enes. O-GB03 B-0023 TD. 3en M;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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| 11111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 71041; 71041; 71041; 71041; Aug-20 eptoco eptoco 000262 MAY-20 MOV-19 NOV-19 TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A TI-) A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 11111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RESULT 1  AAY71041  LID AAY7  XXX  AAC AAY7  XXX  DT 29.  XXX  DD S Lrv  BY  XXX  XXX  XXX  XXX  XXX  XXX  XXX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | $\sim$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

Balanus amphitrite.

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This is the coding sequence of the barnacle sixth adhesion protein. The protein was isolated from the cement secreted from the shell of barnacles. The protein can be used as an adhesive in water, and in wet environments.
                                                                                                                                                                                                         Barnacle sixth adhesion protein gene - useful as a raw material for
                                                                                                                                                                                                                                                                                                              Sequence 1773 BP; 429 A; 499 C; 524 G; 321 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            1773
11
3
12
0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                Location/Qualifiers
1..1371
/*tag* a
/product* sixth_adhesion_protein
                                                                                                                                                     (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                       Example 4; Page 4-5; 8pp; Japanese.
                                                                                                            98JP-0149138
                                                                                                                                98JP-0149138
                                                                                                                                                                                                                                                                                                                                             333
45.00
53.85%
42.31%
34.88%
                                                                                                                                                                       WPI; 2000-091356/08.
P-PSDB; AAY67238.
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Best Local Similarity:
Query Match:
                                                                    JP11332573-A
                                                                                                            29-MAY-1998;
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                                                                                        07-DEC-1999.
                                                                                                                                                                                                                  adhesives
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3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22

Search completed: October 13, 2002, 02:41:30 Job time : 1028.43 secs

23 LysAlaAspAsnAlaAla 28

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US-09-847-539A-6\_COPY\_59\_86 (1-28) x AAZ56162 (1-1773)

98AU-0003634. 99WO-AU00385

21-MAY-1998;

21-MAY-1999;

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WO9961458-A1

(UNSY ) UNIV SYDNEY Reeves PR, Wang L; WPI; 2000-072598/06.

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                                                                                                                                                                                                                                                                                                                                                   AAZ AAZ56331 to AAZ56398 represent nucleic acid molecules (I) encoding all or part of an Escherichia coli flagellin protein except a protein expressed by E. coli H1, H7, H12 or H48 type strains. The presence of E. coli of a particular H serotype in a sample, comprising specifically of a particular H serotype in a sample, comprising specifically containing gene, specific for a particular flagellin gene associated with the H serotype, to any E. coli in the sample which contain the gene, and detecting any hybridised molecules, identifying the presence of that serotype in the sample. (I) are useful for: (I) detecting the presence of E. coli of H serotype in a sample by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both or nucleic acid molecules. (I) is particularly useful for detecting the contain the contain the sample and detecting the hybridised nucleic acid molecules. (I) is particularly useful for detecting the contain the contain the sample and detecting the physiciased nucleic acid molecules. (I) is particularly useful for detecting the contain of O and H antigen. Hybridised (I) when using a pair of (I) is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                   nucleic acid molecule useful for the detection of flagellated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1383 BP; 421 A; 307 C; 314 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-847-539A-6_COPY_59_86 (1-28) x AAZ56340 (1-1383)
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                    bacterial strains in food, faeces, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flagellin; fliC; antigen; detection;
                                                                                                                                                                                                                                                                                                                        Claim 3; Page 193; 245pp; English
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                                                                            99WO-AU00385
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Best Local Similarity:
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W09961458-A1
                                                                          21-MAY-1999;
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                                     02-DEC-1999
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AAZ56331 to AAZ56398 represent nucleic acid molecules (1) encoding all cart of an Escherichia coli flagellin protein except a protein except a protein cart of an Escherichia coli Hill Hy, Hill or Hill the strains. The present invention also describes a method of detecting the presence of E. coli of a particular H serotype in a sample, comprising specifically interested and electing and the presence of E. coli of H serotype, to any E.coli in the sample which contain the gene, specific for a particular flagelling appearance of the card detecting any hybridised molecules, identifying the presence of that serotype in the sample. (1) are useful for: (1) detecting the presence of that serotype in the sample. (1) are useful for: (1) detecting the presence of that serotype in the sample. (1) for detecting the presence of that serotype in the sample by hybridising at least one or a pair of in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both O and H-serotypes of E. coli by hybridising at least one or a pair of (1) to any E. coli by hybridising at least one or a pair of (1) to any E. coli present in the sample and detecting the hybridised nucleic acid molecules. (1) is particularly useful for detecting the combination of O and H antigen. Hybridised (1) when using at least one (1) is detected by southern blot analysis and, when using a pair of (1), is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
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Novel nucleic acid molecule useful for the detection of flagellated bacterial strains in food, faeces, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1383 BP; 421 A; 307 C; 314 G; 341 T; 0 other;
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Conservative:
Mismatches:
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                                                                                                                                   Claim 3; Page 212; 245pp; English
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Best Local Similarity:
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99WO-AU00385 98AU-0003634.

21-MAY-1999; 21-MAY-1998;

02-DEC-1999

(UNSY ) UNIV SYDNEY.

WPI; 2000-072598/06. Reeves PR, Wang L;

Claim 3; Page 222; 245pp; English

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Novel nucleic acid molecule useful for the detection of flagellated bacterial strains in food, faeces, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                 AA256331 to AA256398 represent nucleic acid molecules (I) encoding all expressed by E. coll HI, 47, H12 or 446 type strains. The present to respect a protein expressed by E. coll HI, 47, H12 or 446 type strains. The present of more than a method of detecting the presence of E. coll of a particular H serotype in a sample, comprising specifically from a hybridising a nucleic acid, preferably at least a pair, derived from a lagellating gene, specific for a particular flagellin gene associated with the H serotype, to any E. coll in the sample which contain the gene, and detecting any hybridised molecules, identifying the presence of that serotype in the sample by hybridising at least one or a pair of (I) to any E. coll in the sample by hybridising at least one or a pair of (I) to any E. coll in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the hybridised on the serotypes of E. coll by hybridising at least one or a pair of (I) to any E. coll by hybridising at least one or a pair of (I) to any E. coll by hybridising at least one or a pair of (I) to any E. coll by hybridising at least one or a pair of (I) to any E. coll by hybridising at least one or a pair of (I) to any E. coll present in the sample and detecting the hybridised nucleic acid molecules. (I) is particularly useful for detecting the combination of O and H antigen. Hybridised (I) when using at least one (I) is detected by polymerase chain reaction (FCR). AA256399 to AA256420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epresent primers used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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                                                                                                                                                                                                                                                                                        Novel nucleic acid molecule useful for the detection of flagellated bacterial strains in food, faeces, etc.
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                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 200-201; 245pp; English.
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                                                                                                                                            UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                        WPI; 2000-072598/06
                                                                                                                                                                                           Wang L;
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Best Local Similarity:
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                                                                                               21-MAY-1998;
                                               21-MAY-1999;
02-DEC-1999
                                                                                                                                                                                           Reeves PR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ56376
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AAZ56311 to AAZ56398 represent nucleic acid molecules (I) encoding all captrof an Escherichia coli flagellin protein except a protein captrof or part of an Escherichia coli flagellin protein except a protein captrof in also deacribes a method of detecting the presence of E. coli of a particular H serotype in a sample, comprising specifically captrofically a least a part, derived from a liagellating gene, specific for a particular flagellin gene associated with the H serotype, to any E.coli in the sample which contain the gene, and detecting any hybridised molecules, identifying the presence of that serotype in the sample. (I) are useful for: (I) detecting the presence of E. coli of H serotype in a sample by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both 0 and H-serotypes of E. coli by hybridising at least one or a pair of (I) to any E. coli by hybridising at least one or a pair of (I) to any E. coli by hybridising at least one or a pair of (I) is aparticularly useful for detecting the combination of 0 and H antigen. Hybridised (I) when using at least one (I) is detected by southern blot analysis and, when using at pair of (I), is detected by polymerase chain reaction of (ER). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1123 GATGCAGCAAAATCGTTGCAATCTACCACCCACCGGTCGAAACTATCGACAAAGCATG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-847-539A-6_COPY_59_86 (1-28) x AAZ56376 (1-1380)
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Matches:
Conservative:
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Indels:
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45.00
64.00%
36.00%
34.88%
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99WO-AU00385. 98AU-0003634.

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21-MAY-1999;
                                       21-MAY-1998;
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                                                                                                                                                                                     AAZ56311 to AAZ56398 represent nucleic acid molecules (I) encoding all cypart of an Escherichia coli flagellin protein except a protein expersade by E. coli HI, H7, H12 or H48 type strains. The present of invention also describes a method of detecting the presence of E. coli of a particular H serotype in a sample, comprising specifically particular a nucleic acid, preferably at least a pair, derived from a flagellating gene, specific for a particular flagellin gene associated with the H serotype, to any E. coli in the sample which contain the gene, and detecting any hybridised molecules, identifying the presence of that serotype in the sample. (I) are useful for: (I) detecting the presence of E. coli of H serotype in a sample by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both 0 and H-serotypes of E. coli by hybridising at least one or a pair of (I) to any E. coli by hybridised (I) when using a pair of (I) cony E. coli by hybridised (I) when using a pair of (I) is detected by southern blot analysis and, when using a pair of (I), is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3scherichia coli flagellin protein nucleotide sequence SEQ ID NO:13.
                                                                                                                            Novel nucleic acid molecule useful for the detection of flagellated bacterial strains in food, faeces, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1365 BP; 412 A; 289 C; 312 G; 352 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                 Claim 3; Page 204; 245pp; English
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99WO-AU00385
                         98AU-0003634
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64.00%
36.00%
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                                                  UNSY ) UNIV SYDNEY.
                                                                                                    API; 2000-072598/06
                                                                            Reeves PR, Wang L;
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Best Local Similarity:
Query Match:
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21-MAY-1999;
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                          21-MAY-1998;
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expressed by E. coli H1, H7, H12 or H48 type strains. The protein except a protein expressed by E. coli H1, H7, H12 or H48 type strains. The protein expressed by E. coli H1, H7, H12 or H48 type strains. The protein control of a particular H serotype in a sample, comprising specifically hybridising a nucleic acid, preferably at least a pair, derived from a flagellating gene, specific for a particular flagellin gene associated with the H serotype, to any E. coli in the sample which contain the gene, and detecting any hybridised molecules, identifying the presence of that serotype in the sample. (I) are useful for: (I) detecting the presence of E. coli of H serotype in a sample by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both O and H serotype of E. coli by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules. (I) is particularly useful for detecting the combination of O and H antigen. Hybridised (I) when using a pair of (I), is detected by southern blot analysis and, when using a pair of (I), is detected by oblymerase chain reaction (PCR). AAZS6399 to AAZS6420 represent primers used in the exemplification of the present invention.
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                                                                                                                                                                                                                        Novel nucleic acid molecule useful for the detection of flagellated bacterial strains in food, faeces, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:21.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 195; 245pp; English
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                                                                                                                                                     WPI; 2000-072598/06.
(UNSY ) UNIV SYDNEY
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Best Local Similarity:
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                                                                              Reeves PR,
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AA256331 to AA256398 represent nucleic acid molecules (I) encoding all cypart of an Escherichia coli flagellin protein except a protein expressed by E. coli H1, H7, H12 or H48 type strains. The present to revention also describes a method of detecting the presence of E. coli of a particular H serotype in a sample, comprising specifically.

Comparising a nucleic acid, preferably at least a pair, derived from a flagellating gene, specific for a particular flagellin gene associated with the H serotype, to any E.coli in the sample which contain the gene, and detecting any hybridised molecules, identifying the presence of that serotype in the sample. (I) are useful for: (I) detecting the presence of that serotype in a sample by hybridising at least one or a pair of (I) to any E. coli in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both O and H serotypes of E. coli by hybridising at least one or a pair of (I) to any E. coli present in the sample and detecting the hybridised nucleic acid molecules. (I) is particularly useful for detecting the combination of O and H antigen. Hybridised (I) when using at least one combination of O and H antigen. Hybridised (I) when using at least one (I) is detected by polymerase chain reaction (POR). AA256399 to AA256420 is because the primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryvae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AspalaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 417 BP; 120 A; 108 C; 95 G; 94 T; 0 other;
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Mismatches:
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                    Claim 3; Page 190; 245pp; English.
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45.00
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Best Local Similarity:
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(NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.

99US-0273623

22-MAR-1999;

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Expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in one or more second filamentous fungal cells. The method uses fluorescence—labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes from FF cells allows the production of potential of potential of the microcrganisms to be improved. New genes may be cliscovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be considered. The expression of genes can be used to study how FF cells dentified and gene copy number variation and stability can be considered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore conspined in culture conditions, environmental stress, spore candom consorting using ESTS provides several advantages over genomic or random consorting including alimination of redundancy as one spot on a raray equals one gene or open reading frame, and organisation of the canlysis of the results. AAF11248 to AAF11247 represents ESTS from Aspergillus or SaPariany and AAF11487 to Presents ESTS from AAF14879 to AAF1851 to Present ESTS from Aspergillus suck and SaPariany and Inspecifically claimed in the present invention.
                                                                       Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olsen PB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GlualaLeualaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla
Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461
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Matches:
Conservative:
Mismatches:
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Kauppinen S,
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                                                                                                                                                   Claim 86; Page 763-764; 3161pp; English
                                                                                                               substrate of expressed sequence tags -
Shuster JR,
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45.00
62.50%
41.67%
34.88%
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 Rey MW,
                                   WPI; 2000-594572/56
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Best Local Similarity:
Query Match:
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 Berka RM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N. meningitidis B full length genome DNA sequence SEQ ID NO:1068,
                                                                                                                                                                                                                                                                                                                           Sequence 349980 BP; 80289 A; 91081 C; 97378 G; 81232 T; 0 other;
   coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-847-539A-6_COPY_59_86 (1-28) x AAH68525 (1-349980)
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Mismatches:
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Matches:
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46.00
62.50%
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| 225495 TTCGAGAACGCT 225506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
Neisseria DNA sequences and their corresponding proteins; AAA81254 to
AAA81259 and AAA81304 to AAA81312 represent PCR primers used in the
isolation of Neisseria meningitidis DNA sequences; and AAA8132 to
AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
sequences, which are all used in the exemplification of the present
invention. The nucleic acid sequences, protein sequences, and antibodies
against them, can be used in the manufacture of a composition. The
composition can be used as a medicament (or in the manufacture of a
medicament) for treating, preventing or disquesting infection due to
Neisserial bacteria. For example, some of the identified proteins could
be components of vaccines against Meningococcus B; against all serotypes;
and/or against all pathogenic Neissariae. Identification of sequences
from the bacterium will also facilitate production of bloogical probes,
particularly organism-specific probes. Attempts to make efficacious
Meningococcus B vaccines have falled mally due to antigen tolerance.
Multivalent vaccines have also been tried but none have successfully
overcome antigenic variability. The provision of further, complete
exposed proteins that may be presumed targets for the immune system and
which are not antigenically variable or at least more conserved than
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule useful for the detection of flagellated bacterial strains in food, faeces, etc.
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Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              other more variable regions
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42.31%
35.66%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
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Scarlato

Tettelin H, Venter JC; Ratti G, Scarselli M,

Peterson J, C, Mora M,

Frazer CM, Hickey E, Masignani V, Galeotti Rappuoli R, Pizza M;

WPI; 2000-318079/27.

CHIR ) CHIRON CORP.

98US-0103794.

09-0CT-199B; 30-APR-1999; Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea  $\cdot$ 

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA

Claim 7; Page 866-1272; 1760pp; English.

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EP1108790-A2,
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Tateishi N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomics sequence, as the sequence was too long to go in a record on its own it was split into B sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21607 are repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated the beginning of AAF21608, and so on). AAF2155 to AAF2188 encode the Neisseria proteins given in AAB58550 to AAB58931, and AAF21889 to the PAR21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V;
Rappuoli R;
                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections - \,
                                                                                                                                                            3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
           Sequence 69936 BP; 16512 A; 19259 C; 17399 G; 16763 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis B nucleotide sequence SEQ ID NO:108.
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Scarlato V,
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Mismatches:
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Ratti G, Scarselli M,
                                                             Matches:
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
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                                                2.28e+04
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65.38%
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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                                                                        Percent Similarity:
Best Local Similarity:
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                                   Alignment Scores:
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria constitution of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 111891 GCTTFGGAAGCGCGTTFGGAAAAACTCGAAGCCGCGCAAAATCCCGAAAAACTCGAAGCGGCAGCATG 111950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoi
                                                                                                                                                                                                                                                                                                                                                                         Sequence 349980 BP; 84410 A; 84863 C; 94187 G; 86520 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH68525 standard; DNA; 349980 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 111951 GAAGCGGCTGAAGCCGCT 111968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.69e+05
46.00
65.38%
42.31%
35.66%
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03-AUG-2000; 2000JP-0280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LysAlaAspAsnAlaAla 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organic acid synthesis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                   1540 ATTGAGCCTTACGCACCTGAGGCAGACGTGAAGAGGGGCGAGTCCGCAATCTACAAG 1599
 23
                                                                                                                                                                                                                                                                                                                                                                                          Yokoi H;
4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                                                                                                                                                                                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                         Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                            C glutamicum coding sequence fragment SEQ ID NO: 556
                                                                                                           AAH65521 standard; DNA; 2160 BP
                                                                                                                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                       16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                            organic acid synthesis; ds.
                                                                                                                                                                                                                                  Corynebacterium glutamicum.
                                                                                                                                                       (first entry)
                                                               1600 TTCGAGAACGCT 1611
                                          24 AlaAspAsnAla 27
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-376931/40.
P-PSDB; AAG90302.
                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                      EP1108790-A2.
                                                                                                                                                                                                                                                                            20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa S,
Tateishi N,
                                                                                                                                 AAH65521;
                                                                                                 AAH6552]
                                                                                      RESULT
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacteria are useful for producing amino acids, nucleic acids, vitamine, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Claim 8; SEQ ID NO: 556; 246pp + Sequence Listing; English. Patent Office. European

Sequence 2160 BP; 462 A; 569 C; 621 G; 508 T; 0 other;

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2160
9
6
9
0
        Length:
Matches:
Conservative:
Mismatches:
                                          Indels:
               46.00
62.50%
37.50%
35.66%
                        Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                         Query Match:
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US-09-847-539A-6_COPY_59_86 (1-28) x AAH65521 (1-2160)
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAAB1453 to AAAB2414

represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAAB1260 to AAAB1303 and AAB1563 to present to AAB1261 to AAAB2563 represent to AAAB1304 to AAAB1301 represent PCR primers used in the sequences; and AABB1324 to AAAB1452 represent meningitidis DNA sequences; and AAAB1324 to AAAB1452 represent Neisseria meningitidis MenB polynucleotide ORF sequences; which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used as medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection of sequences against Menhagococcus B; against all servoypes; and/or against all pathogenic Neisseriae. Identification of sequences and/or against all pathogenic Neisseriae. Identification of sequences and/or against all pathogenic Neisseriae. Identification of sequences of particularly organism specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than and the argets for the immune system and conserved than and the argets for the immune system and conserved than and the argets for the immune system and conserved than and the argets for the immune system and conserved than and the argets for the immune system and conserved than and the argets for the immune system and conserved than and the argets for the argets for the argets for the argets for the 
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Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes methods of obtaining immunogenic
                                                                                                                                                                                                                                                                                                                                                                                          N. meningitidis partial DNA sequence gnm_27 SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 547-567; 1760pp; English.
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C, Mora M,
                                                                                                                                                                                                                                              AAA81479 standard; DNA; 69936 BP.
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                                                                                                                                                                                                                                                                                                                                          04-DEC-2000 (first entry)
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Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis.
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                                                                                                                                              576 TTCGAGAACGCT 565
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                                                                                               24 AlaAspAsnAla
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30-APR-1999;
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                                                                                                                                                                                                                                                                                           AAA81479;
                                                                                                                                                                                                                       AAA81479/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                      expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clausen IG,
                                                                                                     gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kauppinen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 87; Page 1728; 3161pp; English.
                                                                   Aspergillus niger EST SEQ ID NO:3866.
                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shuster JR,
                                                                                                                                                                                                                                                                                                                          22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                                                                                                                                              99US-0273623.
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      3erka RM, Rey MW,
                                                                                                                                                                                                               Aspergillus niger
                                                                                                                                                                                                                                                  WO200056762-A2.
                                                                                                                                                                                                                                                                                                                                                              22-MAR-1999;
                                 13-MAR-2001
                                                                                                                                                                                                                                                                                      28-SEP-2000
AAF11343;
                                                                                                       Multiple
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SQ Sequence 636 BP; 169 A; 155 C; 161 G; 149 T; 2 other;
Alignment Scores:
61.2 Length: 636
Score: 46.00 Matches: 11
Percent Similarity: 64.00% Conservative: 5
Best Local Similarity: 44.00% Mismatches: 9
Query Match: 21 Gaps: 0
BB:
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the

561 G; 453 T; 0 other;

Sequence 2115 BP; 492 A; 609 C;

European Patent Office.

Length: Matches: Conservative: Mismatches:

> 46.00 62.50% 37.50% 35.66%

> > Best Local Similarity:

Query Match:

Percent Similarity:

Pred. Score:

Alignment Scores:

Indels: Gaps:

Claim 8; SEQ ID NO: 555; 246pp + Sequence Listing; English.

1 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20

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US-09-847-539A-6\_COPY\_59\_86 (1-28) x AAF11343 (1-636)

US-09-847-539A-6\_COPY\_59\_86 (1-28) x AAH65520 (1-2115)

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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
Yokoi H;
                                                                                                                                                                                                                                                                                                                                                   amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                          C glutamicum coding sequence fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                AAH65520 standard; DNA; 2115 BP.
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                                                                                                                                                                                                                                                                                                                                                                           organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                   (first entry)
                                                                                              209 GCCTATAAAGCTGAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizoguchi
Senoh A,
                                                          21 ValValLysAlaAsp 25
                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-376931/40.
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03-AUG-2000;
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Tateishi N,
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                                                                                                                                       RESULT 26
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AA199682;

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AA199682/C
ID AA199682 standard; DNA; 4411529 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nuclectide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nuclectide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LeualaaspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn 26
                                                                                                                                                                                                            Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
                                                                                                                                                                         Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
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                                                                      BP.
                                                                      DNA; 4403765
1897 GCTGCTGATGCGCTTGCA 1880
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47.00
54.55%
40.91%
36.43%
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                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                         (first entry)
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                                                                    AAI99683 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                         15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                     24 - JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1998;
                                                                                                                                                                                                                                                                                               US6294328-B1
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                                                                                                                                                                                                                                                                                                                                   25-SEP-2001,
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                                                                                                      AA199683;
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                                    RESULT
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Db 4044185 TTGATGGACCCGCCGACCTGCTGGAAGGCGAACAGGTAACCATCGTCGATATCGACAAC 4044126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nuclectide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nuclectide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37PV (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=629432881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LeualaaspGlnThraspAlaLeuGlnSerGluGluAlaAlaValValLysAlaAspAsn 26
                                                                                                                             Mycobacterlum tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
                                                                Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4411529
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54.55%
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                                                                                                                                                                                                                           Mycobacterium tuberculosis.
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Best Local Similarity:
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15-JAN-2002
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ID NO 29017.

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ABL25849,

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sequences (ABL01840-ABL16175) and the encoded proteins (ABB77737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 29017; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ
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Matches:
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11-JUL-2000; 2000US-0614150.
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                                                      23 LysAlaAspAsnAlaAla
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                                                                                                                                                                                                                                                                                                                                pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2.
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                                                                                                                                                                                                                                                                                                             Drosophila;
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                                                                                                                                                                                                  ABL25848;
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The sequence data for this patent did not form part of the printed security in the contraction, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                        AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaVal 22
                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 29020
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 Gaps:
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ABL25849 standard; DNA; 1616 BP.
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11-JUL-2000; 2000US-0614150.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila;
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4229 112 113 00

3 AlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValVal 22

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AAS94455 standard; cDNA; 3711

RESULT 20

13-FEB-2002

AAS94455;

51291 GGAGTTGAAAAGAAAC 51308

21 ValValLysAlaAspAsn 26

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Dehoux P;
Cossart P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchrieser C, Frangeul L, Couve E, Rusniok C, Faihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenlo E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                             Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                              vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                                     Listeria monocytogenes EGD-e genome sequence.
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ABA03041 standard; DNA; 2944528 BP
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                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200177335-A2.
                                                                                                                                          05-FEB-2002
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The present sequence is the genome sequence of Listeria monocytogenes ECD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and blodegradation, especially blosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related the Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly organisms. 

ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other; 2944528 Conservative: Mismatches: Matches: Indels: Length: 3.25e+05 51.00 65.38% 38.46% 39.53% Percent Similarity: Best Local Similarity: Duery Match:

US-09-847-539A-6\_COPY\_59\_86 (1-28) x ABA03041 (1-2944528)

Db 51231 GCTGAAACAAAAGAACAACTAAGTGATGAAACAGATCGACTTGACCGAGAAGATGCAGGT 51290 

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The cand gene mapping and in recombinant production of (II). The polypeptides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) or to treat disease states involving (II) and its binding mathodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cand to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention classes the printed diagnostic coding sequences of the invention of the printed product of the product of the product of the product of the printed product of the invention of the printed product of the product of the product of the product of the product of the product of the printed product of the product of the printed product of the product of the printed product of the printed product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the
                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG30268.
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ABL12682 standard; cDNA; 4221
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                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 33553.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 33553; 21pp + Sequence Listing; English
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11-JUL-2000; 2000US-0614150.
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                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 32528
                                                                                               developmental biology; cell signalling; insecticide;
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4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                        US-09-847-539A-6_COPY_59_86 (1-28) x ABL25210 (1-18603)
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                         polynucleotide SEQ ID NO 32531.
                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
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ABL12683/c
ID ABL12683 standard; cDNA; 1960 BP.
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53.85%
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Best Local Similarity:
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 27106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 2396
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Mismatches:
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Matches:
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                      Alignment Scores:
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| 9- MAY - 1999<br>1- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999<br>3- JUN - 1999 | PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 21-JUN-1999; PR 22-JUN-1999; PR 23-JUN-1999; PR 24-JUN-1999; PR 24-JUN-1999; PR 25-JUN-1999; PR 26-JUN-1999; PR 26-JUN-1999; PR 01-JUL-1999; PR 02-JUL-1999; PR 12-JUL-1999; PR 13-JUL-1999; PR 14-JUL-1999; PR 15-JUL-1999; PR 16-JUL-1999; | 9-70L-1999 9-70L-1999 9-70L-1999 9-70L-1999 9-70L-1999 0-70L-1999 |

| OUS-0147302<br>OUS-01471302<br>OUS-01471303<br>OUS-0147303<br>OUS-01474303<br>OUS-01474313<br>OUS-0148171<br>OUS-0148341<br>OUS-0148865<br>OUS-0148865<br>OUS-0148665<br>OUS-0148665<br>OUS-0148665<br>OUS-0148665<br>OUS-0148665<br>OUS-0148665<br>OUS-0148665 | 9905 - 0149723<br>9905 - 0149723<br>9905 - 0149929<br>9905 - 0149930<br>9905 - 015966<br>9905 - 0151065<br>9905 - 0151066<br>9905 - 0151080<br>9905 - 0151080<br>9905 - 0151303<br>9905 - 0153303<br>9905 - 0153403<br>9905 - 0154018<br>9905 - 0154018<br>9905 - 0155466<br>9905 - 0155466                                                                                                                        | 90.5 - 01.581.579 90.5 - 01.581.579 90.5 - 01.592.93 90.5 - 01.592.93 90.5 - 01.592.93 90.5 - 01.593.93 90.5 - 01.593.93 90.5 - 01.593.93 90.5 - 01.60.740 90.5 - 01.60.740 90.5 - 01.60.740 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.60.980 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 90.5 - 01.61.950 |
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| 1-AUG-1999<br>                                                                                                                                                                                                                                                  | 20 - AUG - 1999;<br>20 - AUG - 1999;<br>23 - AUG - 1999;<br>23 - AUG - 1999;<br>25 - AUG - 1999;<br>27 - AUG - 1999;<br>27 - AUG - 1999;<br>30 - AUG - 1999;<br>31 - AUG - 1999;<br>31 - SEP - 1999;<br>32 - SEP - 1999;<br>32 - SEP - 1999;<br>34 - SEP - 1999;<br>36 - OCT - 1999;<br>36 - OCT - 1999;<br>37 - AUG - 1999;<br>38 - SEP - 1999;<br>39 - SEP - 1999;<br>30 - OCT - 1999;<br>30 - OCT - 1999;<br>30 - OCT - 1999;<br>31 - SEP - 1999;<br>32 - SEP - 1999;<br>33 - SEP - 1999;<br>34 - SEP - 1999;<br>36 - OCT - 1999;<br>37 - SEP - 1999;<br>38 - SEP - 1999;<br>38 - SEP - 1999;<br>39 - OCT - 1999;<br>30 - OCT - 1999;<br>30 - OCT - 1999; | 2. OCT 11999<br>3. OCT 11999<br>3. OCT 11999<br>4. OCT 11999<br>4. OCT 11999<br>4. OCT 11999<br>1. OCT 11999<br>1. OCT 11999<br>1. OCT 11999<br>2. OCT 11999<br>5. OCT 11999<br>6. OCT 11999<br>8. OCT 11999<br>8. OCT 11999<br>8. OCT 11999<br>8. OCT 11999<br>9. OCT 11999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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                                                                                                                                                                                                                                                                                                                                                                                                                             Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 77144.
                                                                                                             US-09-847-539A-6_COPY_59_86 (1-28) x ABL13526 (1-6398)
                                Conservative:
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99US-0123180.
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                               Percent Similarity:
Best Local Similarity:
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27-MAY-1999;
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   Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                           5 GlualaLeualaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLysAla 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 35060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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                Sequence 3349 BP; 808 A; 953 C; 851 G; 737 T; 0 other;
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12
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                                                                                             Conservative:
Mismatches:
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Matches:
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11-JUL-2000; 2000US-0614150.
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                                             Alignment Scores:
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Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFS are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the
           identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                           229 ATACAAGCCCTACAGGAGCAAATTGACGCTTTAGATTCTCAAGAAAAGTCGTTAGCAAA 288
predicted coding regions defined by computer evaluation. To
                                                                                                                                                                                                                                                                                                          4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe; diagnostic; ORF; cell envelope protein;
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                                                                                                                      250 A; 115 C; 119 G; 182 T; 0 other;
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Matches:
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06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                           4 LeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAlaValValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 35063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 35063; 21pp + Sequence Listing; English.
                                                                                                                    1239
12
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0
                                                                          BP; 472 A; 234 C; 206 G; 327 T; 0 other;
                                                                                                                                                                                                                              US-09-847-539A-6_COPY_59_86 (1-28) x AAX30461 (1-1239)
                                                                                                                                                  Conservative:
Mismatches:
Indels:
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Matches:
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ABL13527 standard; cDNA; 3349 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                    1.72
57.00
69.57%
52.17%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                   205 TGGGATAAC 213
                                                                                                                                                                                                                                                                                                                       24 AlaAspAsn 26
                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABB69424
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                                                                                                                                                    Percent Similarity:
                                                                           Sequence 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                         Aliqnment Scores:
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                 SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20
                                                                                                                                                                                                                                                                                                        Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                             H. pylor1 secreted or periplasmic protein ORF 35336707.aa.
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547..549, aa: Asp)
given"
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/*tag= a
/transl_except= (pos: 5.
/transl_except= (pos: 5.
/note= "no stop codon g
559..561
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/note= "encodes Asn"
574..576
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/note= "encodes Asn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                      616 GTTGTTAAAGCGGATAACGCTGCT 639
                                                                  21 ValValLysAlaAspAsnAlaAla 28
                                                                                                                                                                        AAT67618 standard; DNA; 576 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
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                                                                                                                                                                                                         AAT67618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                      RESULT 7
                                                                                                                                                        AAT67618
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The present sequence encodes a H. pylori secreted or periplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides,
                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. pylori secreted or periplasmic protein ORF 02ce10216orfl.
                                                                     576
12
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  217 A; 97 C; 95 G; 161 T; 6 other;
                                                                     Length:
Matches:
Conservative:
Mismatches:
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/note= "no stop codon given"
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1..666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT67891 standard; DNA; 666 BP.
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95US-0487032
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69.57%
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P-PSDB; AAW20638.
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                                                                                                                  Percent Similarity:
Best Local Similarity:
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Sequence 576 BP;
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07-JUN-1995;
                                               Alignment Scores:
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29-AUG-2000

AAD00561;

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related alpha2M binding process. If the process progenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain AP49. The protein has alpha2M binding region and is useful in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
The patent discloses a new family of proteins termed GRAB (protein G
                                                                                                                                                                                                                                                                               Streptococcus pyogenes strain AP49 partial GRAB protein encoding DNA
                                                                                                                                                                                                                                                                                                                GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.
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Matches:
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Gaps:
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                                                                      379 GTTGTTAAAGCGGATAACGCTGCT 402
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                                                                                                                                                                 BP
                                                        21 ValValLysAlaAspAsnAlaAla
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/product=
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2000
                                                                                                                                                                                                       AAD00563;
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                                                                                                                                                    AAD00563
                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain KTLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a protective immune response binding protein -
                                                                                                                                                                                                                                          Streptococcus pyogenes strain KTL9 partial GRAB protein encoding DNA.
                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                           GRAB protein; protein G related alpha2M binding protein; vaccalpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 A; 151 C; 178 G; 179 T; 0 other;
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/note= "Does not include stop codon"
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                     393 GTTGTTAAAGCGGATAACGCTGCT 416
                   ValvalLysAlaAspAsnAlaAla 28
                                                                                                                              AAD00561 standard; DNA; 777 BP.
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                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
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02-NOV-1999; 02-NOV-1998;

Bjorck LH,

11-MAY-2000

853 28 0 0 0 0

SerAspAlaLeuGluAlaLeuAlaAspGlnThrAspAlaLeuGlnSerGluGluAlaAla 20

Alignment Scores:

Query Match:

composition

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Streptococcus pyogenes
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                                                                        sig_peptide
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                                                                                             mat_peptide
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                                                                                                                                                                                                                                                             New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 654 BP; 234 A; 118 C; 143 G; 159 T; 0 other;
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                                                                               /product "Mature GRAB protein"
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Indels:
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Matches:
                             "GRAB protein"
Cocation/Qualifiers
11.654
/*tag= a
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100..651
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                                                                                                                                                                                                            Rasmussen M;
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                                                                                                                                                                                        (ACTI-) ACTINOVA LTD
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Best Local Similarity:
Query Match:
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                                                                                                      WO200026240-A2
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                                        s1g_peptide
                                                             mat_peptide
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective manner response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequence
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complement (101..127)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /bound_molety= "Primer 5 represented in AAD00569"
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                                                                                                                                                                                      /product= "Mature GRAB protein"
complement (101..124)
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                                                                 "GRAB protein"
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                                                                                                                                                                                                                                                                                                                                                  complement (160..184)
Location/Qualifiers
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/product= 60..158
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Indels:
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Matches:
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The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is a DNA encoding partial GRAB protein from a sample. The present sequence is a DNA encoding partial GRAB protein from S. pyogenes strain KTL3.
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Matches:
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                       "GRAB protein"
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 13, 2002, 02:10:56; Search time 40.4278 Seconds

(without alignments)
1189.122 Million cell updates/sec
1189.122 Million cell updates/sec
1280-847-539A-6_COPY_59_86

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Scoring table: BLOSUM62
Scoring table: BLOSUM60.
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Streptococcus pyogenes strain AP1 partial GRAB protein encoding DNA.

GRAB protein; protein G related alpha2M binding protein; vaccine; alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic; immune response; Streptococcus pyogenes infection; ds.

Location/Qualifiers 1..468

Key

Streptococcus pyogenes.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| No.   Score   March Length DB   D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |               |             | •       |         |    | SUMMARIES   |                    |
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| 1 129 100.0 469 21 AAAD00564 Streeptococci   2 129 100.0 654 21 AAAD00560 Streeptococci   3 129 100.0 654 21 AAAD00560 Streeptococci   5 129 100.0 777 2 AAAD00563 Streeptococci   6 129 100.0 777 2 AAAD00563 Streeptococci   8 129 100.0 777 2 14.2 666 18 AAR70661 H. Pylori   10 57 44.2 1539 19 AAR70661 H. Pylori   11 54 41.9 3349 23 ABL13227 Dtrosphila   12 52 40.3 1002 21 AAR70661 H. Pylori   13 52 40.3 1002 21 AAR70661 H. Pylori   14 52 40.3 1002 21 AAR70661 H. Pylori   15 52 40.3 1002 21 AAR70661 H. Pylori   16 51 39.5 40.3 1610 23 ABL13226 Arebidoshila   17 52 40.3 1610 23 ABL13226 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12681 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12681 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12682 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12682 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12682 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12683 Dtrosphila   18 51 39.5 40.3 1610 23 ABL12683 Dtrosphila   18 51 39.5 40.3 1610 22 AAB12683 Dtrosphila   18 51 39.5 40.3 1610 21 AAA56543 Dtrosphila   18 51 34.9 410 410 21 AAA56543 Dtrosphila   18 51 34.9 410 410 21 AAA56543 Dtrosphila   18 51 34.9 410 410 21 AAA56643 Dtrosphila   18 51 34.9 410 410 21 AAA56643 Dtrosphila   18 51 34.9 410 410 21 AAA56643 Dtrosphila   18 51 34.9 410 410 21 AAA5643 Dtrosphila   18 51 34.9 410 210 21 AAA5643 Dtrosphila   18 51 3 |               | 1           |         | ÷       |    |             |                    |
| 129 100.0 504 21 AANDOSSO STREPPROCOCCE 129 100.0 764 21 AANDOSSO STREPPROCOCCE 129 100.0 764 21 AANDOSSO STREPPROCOCCE 129 100.0 764 21 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 764 12 AANDOSSO STREPPROCOCCE 129 100.0 1012 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSSO STREPPROCOCCE 129 1010 AANDOSS | ۰ ۱           | 7 (         | 98      | 465     |    | AAD00562    | reprococcus        |
| 1 129 100.0 554 1 AANDOSSO STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STREPPOCOCOG STRE | N C           | N           | 9 8     | 400     |    | AAD00564    | creprococcus       |
| 129   100.0   774   21   ANDOUSES   Streptocook   774   21   ANDOUSES   Streptocook   774   721   ANDOUSES   Streptocook   774   721   ANDOUSES   Streptocook   774   721   ANDOUSES   Streptocook   774   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775   775     | n •           | 74 (        | 38      | 400     |    | AADUUSBU    | creprococcus       |
| ## 129 100.0 #5.3 11 AAD00563 Streptocook  ## 129 100.0 #5.3 11 AAD00563 Streptocook  ## 129 100.0 #5.3 12 AAD0563 Streptocook  ## 129 100.0 #5.3 12 AAD0563 Streptocook  ## 120 120 120 120 AAD0563 Streptocook  ## 120 120 120 120 AAD0563 Streptocook  ## 120 120 21 AAD05221 AAD0563 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 22 AAJ0563 Streptocook  ## 120 120 22 AAJ0563 Streptocook  ## 120 120 22 AAJ0563 Streptocook  ## 120 120 22 AAJ0563 Streptocook  ## 120 120 22 AAJ0563 Streptocook  ## 120 120 22 AAJ0563 Streptocook  ## 120 120 21 AAD05221 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 Streptocook  ## 120 120 22 AAJ0623 | <b>+</b> W    | чc          | 38      | 107     |    | AADOOE61    |                    |
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| 10 54 41.9 3349 23 ABLI3527 Drosophila 12 52 40.3 1002 21 AAC53428 Arabidopsil 13 52 40.3 1002 21 AAC53428 Arabidopsil 14 52 40.3 16135 23 ABLI2531 Drosophila 15 52 40.3 16135 23 ABLI2531 Drosophila 15 52 40.3 16135 23 ABLI2583 Drosophila 16 51 39.5 2944528 24 ABA03041 Drosophila 17 51 39.5 2944528 24 ABA03041 Drosophila 18 51 39.5 2944528 24 ABA03041 Drosophila 19 51 39.5 2944528 24 ABA03041 Drosophila 19 51 39.5 2944528 24 ABA03041 Drosophila 22 ABLI25849 Drosophila 23 ABLI25849 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 25 ABLI25849 Drosophila 26 ABA03045 Drosophila 27 ABLI25849 Drosophila 27 ABLI25849 Drosophila 28 ABLI25849 Drosophila 29 ABLI25849 Drosophila 20 ABLI25849 Drosophila 20 ABLI25849 Drosophila 20 ABLI25849 Drosophila 20 ABLI25849 Drosophila 21 ABLI25849 Drosophila 22 ABLI25849 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA03045 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophila 24 ABA0304 Drosophil | 6             | 57          |         | 1239    |    | AAX30461    |                    |
| 11   54   41.9   6398   23   ANDL13526   Arabidopsil   13   52   40.3   1002   21   AAC33266   Arabidopsil   14   52   40.3   1230   21   AAC33266   Arabidopsil   15   52   40.3   1230   23   ABL25210   Drosophila   16   51   39.5   2960   23   ABL25210   Drosophila   16   51   39.5   2960   23   ABL25210   Drosophila   18   51   39.5   2944528   24   ABA03041   Drosophila   18   51   39.5   2944528   24   ABA03041   Drosophila   23   37.2   24   23   ABL25849   Drosophila   23   44   4403765   22   AAL99682   AAC99682   AAC9988   AC9988      |               | 54          |         | 3349    |    | ABL13527    |                    |
| 12 52 40.3 1002 21 AACS4228 Arabidopsis 14 52 40.3 1002 21 AACS4228 Arabidopsis 15 40.3 16135 23 ABL25211 Drosophila 16 51 39.5 2018 23 ABL25211 Drosophila 17 51 39.5 2018 23 ABL25631 Drosophila 18 51 39.5 204652 24 ABL2683 Drosophila 18 51 39.5 204652 24 ABL2684 Drosophila 20 50 38.8 37.2 4429 23 ABL2684 Drosophila 21 48 37.2 4429 23 ABL2684 Drosophila 22 44 441529 23 AALS484 Drosophila 22 44 441529 23 AALS484 Drosophila 23 44.3 11.2 4ABL2684 Drosophila 24 44 45 34.9 1380 21 AAR6520 C G glutamic 25 46 35.7 4299 23 AAR6520 C G glutamic 27 46 35.7 42990 21 AAR6520 C G glutamic 27 46 35.7 42990 21 AAR61499 Nroeliseria 19 45 34.9 1368 21 AAR6533 Brosophila 23 44.9 1368 21 AAR6533 Brosophila 24 45 34.9 1380 21 AAZ56334 Brosophila 24 45 34.9 1380 21 AAZ56334 Brosophila 24 45 34.9 1383 21 AAZ56334 Brosophila 24 45 34.9 4661 20 AAZ56336 Brosophila 24 45 34.9 4661 20 AAZ56336 Brosophila 24 45 34.9 4661 20 AAZ56336 Brosophila 24 45 34.9 4661 20 AAZ56336 Brosophila 24 45 34.9 4661 20 AAZ56336 Brosophila 24 45 34.9 4661 20 AAZ56336 Brosophila 24 46 34.9 4661 20 AAZ56336 Brosophila 24 46 34.9 4661 20 AAZ56336 Brosophila 24 46 34.9 4661 20 AAZ56336 Brosophila 24 46 34.9 4661 20 AAZ56336 Brosophila 24 46 34.9 4661 20 AAZ56336 Brosophila 24 46 34.9 4661 20 AAZ56336 Brosophila 24 46 46 34.9 4661 20 AAZ56336 Brosophila 24 46 46 34.9 4661 20 AAZ56336 Brosophila 24 46 46 34.9 4661 20 AAZ56336 Brosophila 24 46 46 34.9 4661 20 AAZ56336 Brosophila 24 46 46 34.9 4661 20 AAZ56336 Brosophila 24 46 46 46 46 46 46 46 46 46 46 46 46 46                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               | 54          |         | 6398    |    | ABL13526    |                    |
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| 22 48 37.2 429 22 AA199683 Mycobactes 24 47 36.4 4401529 22 AA199683 Mycobactes 25 46 35.7 2165 22 AA199683 Mycobactes 26 46 35.7 2160 22 AA165520 C glutamic 27 46 35.7 2160 22 AA465521 C glutamic 28 46 35.7 2160 22 AA465521 C glutamic 29 46 35.7 2160 22 AA465521 C glutamic 29 46 35.7 349980 22 AA468525 C glutamic 31 46 35.7 349980 22 AA468525 C glutamic 31 46 35.7 349980 22 AA468525 C glutamic 31 46 35.7 143768 21 AAA56355 C glutamic 31 45 34.9 1368 21 AAA56355 C glutamic 33 45 34.9 1368 21 AAA56355 C glutamic 33 45 34.9 1368 21 AAA56350 C glutamic 37 45 34.9 1380 21 AAA56350 C glutamic 39 45 34.9 1383 21 AAA56340 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 40 45 34.9 1383 21 AAA56360 C glutamic 50 50 50 50 50 50 50 50 50 50 50 50 50                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |               | 8 7         |         | 1616    |    | ABL258      | Drosophila melanog |
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| 33 45 34.9 461 21 AAR08476 Fusarrum variant 45 34.9 461 21 AAR56356 Escherichts 36 45 34.9 1365 21 AAR56356 Escherichts 37 45 34.9 1380 21 AAR56351 Escherichts 37 45 34.9 1380 21 AAR56376 Escherichts 39 45 34.9 1383 21 AAR56360 Escherichts 39 45 34.9 1383 21 AAR56360 Escherichts 40 45 34.9 1383 21 AAR56360 Escherichts 41 45 34.9 2194 21 AAR56360 Escherichts 42 45 34.9 2599 21 AAR56360 Escherichts 44 45 34.9 4621 20 AAV69919 Murine pCII PCII 45 34.9 5091 23 ABL07051 Drosophila DO0562 AAD00562 standard; DNA; 469 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 100           |             |         | 7       |    | AAA6143     | acherichia coll    |
| 34 45 34.9 1365 21 AA256356 Escherichte   35 45 34.9 1368 21 AA256356 Escherichte   36 45 34.9 1380 21 AA256343 Escherichte   37 45 34.9 1380 21 AA256340 Escherichte   38 45 34.9 1383 21 AA256340 Escherichte   40 45 34.9 1383 21 AA256340 Escherichte   41 45 34.9 1383 21 AA256368 Escherichte   42 45 34.9 173 21 AA256364 Escherichte   43 45 34.9 2599 21 AA256382 Murine pCT   44 45 34.9 4860 20 AAX26000 Murine pCC   45 34.9 5091 23 ABLO7051 Drosophila   AAD00562 AAD00562 standard; DNA; 469 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |               |             |         | 461     |    | AAFOR476    | Fusarium venenatum |
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| 37 45 34.9 1380 21 AAZ56376 Escherichid   38 45 34.9 1383 21 AAZ56340 Escherichid   39 45 34.9 1383 21 AAZ56340 Escherichid   40 45 34.9 1383 21 AAZ5636                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 36            |             |         | 1380    |    | AA256351    | a coli             |
| 38 45 34.9 1383 21 AAZ56340 Escherichid   40 45 34.9 1383 21 AAZ56348 Escherichid   40 45 34.9 1383 21 AAZ56368 Coding seq   41 45 34.9 173 21 AAZ56364 Escherichid   42 45 34.9 2599 21 AAZ56382 Escherichid   43 45 34.9 4860 20 AAX99919 Murine pCC   45 45 34.9 5091 23 ABL07051 Drosophila   ALIGNMENTS   ALIGNMENTS   AAD00562 standard; DNA; 469 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 37            |             |         | 1380    |    | AAZ56376    | a coli             |
| 39 45 34.9 1383 21 AAZ56158B ESCHETICHIA 45 34.9 1733 21 AAZ56162 COding seq 41 45 34.9 1733 21 AAZ56162 COding seq 41 45 34.9 2145 21 AAZ56384 ESCHETICHIA 42 45 34.9 2145 21 AAZ56382 Murine p/CII 44 45 34.9 4860 20 AAX26000 Murine p/CII 45 45 34.9 4860 20 AAX26000 Murine p/CII 45 34.9 5091 23 ABLO7051 Drosophila Drosophila AAD00562 standard; DNA; 469 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 38            |             | •       | 1383    |    | AAZ56340    | 00                 |
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| 44 45 34.9 4860 20 AAX26000 Murine p/CT 45 45 34.9 5091 23 ABL07051 Drosophila Drosophila ALIGNMENTS  SULT 1 ALIGNMENTS  AAD00562 standard; DNA; 469 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 4.4           |             |         | 4621    |    |             | _                  |
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| ALIGNMENT 1<br>200562<br>AAD00562 standard; DNA; 469 BP.<br>AAD00562;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 45            |             | 34.9    | 5091    |    |             | Drosophila melanog |
| ALIGNMENT 1<br>200562<br>AAD00562 standard; DNA; 469 BP.<br>AAD00562;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |               |             |         |         |    |             |                    |
| SULT 1<br>200562<br>AAD00562 standard; DNA; 469<br>AAD00562;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |               |             |         |         |    | ALIGNMENTS  |                    |
| ADD00562 standard; DNA; 469 ADD00562; ADD00562;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PECIIL        | _           |         |         |    |             |                    |
| AAD00562 standard; DNA; 469 AAD00562;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | APDOOF        | 1 ()        |         |         |    |             |                    |
| AAD00562;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |               | 00562       | tandaro | DNA     | 69 | ВР,         |                    |
| AAD00562;<br>29-8113-2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |               |             |         |         |    |             |                    |
| 29-ATG-2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | -             | ND00562;    |         |         |    |             |                    |
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C; Date: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 22-oct-1999
C; Accession: T1496
C; Accession: T1496
R; Lindler, LE.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A; Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid A; Reference number: 218269; MUID: 99043898
A; Reference number: 218269; MUID: 99043898
A; Accession: T14968
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-978 <LIN>A; Cross-references: EMBL: AF074611; NID: 93883003; PID: 93883051; PIDN: AAC82711.1
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J. Bacteriol. 173, 7650-7664, 1991
A:Title: Molecular and genetic analysis of a region of plasmid pCF10 containing positive
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                                                                                                                                 terococcus faecalis.

A;Reference number: A41662; MUID:92041679

A;Accession: G41662; MUID:92041679

A;Accession: G41662

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-891 < KAO>

A;Cross-references: GB:M64978; NID:g150552; PIDN:AAA65847.1; PID:g150554

C;Genetics:
A;Genome: plasmid
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C;Species: Yersinia pestia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
8.8;
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9.4%; Score 73; DB 3
Best Local Similarity 21.2%; Pred. No. 8.8;
Matches 21; Conservative 20; Mismatches
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A;Genome: plasmid pMT1
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Best Local S.
Matches 20
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Gaps
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                   46; Indels
Best Local Similarity 24.7%; Pred. No. 12;
Matches 21; Conservative 18; Mismatches
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62 LEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAASDAWEKA 121

122 ATPIALDVKKTKDTKPVVKKEERQN 146

879 KGLMEERTKDIKAKSAKIEKYREON 903

Page 10

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tail fiber protein homolog - Yersinia pestis plasmid pWTl
C;Species: Yersinia pestis
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14650
C;Accession: T14650
C;Atcession: T14650
C;Atcession: T14650
C;Atcession: T14650
C;Species: T14650
C;Atcession: T14650
C;Atcession: T14650
C;Atcession: T14650
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                                                                                                                                              hypothetical protein M01B12.4 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Accession: T33170
B.Becker, M.; Graves, T.; Czersky, P.
Submitted to the EMBL Data Library, May 1998
A.Description: The sequence of C. elegans cosmid M01B12.
A.Reference number: 221297
A.Accession: T33170
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: BMBL.AF067624; PIDN:AAC17562.1; GSPDB:GN00019; CESP:M01B12.4
A.Experimental source: strain Bristol N2; clone M01B12
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNAAS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 PRKLPFGKPEAARKSASPVAAQEPTAPVVVVAPVEAIPEVPAVQEEVLTVEEPAAPAREA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 PEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADN 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 73; DB 2; Length 719; 25.8%; Pred. No. 6.9; Live 12; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1
A;Introns: 5/3; 41/2; 135/3; 234/1; 438/3; 590/2; 626/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.4%; Score 73; DB 2;
ilarity 33.3%; Pred. No. 8.4;
Conservative 12; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-860 < HUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AASDALEALADQTDALQSEEAEVVQSDNAASDA 117
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99 ALQSEEAEVVOSDNAASDAWEKAATPIAL 127
                            : | | | :::
428 HVTDVNEAVQQIDDATDAQAASADTTVSM 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.4%
Best Local Similarity 25.8%
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:M01B12.4
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Best Local Simi
Matches 20;
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C.Species: Halobacterlum sp. NRC-1
C.Species: Halobacterlum sp. NRC-1
C.Species: Halobacterlum sp. NRC-1
C.Species: Halobacterlum sp. NRC-1
C.Species: Halobacterlum sp. NRC-1
C.Species: Halobacterlum sp. NRC-1
C.Accession: D84255
R.M. V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A.Reference number: A84160; MUID:20504483
A.Reference number: A84160; MUID:20504483
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A;Molecule type: DNA
A;Residues: 1.536 cSTO>
A;Cross-references: GB:AE004437; NID:g10581193; PIDN:AAG19968.1; GSPDB;GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000007; PIDN:BAB34546.1; PID:g13360583; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
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                                              EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA
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C;Superfamily: Halobacterium salinarum transducer protein htrI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Indels
                                                                                                              86 ASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVK 130
                                                                                                                                                     87 DAGEAAVVAPEKVENAATENAEAKVEAVAVAAPEKVEVAVEAEKK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73; DB 2;
Pred. No. 4.1;
7; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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Best Local Similarity 35.3%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <HAY>
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Best Local 9
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hypothetical protein 21382 [imported] - Escherichia coll (strain 0157:H7, substrain E
C;Species: Escherichia coll
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85631
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <STO>
A;Cross-references: GB:AE005174; NID:g12514226; PIDN:AAG55515.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
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C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C; Accession: T46231
S; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemck submitted to the Protein Sequence Database, December 1999
A; Reference number: Z23026
A; Reference number: Z23026
A; Reference number: Z3026
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9.5%; Score 74; DB 2; Length 375;
Best Local Similarity 35.3%; Pred. No. 2.7;
Matches 24; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 9.4%; Score 73; DB 2; Length 166; Best Local Similarity 21.9%; Pred. No. 1.4; Matches 23; Conservative 22; Mismatches 60; Indels
                                                                                                                                                                                                      Length 509;
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A;Experimental source: cultivar Columbia; BAC clone T9C5
                                                                                                                                                                                                                                                                                                           49;
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                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                           9.7%; Score 75; DB 2 26.4%; Pred. No. 2.9; tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 EVVQSDNAASDAWEKAATPIALDVKKTKDTK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : : |:||| :| ||| || EPEQVLPSEAMVVEEAATLVASAAKKSKSKK 221
                                                                                                                                                                                                                                                           Best Local Similarity 26.4%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 SDNAASDA 117
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A; Introns: 32/3
A; Note: T9C5.130
                                                                                                     A; Map position: 1
                                                                                                                                                                                                                Query Match
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     C; Genetics;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   two-component sensor histidine kinase alr4716 [imported] - Anabaena sp. (strain PCC 7120 C.Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C.Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C.Species: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 11-Jan-2002 R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tasuda, M.; Tabata, S. DNA Res. B, 205-213, 2001 Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNKNOWN protein, 66348-64527 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: 696552
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Bansen, N.F.; Hughes, B.; Huizar, L.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A; Molecule type: DNA
A; Mosleule type: DNA
A; Residues: 1.468 <KUR>
A; Cosstances: CKUR>
A; Cross-references: CB:BA000019; PIDN:BAB76415.1; PID:917133853; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: alr4716
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A;Molecule type: DNA
A;Residues: 1-509 <STO>
A;Cross-references: GB:AE005173; NID:g10092363; PIDN:AAG12772.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                            37 IDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :||: | ::::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| | :::|| :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | ::
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                                                                                                                                                                                                      Length 406;
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                                                                                                                                                                                                Query Match 9.7%; Score 75; DB 2; Length 406
Best Local Similarity 18.5%; Pred. No. 2.3;
Matches 15; Conservative 29; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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Pred. No. 2.6;
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9.7%; Score 75; DB 3
Best Local Similarity 25.6%; Pred. No. 2.6;
Matches 21; Conservative 19; Mismatches
                                          A;Cross-references: SGD:S0001800; MIPS:YKR092c
A;Map position: 11R
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A; Gene: SGD: SRP40
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chromosomal protein XCAP-C - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
C;Accession: A55094
R:Hirano, T.; Mitchison, T.J.
Cell 79, 449-4458, 1994
A;Title: A heterodimeric colled-coil protein required for mitotic chromosome condensa A;Reference number: A55094; MUID:95042742
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NiAlternate names: protein YKR092c; protein YKR412a
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision
C;Date: 03.May.1994 *sequence_revision 03.May-1994 *text_change 21-Jul-2000
C;Accession: S38170; S40645; S37702
R;Baladron, v.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garci Submitted to the Protein Sequence Database, March 1994
A;Reference number: S38158
                            Gaps
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A, Molecule type: mRNA
A, Residues: 1-1290 < HIRA
A, Residues: 1-1290 < HIRA
A, Cross-references: GB: U13673; NID: 9563811; PIDN: AAA64679.1; PID: 9563812
C, Superfamily: chromosome segregation protein SMC1
C, Keywords: chromosomal protein; DNA condensation; heterodimer
KLALRNEERA IDELKKQA IEDKEATTA IEAASSDALEALADQTDALQSEEAAVVKADNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.8%; Score 76; DB 2; Length 129 Best Local Similarity 21.3%; Pred. No. 6.2; Matches 16; Conservative 24; Mismatches 35; Indels
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A;Rosidues: 1-399,'N',401-406 <LAL>
A;Cross-references: EMBL:L11275; NID:9295670; PID:9295671
C;Genetics:
                                                                                          87 SDALEALADQTDALQSEEAEVVQS 110
                                                                                                                      458 MDSLKKETQGLQEEK 472
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 26-Aug-1999
C;Accession: 141024
R;Pilal, H.; Braun, V.
Mol. Microbiol. 16, 57-67, 1995
A;Title: Novel colicin 10: assignment of four domains to TonB- and TolC-dependent uptake
A;Reference number: 141024; MUID:95379494
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C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Date: O'S-May-1995 #sequence_revision 05-May-1995 #text_change 21-Jul-2000
C:Accession: A47168
R:Rezaee, M.: Stockwaw, K.: Halligan, N.: Markwald, R.R.; Krug, E.L.
B:Boll Chem. 268, 14404-14411, 1993
A:Title: Identification of an extracellular 130-kDa protein involved in early cardiac rA:Reference number: A47168; MUID:93300839
A:Accession: A47168
A:Accession: A47168
A:Molecule type: mRNA
A:Rossion: T-725 <REA
A:Cross-references: GB:Ll3973; NID:9304369; PIDN:AAA48557.1; PID:9304370
C:Keywords: cardiac muscle; heart
                                                                A;Map position: 3
A;Introns: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3;
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                                                                                                                                                                                                                            27 KLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAA 86
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                                                                                                                                       Length 1133;
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                                                                                                                                                                                 40;
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                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: 141024
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-490 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.8%; Score 76; DB 2; 29.8%; Pred. No. 3.3;
                                                                                                                                    Query Match 9.9%; Score 77; DB 2
Best Local Similarity 26.0%; Pred. No. 4.2;
Matches 20; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
9.8%; Score 76; DB 2
Best Local Similarity 31.9%; Pred. No. 2.1;
Matches 22; Conservative 15; Mismatches
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17; Mismatches
  A; Experimental source: clone K01A11
                                                                                                                                                                                                                                                                                                                                                   316 REQMDRLQKVHNAGQED 332
                                                                                                                                                                                                                                                                                                                    87 SDALEALADQTDALQSE 103
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Best Local Similarity 29.89
Matches '25; Conservative
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C.Keywords: bacteriocin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 DVQSKQAIV 231
                                          A; Gene: CESP: F59A2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: cta
C; Superfamil
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F;1-318,334-771/Product: h-caldesmon, alternative splice form *status predicted summar; P;1-390/Region: 13-residue repeats
F;261-390/Region: tropomyosin binding
F;522-636/Region: tropomyosin binding
F;522-636/Region: tropomyosin binding
F;527-682,717/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) *status exper
F;688,711/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) *status experimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C.Jacobs, A.J.; Kamholz, J.; Selzer, M.E. Brain Res. Mol. Brain Res. 29, 43-52, 1995 A;Title: The single lampray neurofilament subunit (NF-180) lacks multiphosphorylation A;Reference number: 151116; MUID:95287814 A;Reference number: 151116 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1110 c.JAC> A;Residues: 1-1110 c.JAC> A;Cross-references: EMBL:019361; NID:g632548; PIDN:AAA80106.1; PID:9632549
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Taron 172976; Taron 15.0ct-1999 #text_change 29.0ct-1999
C;Accession: T22976; Taron 187
R;Lightning, J.
Submitted to the EMBL Data Library, June 1994
A;Reference number: 219645
A;Accession: T22976
A;Retauts: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1133 <WILL>
A;Residues: 1-1133 <WILL>
A;Residues: 1-1133 <WILL>
A;Reperimental source: clone F59A2
B;Experimental source: clone F59A2
A;Reference number: 219700
A;Accession: T22157
A;Accession: T22157
A;Accession: T23157
A;Reference number: 219700
A;Accession: T23157
A;Reference number: 219700
A;Accession: T23157
A;Reference number: 219700
A;Accession: T23157
A;Reference number: 219700
A;Accession: T23157
A;Reference number: 219700
A;Accession: T23157
A;Residues: 1-1133 <WILZ>
A;Residues: 1-1133 <WILZ>
A;Residues: 1-1133 <WILZ>
A;Cross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6
A;Cross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
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                                                                                                                                                                                                                                                                                                                    DB 1; Length 771;
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24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 ASDALEALADQTDALQSEEAEVVQSDNAASD 116
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Matches 21; Conserv
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A; Mostdues: 466-771 cHA2>
A; Rosidues: 466-771 cHA2>
A; Cross-references: GB-M2664; NID:g211897; PIDN:AAA48811.1; PID:g211898
R; Mak, A.S.; Carpenter, M.; Smlllie, L.B.; Wang, J.H.
B; Dalol. Chem. 266, 19971-19975, 1991
A; Title: Phosphorylation of caldesmon by p34(cdc2) Kinase. Identification of phosphoryla
A; Reference number: A41064; MUID:92041815
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A Residues: 462-477, '0',479-563;674-762,'A',763-771 CTAK>

A Residues: 462-477,'D',479-563;674-762,'A',763-771 CTAK>

C; Comment: This protein plays a vital role in the regulation of smooth muscle and nonmus C; Comment: The binding of caldesmon to F-actin is modulated by calcium and calmodulin.

C; Comment: Two calmodulin molecules can bind to nonoverlapping domains of each caldesmon C; Superfamily: caldesmon c; Superfamily: caldesmon attin binding; alternative splicing; calmodulin binding; cytoskeleton; muscl

F;1-771/Product: h-caldesmon #status predicted <HMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-318,334-771 CBRY>
A; Residues: 1-318,334-771 CBRY>
A; Residues: 1-318,334-771 CBRY>
A; Residues: 1-318,334-771 CBRY>
A; Residues: 1-318,334-771 CBRY>
A; Residues: 1-318,334-64 CB Codon GAA for residue 743 as Leu
A; Note: this alternative splice form is a high molecular weight caldesmon (h-caldesmon)
B; Hayashi, K; Yamada, S.; Kanda, K.; Kimizuka, F.; Kato, I.; Sobue, K.
Biochem. Blophys. Res. Commun. 161, 38-45, 1989
A; Title: 35Kba fragment of h-caldesmon conserves two consensus sequences of the tropomyc
A; Reference number: A32445; MUID:89273666
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A; Residues: 74-419 <HAR>
R; Takaqi, T.; Yazawa, M.; Ueno, T.; Suzuki, S.; Yaqi, K.
B: Blochem. 106, 778-783, 1989
A; Title: Amino acid sequence studies on cyanogen bromide peptides of chicken caldesmon
A; Reference number: PX0022; MUID:90130380
                                                                                                                                                                                                                                                                                         N:Alternate names: caldesmon, smooth muscle; calmodulin- and actin-binding protein C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 27-Feb-1990 #sequence_revision 27-Jun-1994 #text_change 22-Jun-1999
C; Accession: A33430; A32642; A32445; A41064; A60461; PC2003; PX0022
R; Hayashi, K.; Kanda, K.; Kimizuka, F.; Karco, I.; Sobue, K.
Blochem. Biophys. Res. Commun. 164, 503-511, 1989
A; Title: Primary structure and functional expression of h-caldesmon complementary DNA. A; Reference number: A33430; MUID:90026426
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A;Residues: 2-17, X; 19-38;466-485 <WAN>
A;Residues: 2-17, X; 19-38;466-485 <WAN>
R;Haruna, M.; Hayashi, K.
Biochem. Biophys. Res. Commun. 197, 145-153, 1993
A;Title: Common structural and expressional properties of vertebrate caldesmon genes.
A;Reference number: PC2003; MUID:94071934
A;Accession: PC2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-771 <HAY>
A;Cross-references: GB:M28417; NID:g211895; PIDN:AAA48810.1; PID:g211896
A;Experimental source: gizzard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: part of this sequence was confirmed by protein sequencing R; Bryan, J.; Imai, M.; Lee, R.; Moore, P.; Cook, R.G.; Lin, W.G. J. Blol. Chem. 264, 13873-13879, 1989
A; Title: Cloning and expression of a smooth muscle caldesmon. A; Reference number: A32642; MUID:89340480
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A;Residues: 597-600;7718-65;711-721 <MAK>
K;Wang, C.L.A.; Wang, L.W.C.; Lu, R.C.
Biochem. Biophys. Res. Commun. 162, 746-752, 1989
A;TitLe: Caldesmon has two calmodulin-binding domains.
A;Reference number: A60461; MUID:89334885
                                                 210 AGNAARDA 217
                                                                                                                                                                                                                                                                       h-caldesmon - chicken
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probable tail fiber protein of prophage CP-933U Z3074 [imported] - Escherichia coll (C;Species: Escherichia coll C;Species: Escherichia coll C;Species: Escherichia coll C;Species: Escherichia coll C;Species: Esselon: E85816 (C;Accession: E8
                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: E90968
B; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g A; Reference number: A99629; MuID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:BA000007; PIDN:BAB36140.1; PID:913362185; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                                                     50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 2; Length 437
Pred. No. 1.1;
7; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
       36;
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Best Local Similarity 36.8%; Pred. No. 1.1;
Matches 25; Conservative 7; Mismatches
          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%;
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Best Local Similarity 36.83
Matches 25; Conservative
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-437 <HAY>
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AGNAARDA 215
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       25;
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          Matches
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Dana Res. B, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gench R;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable tail fiber protein [imported] - Escherichia coli (strain 0157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S66805
A;Molecule type: DNA
A;Residues: 1-113 <DUR>
A;Residues: 1-113 <DUR>
A;Cross-references: EMBL:274851; NID:91419974; PID:e251901; PID:91419975; MIPS:YOL109w
A;Experimental source: strain S288C
                                                                 A.Cross-references: GB:X16421, EMBL:M26048; NID:g43333; PIDN:CAA34442.1; PID:g43334
A.Note: the authors translated the codon CGT for residues 221 and 223 as Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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A;Molecule type: DNA
A;Residues: 1-407 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35654.1; PID:913361697; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NiAlternate names: hypothetical protein 00738
C:Species: Saccharomyces cerevisiae
C:Species: Saccharomyces cerevisiae
C:Species: Saccharomyces cerevisiae
C:Sacession: S66805
R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66791
                                                                                                                                                                                                                                                                                                                                                              86 ASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 ESKAPESSTTEESTSTESSTTTENSSTGSSSTESSSTEESTVPESSTQESTPANTESSSS 337
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 78; DB 2; Length 113; larity 37.3%; Pred. No. 0.26; Conservative 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YOL109w – yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein 00738
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                                                                                                                                                                                                                                                    73;
                                                                                                                                                                                   DB 2;
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Pred. No. 1.1;
                                                                                                                                                                           10.2%; Score 79; DB 2 ilarity 16.9%; Pred. No. 1; Conservative 30; Mismatches
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A,Cross-references: SGD:S0005469; MIPS:YOL109w
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36.8%;
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserv
A; Molecule type: DNA
A; Residues: 1-507 <FUE>
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
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A;Gene: ECs2231
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82 ADNAASDALEALADQTDALQSEEAEVVQS 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 ALTEEWQTLCATLGVQLQPQED 597
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Matches 20; Conserv
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
R;Stover, CK:; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
", Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: E83525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A;Experimental source: strain PA01
                                                                                                                                                                                                          A;Reaidues: 1-269 <ROW>
A;Cross-references: GB:Z47047; EMBL:238113; NID:g603997; PID:g763335; GSPDB:GN00009; MIE
C;Genetics:
probable temperature shock-inducible protein YIL011w - yeast (Saccharomyces cerevisiae)
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                          C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 05-Nov-1999
C;Accession: S48444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tola protein Pa0971 [imported] - Pseudomonas aeruginosa (strain Pa01)
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                                                                                                                                                                                                                                                                                                                                A.Map position: 9L
C.Superfamily: serine-rich protein
C.Keywords: transmembrane protein
F:6-22/Domain: transmembrane *status predicted <TMI>F:6-22/Domain: transmembrane *status predicted <TMI>F:253-269/Domain: transmembrane
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29.8%; Pred. No. 0.54;
tive 14; Mismatches 4!
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                                                                                                  R;Rowley, N. Submitted to the EMBL Data Library, August 1994 A;Reference number: S48442 A;Accession: S48444
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Best Local Similarity 29.88
Matches 25; Conservative
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608
A;Reference number: AB0502; PMID:11677608
A;Accession: AB051
A;Accession: AB0551
A;Accession: AB0551
A;Accession: AB0551
A;Genetics: Sreadles: 1-1034 cAPAR>
A;Genetics: GB:AL513382; PIDN:CAD08850.1; PID:g16501663; GSPDB:GN00176
C;Genetics: STY0429
C;Superfamily: SbcC Protein
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R; Connor, R.; Churcher, C.M.
Bubmitted to the EMBL Data Library, April 1995
A; Reference number: S53969
A; Accession: S53975
A; Molecule type: DNA
A; Residues: 1-389 <CON>
A; Cross-references: EMBL: 249212; NID: 9798940; PID: 9798947; GSPDB: GN00013; MIPS: YMR305
C; Genetics:
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Cispecias: Enterococcus faecium
Cispecias: Enterococcus faecium
Cispecias: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Oct-1999
Ciate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Oct-1999
Ciate: 07-Sep-1990 #sequence_revision 07-Sep-1990 Whencher Pi Mosech, H.U.; Solloz, M.
R.Fuerst, P.; Mosech, H.U.; Solloz, M.
Nucleic Acids Res. 17, 6724, 1989
Nucleic Acids Res. 17, 6724, 1989
A.Title: A protein of unusual composition from Enterococcus faecium.
A.Reference number: S05542; MUID:89385998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YMR305c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM9952.07c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GNSGETIVPVNENAVVATTSSTAVASQATTSTEPPTSANVVTSQQQTSTLQSSEAASTV 105
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10.2%; Score 79; DB 2; Length 389;
Best Local Similarity 23.6%; Pred. No. 0.78;
Matches 21; Conservative 16; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
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C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>
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probable tail fiber protein GP37 - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: G64887; T09189
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A;Rose, D.J; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Residues nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1122 <BLAT>
A;Residues: 1-1122 <BLAT>
A;Residues: 1-1122 <BLAT>
A;Cross-references: GB:AE000234; GB:U00096; NID:91787633; PIDN:AAC74454.1; PID:917876
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain MC-12, substr
                                                                                                                                  streptococcal surface protein - Streptococcus dysgalactiae
C;Species: Streptococcus dysgalactiae
C;Species: Streptococcus dysgalactiae
C;Date: 13-4mn-1995 #sequence_revision 13-Jan-1995 #text_change 19-May-2000
C;Accession: S42574
R;Jonsson, H.; Mueller, H.P.
Eur. J. Biochem. 220, 819-826, 1994
A;Title: The type-III Fo receptor from Streptococcus dysgalactiae is also an alpha(2)
A;Accession: S42574
A;Status: preliminary
A;Status: preliminary
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A;Residues: 3-1122 <AIB>
A;Cross-references: GB:AE000234; GB:U00096; NID:91787633; PIDN:AAC74454.1; PID:917876
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Mresiduces: 1-664 <10N>
A;Residuces: 1-664 <10N>
A;Cross-references: EMBL:229666; NID:g470220; PIDN:CAA82764.1; PID:g470221
C;Superfamily: M5 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 85; DB 2; Length 664, Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.9%;
Best Local Similarity 56.2%;
Matches 18; Conservative
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252 ETSAASSASSATA 268
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A;Modecule type: DNA
A;Modecule type: DNA
A;Cross-references: GB:AE005174; NID:912514847; PIDN:AAG56007.1; GSPDB:GN00145; UWGP:215
A;Experimental source: strain 0157:H7, substrain EDL933
A;Gene: Z1918
                                                                                                                                                                                                                                                                                                                                                             C; Species: Escherichia coli
C;Date: 18-Jul-2001 *sequence_revision 18-Jul-2001 *text_change 18-Jul-2001
C;Accession: B90835
C;Accession: B90835
R;Hayashi, T :; Makino, K :; Ohnishi, M :; Kurokawa, K :; Ishii, K :; Yokoyama, K :; Han, C :G. gasawara, N :; Yasunaga, T :; Kuhara, S :; Shiba, T :; Hattori, M :; Shinagawa, H :
DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                probable tail fiber protein [imported] – Escherichia coli (strain 0157:H7, substrain RIM
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ilarity 32.5%;
Conservative 1
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Best Local Similarity
Matches 25; Conservat
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A;Molecule type: DNA
A;Residues: 1-971 <HAY>
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As Description: Primary structure of the herpesvirus saimiringenome.

A; Description: Primary structure of the herpesvirus saimiringenome.

A; Reference number: A36806

A; Rolecule type: DNA

A; Residues: 1-407 < ALB>
A; Cross references: GB: X64346; NID: 960320; PIDN: CAA45696.1; PID: 960394

A; Rabrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Blesinger, B.; Newman, C.;

A; Title: Primary structure of the herpesvirus saimiringenome.

A; Reference number: A37309; MuiD: 9233688

A; Contents: annotation; possible protein-coding frames

A; Contents: annotation; possible protein-coding frames

A; Nicholas, J.; Cameron, K.R.; Honess, R.W.

Nature 355, 362-365, 1992

A; Title: Herpesvirus saimiri encodes homologues of G protein-coupled receptors and cy

A; Reference number: S20243; MUID: 92115001
                    probable tail fiber protein [imported] - Escherichia coli (strain 0157:H7, subatrain C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                Cyaccession: H90854
R.Hayashl, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Ress. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-437 < HAY>
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                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:BA000007; PIDN:BAB35231.1; PID:g13361273; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immediate-early protein - saimirtine herpesvirus 1 (strain 11)
C;Species: saimirtine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Accession: G36813; S20244
R;Albrecht, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Redidues: 1-407 <NIC>
A; Redidues: 1-407 <NIC>
A; Cross-references: GB:S76368; NID:9243351; PIDN:AAB21116.1; PID:9243353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.7%; Pred. No. 0.071;
Matches 27; Conservative 7; Mismatches 34; Indels
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C; Keywords: early protein
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A; Molecule type: DNA
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C;Species: Streptococcus dysgalactie
C;Accession: 555890
E;Aonsson, H.; Frykberg, L.; Rantamaeki, L.; Guss, B.
Gene 143, 85-89, 1994
A;Title: MAG, a novel plasma protein receptor from Streptococcus dysgalactiae.
A;Reference number: $55890; MUID:94259307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-413 <200>
A;Cross-references: EMBL:L27798; NID:g475117; PIDN:AAA26921.1; PID:g475118
C;Superfamily: M5 protein
                                                                                          50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
                                                                                                                        50 ATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.4%; Score 96; DB 2; Length 440; Best Local Similarity 39.7%; Pred. No. 0.012; Matches 27; Conservative 8; Mismatches 33; Indels
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Pred. No. 0.04;
1; Mismatches 12; Indels
Pred. No. 0.012;
                                             8; Mismatches
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Best Local Similarity 59.4%;
Matches 19; Conservative
                      Best Local Similarity 39.7 Matches 27; Conservative
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209 AGNAARDA 216
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211 AGNAARDA 218
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Length 323;

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A;Molecule type: DNA
A;Residues: 1-401 <SAN>
A;Cross-references: GB:J02459; GB:M17233; GB:W24325; GB:V00636; GB:X00906; NID:g21510
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS0844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 401 - phage lambda
N;Alternate names: orf-401; orf401
C;Species: phage lambda
C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999
C;Accession: G43010; D43016; A04389
R;Daniels, D.
submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A94614
A;Reference number: A94614
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                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-401 <DAN>
R;Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
J. Mol. Biol. 162, 729-773, 1982
J. Mol. Biol. 162, 729-773, 1982
A;Title: Nucleotide sequence of bacteriophage lambda DNA.
A;Reference number: A92891; MUID:83189071
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32.9%; Pred. No. 0.0052;
Live 16; Mismatches 37; Indels
                               , DB 2;
4.5e-06;
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C; Superfamily: phage lambda hypothetical protein 401
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%; Pred. No. 4.5e-
14; Mismatches
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                               16.2%;
42.6%;
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Best Local Similarity 32.9%
Matches 26; Conservative
                                                                                                          Conservative
                                                                      Best Local Similarity
Matches 26; Conserv
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A;Residues: 1-323 csjo>
A;Residues: 1-323 csjo>
A;Cross-references: GB M95520; NID:9153554; PIDN:AAA26847.1; PID:9153555
A;Cross-references: GB M95520; NID:9153554; PIDN:AAA26847.1; PID:9153555
A;Experimental source: group G, strain DG12
A;Note: sequence extracted from NCBI backbone (NCBIN:110938, NCBIP:110939)
F;12-323/Pgoduct: albumin-binding protein (fragment) #status experimental cMAI>
                           A Molecule Lype: DNA
A Residuces: 1-593 <0L5>
A Residuces: 1-593 <0L5>
A Note: the source is designated as Streptococcus G148
A Note: the source is designated as Streptococcus G148
A Note: part of this sequence, including the amino end of the mature protein, was confir
R Sjoebring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.
J. Immunol. 140, 1595-1599, 1988
A Fitle: Isolation and characterization of a 14-kDa albumin-binding fragment of streptoc
A; Reference number: A27604; MUID:88154455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description: it is part of the cell wall structure of group G streptococci and is cova
Superfamily: M5 protein
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 62-101 <53/0>
R; Guss, B.; Eliasson, M.; Olsson, A.; Uhlen, M.; Frej, A.K.; Jornvall, H.; Flock, J.I.;
EMBO J. 5, 1567-1575, 1986
A; Title: Structure of the 1gG-binding regions of streptococcal protein G.
A; Reference number: A26314; MUID: 96300657
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: A44801
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A; Residues: 114-593 <GUS>
A; Cross-references: GB:X04015; NID:g47071; PIDN:CAA27638.1; PID:g47072
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: M5 protein
Reywords: duplication; membrane protein
31-33/Domain: signal sequence #status predicted <SIG>
34-593/Product: protein G #status experimental <MAT>
34-516/Domain: alanine_rich <ALA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.9%; Score 155; DB 2; Best Local Similarity 56.1%; Pred. No. 5.8e-09; Matches 37; Conservative 4; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;498-567/Domain: proline-rich <PRO>F;568-593/Domain: carboxyl-terminal <CTD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117-290/Domain: AB duplication <DUPl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <IGB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 60, 3601-3608, 1992
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IgG binding
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S00128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303-497/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267-290/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F; 358-372/Region: F; 373-427/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :428-442/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443-497/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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Gaps

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 13, 2002, 02:00:41; Search time 42.5134 Seconds (without alignments) 359.374 Million cell updates/sec Run on:

US-09-847-539A-6

777 1 VDSPIEQPRIIPNGGTLTNL......KKEERQNVNTLPTTGEESNP 159 Perfect score:

Sequence:

Scoring table:

283138 seqs, 96089334 residues Searched:

BLOSUM62 Gapop 60.0 , Gapext 60.0

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   |        | Description | IdG-binding protei | protein G precurso | albumin-binding pr | hypothetical prote | $\vdash$ | tail   | plasma protein rec |        | immediate-early pr | probable tail fibe | probable membrane | streptococcal surf |        | tempe  |        | exonuclease SbcC [ | probable membrane | hypothetical prote |        | _      | probable tail fibe | probable tail fibe | h-caldesmon - chic | NF-180 - sea lampr | hypothetical prote |        | rph    | chromosomal protei | SRP40 protein - ye |
|---|--------|-------------|--------------------|--------------------|--------------------|--------------------|----------|--------|--------------------|--------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------------------|-------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|
|   |        | ai<br>ai    | A24496             | S00128             | A44801             | QXBP1L             | D90734   | F85584 | 855890             | H90854 | EDBEQ3             | B90835             | C85693            | 842574             | G64887 | S48444 | E83525 | AB0551             | S53975            | S05542             | S66805 | G90907 | E90968             | E85816             | A33430             | 151116             | T22976             | I41024 | A47168 | A55094             | S38170             |
|   |        | DB          | 7                  | ~                  | ~                  | ~                  | c        | ~      | 7                  | ~      | Н                  | ď                  | ~                 | ď                  | ~      | ~      | N      | ď                  | ~                 | ~                  | 7      | ~      | 7                  | ~                  |                    | 7                  | ~                  | ~      | ~      | N                  | 7                  |
|   |        | Length      | 448                | 593                | 323                | 401                | 438      | 440    | 413                | 437    | 407                | 971                | 973               | 664                | 1122   | 269    | 347    | 1034               | 389               | 207                | 113    | 407    | 437                | 439                | 771                | 1110               | 1133               | 490    | 725    | 1290               | 406                |
| æ |        | Match       | 19.9               |                    | 16.2               | 12.7               | 12.4     | 12.4   | 11.7               |        | 11.3               |                    | 11.3              | 10.9               | 10.9   | 10.3   |        |                    | 10.2              | 10.2               |        |        | 10.0               |                    | •                  |                    |                    | 9.8    | ص<br>ھ | 9.6                | 9.7                |
|   |        | Score       | 155                | 155                | 126                | 66                 | 96       | 96     | 91                 | 83     | 88                 | 88                 | 88                | 82                 | 82     | 80     | 80     | 80                 | 79                | 79                 | 78     | 78     | 78                 | 78                 | 78                 | 77                 | 77                 | 97     | 16     | 9.                 | 75                 |
|   | Result | No.         | п                  | 2                  | m                  | 4                  | S        | 9      | 7                  | œ      | σι                 | 10                 | 11                | 12                 | 13     | 14     | 15     | 16                 | 17                | 18                 | 19     | 20     | 21                 | 22                 | 23                 | 24                 | 25                 | 56     | 27     | 28                 | 53                 |

| two-component sens | unknown protein, 6 | hypothetical prote | hypothetical prote | probable tail fibe | Htr17 transducer [ | hypothetical prote | tail fiber protein | 130K surface exclu | phage lambda-relat | ATPase ScII, chrom | L-shaped tail fibe | probable alpha hel | probable alpha hel | cAMP-dependent pro | cylicin II - bovin |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AD2395             | 696552             | G85631             | T46231             | C90769             | D84325             | T33170             | T14650             | G41662             | T14968             | A54817             | S36851             | F91273             | F86114             | A32461             | 146014             |
| ~ (                | 7                  | N                  | N                  | ~                  | N                  | 7                  | N                  | 7                  | 7                  | ~                  | ~                  | ~                  | 7                  | 7                  | 7                  |
| 468                | 203                | 375                | 166                | 439                | 536                | 719                | 860                | 891                | 978                | 1189               | 1396               | 232                | 232                | 464                | 488                |
| ۲,                 | ` '                | 5.                 | 9.4                | 4.6                | 9.4                | 9.4                | 9.4                | 9.4                | 9.4                | 9.4                | 9.4                | 9.3                | 6.9                | 6.9                | 9.3                |
| o c                | ,                  |                    |                    |                    |                    |                    |                    |                    |                    | -                  |                    | •                  |                    |                    |                    |
| 75 9.              |                    | 74                 | 73                 | 73                 |                    | 73                 | 73                 | 73                 |                    | 73                 |                    |                    |                    | 72                 | 73                 |

## ALIGNMENTS

```
IgG-binding protein - Streptococcus sp. (group G)
```

C; Species: Streptococcus sp.
C; Species: Streptococcus sp.
C; Date: 17-Sep-1987 #sequence\_revision 17-Sep-1987 #text\_change 17-Mar-2000
C; Accession: A24496; A39041
R; Fahnestock, S.R.; Alexander, P.; Nagle, J.; Filpula, D.
J. Bacteriol. 167, 870-880, 1986
A; Title: Gene for an immunoglobulin-binding protein from a group G Streptococcus.
A; Reference number: A24496; MUID:86304178
A; Rocession: A24496
A; Molecule type: DNA
A; Residues: 1-448 < FAH>
A; Residues: 1-448 < FAH>
A; Residues: 1-480 < FAH>
A; Reference number: 266, 399-405, 1991
A; Title: Streptococcal protein G. Gene structure and protein binding properties.
A; Reference number: A39041; MUID:91093154
A; Reference number: A39041; MUID:91093154
A; Residues: 34-42, N', 45-48; 62-76; 186-200 < SJO>
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Revwords: transmembrane protein
C; Keywords: transmembrane protein

Gaps ö Length 448; Match 19.9%; Score 155; DB 2; Length 44 Local Similarity 56.1%; Pred. No. 4.3e-09; Length 44 Mismatches 25; Indels Matches

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1 VDSPIEQPRIIPNGGTLTNLLGNAPEKLALRNEERAIDELKKQAIEDKEATTAIEAASSD 60 QQ ò

61 ALEALA 66 ò

I II I AWEAAA 99 94 Q

protein G precursor - Streptococcus sp. (Streptococcus G148)
N;Alternate names: albumin-binding protein; cell wall-bound protein
C;Species: Streptococcus sp.
A;Variety: Streptococcus sp.
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 19-May-2000
C;Accession: S00128; A27604; A26314
R;Olsson, A.: Eliasson, M.: Guss, B.; Nilsson, B.; Hellman, U.; Lindberg, M.; Uhlen, Eur. J. Biochem. 168, 319-324, 1987
A;Title: Structure and evolution of the repetitive gene encoding streptococcal protein A;Reference number: S00128; MUID:88029445

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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- ALTERNATIVE PRODUCTS: THE PRODUCTION OF THE TWO PROTEIN PRODUCTS FROM THIS REGION IS DUE TO PROGRAMED RIBOSOMAL FRAMESHIFTING.
-1- SIMILARITY: PARTIAL TO PHAGE T4 DNA POLYMERASE ACCESSORY PROTEIN 44 AND TO HUMAN ACTIVATOR 1, 37 AND 40 KDA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) (75 kDa membrane protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERDIENCE FROM N.A.
SSTRAIN-MODPN / NIGG;
MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
Read T.D., Hickey E.K., Peterson J., Utterback T., Berry K.,
Bass S., Linher K., Weldman J., Khouri H., Craven B., Bowman C.,
Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G
Salzberg S.L., Elsen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; DNA-directed DNA polymerase; DNA replication;
ATP-binding; Ribosomal frameshift; Complete proteome.
CHAIN 1 643 DNA POLYMERASE III SUBUNIT TAU.
CHAIN 1 431 DNA POLYMERASE III SUBUNIT GAMMA.
SEQUENCE 643 AA; 71137 MW; D2028BD999E375150 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.8%; Score 68; DB 1; Length 643; 36.5%; Pred. No. 7.3; vative 9; Mismatches 24; Indels
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"Heat shock response of murine Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 AA
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Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                   EMBL; X04487; CAAZ8174.1; -.
EMBL; X04487; CAAZ8175.1; ALT_INIT.
EMBL; X04275; CAAZ7827.1; -.
EMBL; A8200153; AAC73572.1; -.
EMBL; U82664; AA840224.1; -.
EMBL; M38777; AAAZ3457.1; -.
PIR; A25549; DJEC36.
ECOZDBASE; H052.0; 6TH EDITION.
ECOZDBASE; H080.0; 6TH EDITION.
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MEDLINE=91072247; PubMed=2254267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003959; AAA_subfam.
InterPro; IPR000862; RFC.
Pfam; PF00004; AAA; 1.
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P56836;
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'Donnell M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP3X_ECOLI STANDARD; PRT; 643 AA.
P06710; 04771;
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 06, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
DNA polymerase III subunit tau (EC 2.7.7.7) (Contains: DNA polymerase III subunit gammal)
DNAX OR DNAZ OR DNAZX OR B0470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 ELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bactería; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 68; DB 1; Length 232; 25.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 HYPOTHETICAL PROTEIN YJFJ.
25333 MW; 65EB1483D6D29369 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Signal; Complete proteome.
SIGNAL
1 18 POTENTIAL.
                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ppothetical protein yif precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative 14; Mismatches
                                                                                                                                         232 AA
114 ASDAWEKAATPIALDVKKTKDTKPVVKKE 142
                                      449 IRERNAKAKTDYELKLSKYQEELAQYKKD 477
                                                                                                                                                                                                                                               protein yjfJ precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U14003; AAA97078.1; -. EMBL; AE000490; AAC77139.1; -.
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EcoGene; EG12485; yjfJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232
                                                                                                                                                                                                                                                                                                                                                                                                            / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      Escherichia coll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R.;
                                                                                                                                                                                                                                                                  YJFJ OR B4182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                       YJFJ_ECOLI
P39292;
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-K12
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MEDLINE-86312915; PubMed-3018672;
Yin K.-C., Blinkowa A.L., Walker J.R.;
"Nucleotide sequence of the Escherichia coli replication gene dnazx.";
Nucleic Acids Res. 14:6541-6549(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBGUIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLII! COMPLEX. POLII! ASSOCIATES WITH THE GAMMA. COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA, PSI, AND CHI) AND WITH THE BETA CHAIN. THE FINAL COMPOSITION OF THE COMPLEX IS: (ALPHA, EPSILON, THETA)[2]-TAU[2]-(GAMMA, DELTA, DELTA', PSI, PSI, CHI)[2]-BETA[4].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Decessory protein function in the DNA polymerase III holoenzyme from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIBOSOMAL FRAMESHIFTING.
MEDLINE-90245560; Pubmed-1186364;
Blinkowa A.L., Walker J.R.;
Programmed ribosomal frameshifting generates the Escherichia coll
DNA polymerase III gamma subunit from within the tau subunit reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12 / JM109;
MEDLINE-87040775; Pubmed-3534795;
Flower A.M., McHenry C.S.;
"The adjacent dnaz and dnax genes of Escherichia coli are contained within one continuous open reading frame.";
Nucleic Acids Res. 14:8091-8101(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90251627; PubMed-2187190;
Flower A.M., McHenry C.S.,
"The gamma subunit of DNA polymerase III holoenzyme of Escherichia
coli is produced by ribosomal frameshifting.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Doncoan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchihashi Z., Kornberg A.;
"Translational frameshifting generates the gamma subunit of DNA
polymerase III holoenzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli is produced by ribosomal frameshifting.";
Proc. Natl. Acad. Sci. U.S.A. 87:3713-3717(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 87:2516-2520(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:1725-1729(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90207226; PubMed-2181440;
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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CONFLICT
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                                                                 SPAA_STRDO
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                                                                                                                                                          Burne R.A., Penders J.E.C.; "Characterization of the Streptococcus mutans GS-5 fruA gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 AIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSE 103
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                                                                                                                                                                                  exo-beta-D-fructosidase.";
Infect. Immun. 60.4621-4632(1992).
-I- FUNCTION: THIS PROTEIN IS A FRUCTANASE ENZYME WHICH DEGRADES
LEVANS AND INULINS TO FRUCTOSE AND ALSO CLEAVES SUCROSE INTO
GLUCOSE AND FRUCTOSE AND CAN THEREFORE FUNCTION AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRUCTAN BETA-FRUCTOSIDASE.
REMOVED IN MATURE FORM (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BY SIMILARITY.
BIY SIMILARITY.
BIRNOLVED IN BINDING OF SUGARS WITH
BIRA-(2,6) LINKAGES OR BINDING OF
MOLECULAR WEIGHT FRUCTANS (BY
SIMILARITY).
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           Fructan beta-fructosidase precursor (EC 3.2.1.80) (EXO-beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALL-SPANNING DOMAIN (POTENTIAL). CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1423;
13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF03368; B1g_2: 1.
Pfam: PF00251; G1yco_hydro_32; 2.
PROSITE; PS00609; GLYCOSYL_HYDROL_F32; FALSE_NEG.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Hydrolase; G1ycos1dase; Signal: Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SURFACE PROTEINS
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003343; B1g_2.
InterPro; IPR001362; G1yco_hydro_32.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                              MEDLINE-93014178; PubMed-1398976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%;
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                        ructosidase) (Fructanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 20.6% tes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1423
                                                   Streptococcus mutans.
                                                                                                                    SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID-1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1352
1388
                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; (SIGNAL
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ACT_SITE
DOMAIN
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PROPEP
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Matches
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CELL SURFACE ANTIGEN II.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 IEAASSDALEALADQTDALQSEEAAVVKADNAASDALEALADQTDALQSEEAEVVQSDNA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-TERMINAL TWO-THIRDS OF THE SPAA PROTEIN.
-- SIMILARITY: BELDONGS TO THE SPAP/SSPS/SPAA FAMILY.
-- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 423-817 FROM N.A. MEDLINE-90299827: PubMed-1694526; MEDLINE-90299827: PubMed-1694526; Goldschmidt R.M., Thoren-Gordon M., Curtiss R. III; Regions of the Streptococcus sobrinus spaA gene encoding major determinants of antigen I.": Deacterniants of antigen I.": Bacteriol. 172:3988-4001(1990).

-I- SUBCELLULAR LOCATION: Type I membrane protein. Cell Wall.

-I- MISCELLANEOUS: IMMUNODOMINANT DETERMINANTS ARE LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEROTYPE G;
STRAIN=6/15 / SEROTYPE G;
MEDLINE-91310320, PubMed-1855987;
Lapolla R.J., Haron J.A., Kelly C.G., Taylor W.R., Bohart C.,
Hendricks M., Pyati J., Graff R.T., Ma J.K.C., Lehner T.;
"Sequence and structural analysis of surface protein antigen I/II
(SpaA) of Streptococcus sobrinus.";
Infect. Immun. 59:2677-2685(1991).
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                                                                                                                                                                                                                       InterFro; LEADOUS, AAR; 1.
Pfam; PF0053; BRCT; 1.
SWART; SW00292; BRCT; 1.
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E -> EPDECLSCLIFFGIQ (IN REF. 4).
V -> A (IN REF. 5).
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S -> N (IN REF. 3).
T -> A (IN REF. 3).
K -> A (IN REF. 3).
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                                                                                                                                           Lossie A.C., Haugen B.H., Wood W.M., Camper S.A., Gordon D.F.; Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
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   Haque S.J.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
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InterPro: IPR0003559; AAA_subfam.
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InterPro; IPR000862; RFC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Jang W., Weber J.S., Tokito M.K., Holzbaur E.L., Meisler M.H.;
"Mouse pl50Glued (dynactin 1) cDNA sequence and evaluation as a candidate for the neuromuscular disease mutation mnd2.";
Biochem Biophys Res. Commun. 231:344-34(1997).
-!- FUNCTION: REQUIRED FOR THE CYTOPLASMIC DYNEIN-DRIVEN RETROGRADE MOVEMENT OF VESICLES AND ORGANELLES ALONG MICROTUBULES. DYNEIN-DYNACTIN INTERACTION IS A KEY COMPONENT OF THE MECHANISM OF AXONAL TRANSPORT OF VESICLES AND ORGANELLES.
-!- SUBUNIT: LARGE MACROMOLECULAR COMPLEX. OF AT LEAST 10 COMPONENTS.
PLSOGLUED) BINDS DIRECTLY TO MICROTUBULES AND TO CYTOPLASMIC
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Dynactin 1 (150 kDa dynein-associated polypeptide) (DP-150) (DAP-150)
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                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinaei Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS THE DYNACTIN 150 KDA SUBUNIT FAMILY.
-1- SIMILARITY: CONTAINS 1 CAP-GLY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 1; Length 1281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1185 1214 COILED COIL (POTENTIAL).
1281 AA; 141721 MW; 3087FBFF0847D1EC CRC64;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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(Rel. 35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J;
MEDLINE-97223454; PubMed-9070275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR000938; CAP-Gly.
Pfam: PF01302; CAP_GLY; 1.
PROSITE; PS00845; CAP_GLY_1: 1.
PROSITE; PS50245; CAP_GLY_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U60312; AAB57773.1; -.
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1049
1214
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                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                        (p150-glued).
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01-NOV-1997
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Q03174;
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FRUA_STRMU
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Gaps

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21; Indels

11; Mismatches

Conservative

16;

99 ALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEERQN 146

RESULT 35

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-i- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO HAVE A N-TERMINAL SEQUENCE SIGNAL AND A C-TERMINAL TRANSMEMBRANE REGION. BOTH DOMAINS DO NOT EXIST IN THE REVISED SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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006068; 094761;
01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
97 kDa heat shock protein (Egg sperm receptor).
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinodea; Echinocea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                26 EKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQTDALQSEEAAVVKADNA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lennarz W.J.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELL SURFACE RECOGNITION PROTEIN THAT BINDS ACROSOME.
REACTED SPERM AND THEREBY MEDIATES BINDING AND SUBSEQUENT FUSIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foltz K.R., Partin J.S., Lennarz W.J.; "Sea urchin egg receptor for sperm: sequence similarity of binding
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                EMBL: AL16319; CAB6413.1; -.
HSSP; P09651; 1HA1.
InterPro: IPR000504; RRM.
Fam; Pr00076; rrm; 2.
SMART: SM00360; RRM; 2.
PROSITE: PS50102; RRM; 2.
PROSITE: PS50102; RRM: 1.
RIDOSOME blogenesis; RNA-binding; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                              8.9%; Score 69; DB 1; Length 500;
16.7%; Pred. No. 4.3;
Live 28; Mismatches 47; Indels
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9D37FAD0C5161A0B CRC64;
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RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   86 ASDALEALADQTDALQSEEAEVVQSDNAAS 115
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MEDLINE-93197888; PubMed-8383878;
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                                                                                                                                                                                                                                263 341 RN
366 443 RN
339 339 S
500 AA; 52987 MW;
                                                                                        EMBL; 248166; CAA88179.1; -.
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Science 259:1421-1425(1993).
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus.
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                           rRNA processing.
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Activator 1 140 kDa subunit (Replication factor C large subunit) (Al 140 kDa subunit) (Replication factor I large subunit)
(Al-P145) (Differentiation specific element binding protein)
RFCI OR RECLIOR IBF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 ASDALEALADQTDALQSEEAEVVQSDNAASDAWEKAATPIALDVKKTKDTKPVVKKEE 143
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"Cloning of the large subunit of activator 1 (replication factor C)
reveals homology with bacterial DNA ligases.";
Proc. Natl. Acad. Sci. U.S.A. 90:11543-11547(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557 DNGSKETSKDSKDQTSESSKSDKESKDQNSEGSKSDNSSTETDAKAAKKTKKTIKTHE 614
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    889 AA; 98618 MW; 1520EEDF70B0E0CF CRC64;
          Usage
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.9%; Score 69; DB 1

Best Local Similarity 22.0%; Pred. No. 7.9;

Matches 26; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1131 AA
                                                                                                                                                                                            Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00239; HSP70_1; FALSE_NEG.
PROSITE; PS01036; HSP70_2; FALSE_NEG.
PROSITE; PS01036; HSP70_3; 1.
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MEDLINE-94089669; PubMed-8265586;
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                                                                                                                              EMBL; L04969; AAB09737.1; -. HSSP; P19120; 18A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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SEQUENCE FROM N.A.